

GenCore version 5.1.6  
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OM nucleic - nucleic search, using bw model

Run on: April 25, 2005, 13:09:42 ; Search time 228.947 Seconds  
(without alignments)  
517.127 Million cell updates/sec

Title: US-08-887-505b-28

Perfect score: 20  
Sequence: 1 TTGGGACCCACACTACTC 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	2	AAT80332 Oligo HCV
2	20	100.0	20	2	AAT80337 Oligo HCV
3	20	100.0	20	2	AAT80336 Oligo HCV
4	20	100.0	20	2	AAT80338 Oligo HCV
5	20	100.0	20	2	AAT80329 Oligo HCV
6	20	100.0	20	2	AAT80330 Oligo HCV
7	20	100.0	20	2	AAT80333 Oligo HCV
8	20	100.0	20	2	AAT80339 Oligo HCV
9	20	100.0	20	2	AAT80340 Oligo HCV
10	20	100.0	20	2	AAT80238 Oligo HCV
11	20	100.0	20	2	AAT80334 Oligo HCV
12	20	100.0	20	2	AAT80335 Oligo HCV
13	20	100.0	20	2	AAT80331 Oligo HCV
14	20	100.0	20	6	AB865922 Inhibitor
15	20	100.0	20	6	AB865918 Inhibitor
16	20	100.0	20	6	AB865924 Inhibitor
17	20	100.0	20	6	AB865920 Inhibitor
18	20	100.0	20	6	AB865917 Inhibitor
19	20	100.0	20	6	AB865923 Inhibitor
20	20	100.0	20	6	AB865921 Inhibitor

21	20	100.0	20	6	AB865913 Inhibitor
22	20	100.0	20	6	AB865916 Inhibitor
23	20	100.0	20	6	AB865919 Inhibitor
24	20	100.0	20	6	AB865914 Inhibitor
25	20	100.0	20	6	AB865915 Inhibitor
26	20	100.0	20	6	AB865822 Inhibitor
27	20	100.0	20	6	AB865822 Inhibitor
28	20	100.0	20	6	AB865822 Inhibitor
29	20	100.0	20	6	AB865822 Inhibitor
30	20	100.0	20	6	AB865822 Inhibitor
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84	20	100.0	20	6	AB865822 Inhibitor
85	20	100.0	20	6	AB865822 Inhibitor
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87	20	100.0	20	6	AB865822 Inhibitor
88	20	100.0	20	6	AB865822 Inhibitor
89	20	100.0	20	6	AB865822 Inhibitor
90	20	100.0	20	6	AB865822 Inhibitor
91	20	100.0	20	6	AB865822 Inhibitor
92	20	100.0	20	6	AB865822 Inhibitor
93	20	100.0	20	6	AB865822 Inhibitor

C 94	20	100.0	239	6	ABL46065	Abi46065 Hepatitis	C 167	20	100.0	299	10	AAD55565	Aad55565 I657272 H
C 95	20	100.0	239	6	ABL46069	Abi46069 Hepatitis	C 168	20	100.0	301	10	ACD27586	Accd27586 Hepatitis
C 96	20	100.0	239	12	ADK82255	Adk82255 Hepatitis	C 169	20	100.0	305	12	AAT87088	Aat87088 HCV ampli
C 97	20	100.0	239	12	ADK82259	Adk82259 Hepatitis	C 170	20	100.0	305	6	ABN79969	Abn79969 Hepatitis
C 98	20	100.0	240	2	AAV70458	Aav70458 Partial s	C 171	20	100.0	305	6	ABN79970	Abn79970 Hepatitis
C 99	20	100.0	240	2	AAV70456	Aav70456 Partial s	C 172	20	100.0	305	6	ABN79974	Abn79974 Hepatitis
C 100	20	100.0	240	2	AAV70461	Aav70461 Partial s	C 173	20	100.0	306	2	AAO67079	Aao67079 Hepatitis
C 101	20	100.0	240	6	ABL46066	Abi46066 Hepatitis	C 174	20	100.0	306	6	ABES3053	Abes3053 Hepatitis
C 102	20	100.0	240	6	ABL46068	Abi46068 Hepatitis	C 175	20	100.0	308	3	AAA75294	Aaa75294 Novel hep
C 103	20	100.0	240	6	ABL46071	Abi46071 Hepatitis	C 176	20	100.0	308	12	ADN35973	Adn35973 HCV CDNA
C 104	20	100.0	240	12	ADK82261	Adk82261 Hepatitis	C 177	20	100.0	310	6	ABK70877	Abk70877 HCV genom
C 105	20	100.0	240	12	ADK82258	Adk82258 Hepatitis	C 178	20	100.0	312	3	AAZ36198	Aaz36198 Adapted H
C 106	20	100.0	240	12	ADK82256	Adk82256 Hepatitis	C 179	20	100.0	314	3	AAZ36197	Aaz36197 Adapted H
C 107	20	100.0	241	6	AAD43290	Aad43290 HCV target	C 180	20	100.0	323	6	ABK70883	Abk70883 HCV genom
C 108	20	100.0	241	6	AAD43742	Aad43742 HCV ampli	C 181	20	100.0	323	6	ABK70882	Abk70882 HCV genom
C 109	20	100.0	244	2	AAV70454	Aav70454 Partial s	C 182	20	100.0	326	6	ABK70880	Abk70880 HCV genom
C 110	20	100.0	244	2	AAV70449	Aav70449 HCV subty	C 183	20	100.0	326	12	ADP20410	Adp20410 Hepatitis
C 111	20	100.0	244	2	AAV70450	Aav70450 HCV subty	C 184	20	100.0	327	6	AAZ36159	Aaz36159 Adapted H
C 112	20	100.0	244	2	AAV70452	Aav70452 HCV subty	C 185	20	100.0	327	6	ABK70884	Abk70884 HCV genom
C 113	20	100.0	244	6	ABL46062	Abi46062 Hepatitis	C 186	20	100.0	328	2	AAT77074	Aat77074 Hepatitis
C 114	20	100.0	244	6	ABL46059	Abi46059 Hepatitis	C 187	20	100.0	328	2	ABL46275	Abi46275 Hepatitis
C 115	20	100.0	244	6	ABL46060	Abi46060 Hepatitis	C 188	20	100.0	328	6	ABL46278	Abi46278 Hepatitis
C 116	20	100.0	244	6	ABL46064	Abi46064 Hepatitis	C 189	20	100.0	328	6	ABL46273	Abi46273 Hepatitis
C 117	20	100.0	244	12	ADK82254	Adk82254 Hepatitis	C 190	20	100.0	328	6	ABL53724	Abi53724 Hepatitis
C 118	20	100.0	244	12	ADK82351	Adk82351 Hepatitis	C 191	20	100.0	328	8	AAL53724	Aal53724 Hepatitis
C 119	20	100.0	244	12	ADK82350	Adk82350 Hepatitis	C 192	20	100.0	328	6	ABK70871	Abk70871 HCV genom
C 120	20	100.0	244	12	ADK82347	Adk82347 Hepatitis	C 193	20	100.0	329	6	ABK70872	Abk70872 HCV genom
C 121	20	100.0	244	12	ADK82252	Adk82252 Hepatitis	C 194	20	100.0	333	6	ABK70881	Abk70881 HCV genom
C 122	20	100.0	244	12	ADK82350	Adk82350 Hepatitis	C 195	20	100.0	333	6	ABK70879	Abk70879 HCV genom
C 123	20	100.0	244	12	ADK82249	Adk82249 Hepatitis	C 196	20	100.0	333	6	ABK70887	Abk70887 HCV genom
C 124	20	100.0	244	12	ADK82348	Adk82348 Hepatitis	C 197	20	100.0	334	6	ABK70876	Abk70876 HCV genom
C 125	20	100.0	244	12	ADK82348	Adk82348 Hepatitis	C 198	20	100.0	334	6	ABK70869	Abk70869 HCV genom
C 126	20	100.0	252	2	AAO31071	Aao31071 HCV-1 gen	C 199	20	100.0	335	6	ABK70868	Abk70868 HCV genom
C 127	20	100.0	252	2	AAO31069	Aao31069 HCV-1 gen	C 200	20	100.0	335	6	ABK70885	Abk70885 HCV genom
C 128	20	100.0	252	2	AAO31070	Aao31070 HCV-1 gen	C 201	20	100.0	336	6	ABK70885	Abk70885 HCV genom
C 129	20	100.0	252	2	AAO31068	Aao31068 HCV-1 gen	C 202	20	100.0	337	2	AAT76663	Aat76663 HCV genom
C 130	20	100.0	252	2	AAO31081	Aao31081 HCV-1 gen	C 203	20	100.0	337	2	AAV53895	Aav53895 HCV1.1 RN
C 131	20	100.0	252	2	AAO31080	Aao31080 HCV-1 gen	C 204	20	100.0	337	6	ABK70870	Abk70870 HCV genom
C 132	20	100.0	252	2	AAO31067	Aao31067 HCV-1 gen	C 205	20	100.0	337	6	ADSE2863	Adse2863 FEEN-1 re
C 133	20	100.0	252	2	AAO31066	Aao31066 HCV-1 gen	C 206	20	100.0	340	6	ABK70886	Abk70886 HCV genom
C 134	20	100.0	252	2	AAO31072	Aao31072 HCV-1 gen	C 207	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 135	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 208	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 136	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 209	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 137	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 210	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 138	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 211	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 139	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 212	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 140	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 213	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 141	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 214	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 142	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 215	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 143	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 216	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 144	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 217	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 145	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 218	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 146	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 219	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 147	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 220	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 148	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 221	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 149	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 222	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 150	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 223	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 151	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 224	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 152	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 225	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 153	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 226	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 154	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 227	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 155	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 228	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 156	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 229	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 157	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 230	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 158	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 231	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 159	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 232	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 160	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 233	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 161	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 234	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 162	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 235	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 163	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 236	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 164	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 237	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 165	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 238	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 166	20	100.0	256	2	AAO32881	Aao32881 HCV E1 5'	C 239	20	100.0	341	2	AAO62945	Aao62945 HCV genom



C 240	20	100.0	384	6	ABK15314	AbK15314 Hepatitis	C 313	20	100.0	1880	2	AAQ24466	AaQ24466 NANB hepa
C 241	20	100.0	386	2	AAT29117	AaT29117 Hepatitis	C 314	20	100.0	1880	2	AAQ24467	AaQ24467 NANB hepa
C 242	20	100.0	386	9	ADB16253	AbB16263 Cleavase	C 315	20	100.0	2033	2	AAQ64913	AaQ64913 Hepatitis
C 243	20	100.0	393	6	ABA96260	AbA96260 Hepatitis	C 316	20	100.0	2033	2	AAQ67988	AaQ67988 Hepatitis
C 244	20	100.0	412	6	ABA96259	AbA96259 Hepatitis	C 317	20	100.0	2116	2	AAQ12242	AaQ12242 Encodes P
C 245	20	100.0	420	12	AD080848	AD080848 Hepatitis	C 318	20	100.0	2327	6	ABQ78074	AbQ78074 Partial p
C 246	20	100.0	422	8	ACC79264	AcC79264 Hepatitis	C 319	20	100.0	2540	2	AAQ29628	AaQ29628 Hepatitis
C 247	20	100.0	483	2	AAQ32446	AaQ32446 HCV core-	C 320	20	100.0	2540	2	AAQ29627	AaQ29627 Hepatitis
C 248	20	100.0	483	2	AAQ32445	AaQ32445 HCV core-	C 321	20	100.0	2540	2	AAQ43889	AaQ43889 NANB hepa
C 249	20	100.0	483	2	AAQ32453	AaQ32453 HCV core-	C 322	20	100.0	2540	2	AAQ43888	AaQ43888 NANB hepa
C 250	20	100.0	483	2	AAQ32447	AaQ32447 HCV core-	C 323	20	100.0	2540	2	AAQ63753	AaQ63753 NANBH ge
C 251	20	100.0	483	2	AAQ32444	AaQ32444 HCV core-	C 324	20	100.0	2540	2	AAQ63752	AaQ63752 NANBH ge
C 252	20	100.0	500	13	ADS34658	AdS34658 Hepatitis	C 325	20	100.0	2674	6	ABQ78073	AbQ78073 Partial p
C 253	20	100.0	500	13	ADS34660	AdS34660 Hepatitis	C 326	20	100.0	2771	6	ABQ78072	AbQ78072 Partial p
C 254	20	100.0	500	13	ADS34661	AdS34661 Hepatitis	C 327	20	100.0	2829	2	AAV60673	AaV60673 Fragment
C 255	20	100.0	500	13	ADS34659	AdS34659 Hepatitis	C 328	20	100.0	3360	2	AAV60677	AaV60677 Fragment
C 256	20	100.0	504	2	AAQ12239	AaQ12239 Clone 164	C 329	20	100.0	3401	2	AAQ64069	AaQ64069 Non-A, no
C 257	20	100.0	552	2	AAQ79755	AaQ79755 Hepatitis	C 330	20	100.0	3401	2	AAQ64069	AaQ64069 Non-A, no
C 258	20	100.0	552	2	AAQ79749	AaQ79749 Hepatitis	C 331	20	100.0	3461	2	AAQ64068	AaQ64068 Non-A, no
C 259	20	100.0	552	2	AAQ79756	AaQ79756 Hepatitis	C 332	20	100.0	3461	2	AAQ64068	AaQ64068 Non-A, no
C 260	20	100.0	552	2	AAQ79757	AaQ79757 Hepatitis	C 333	20	100.0	4887	2	AAQ65322	AaQ65322 Vaccinia
C 261	20	100.0	552	2	AAQ79756	AaQ79756 Hepatitis	C 334	20	100.0	4887	2	AAQ65322	AaQ65322 Vaccinia
C 262	20	100.0	552	2	AAQ79756	AaQ79756 Hepatitis	C 335	20	100.0	5860	6	ABQ78071	AbQ78071 PMU050 co
C 263	20	100.0	552	2	AAQ79756	AaQ79756 Hepatitis	C 336	20	100.0	7141	6	AAQ25333	AaQ25333 Hepatitis
C 264	20	100.0	552	2	AAQ79756	AaQ79756 Hepatitis	C 337	20	100.0	7789	6	AAQ25330	AaQ25330 Hepatitis
C 265	20	100.0	552	2	AAQ79756	AaQ79756 Hepatitis	C 338	20	100.0	7848	6	AAQ25323	AaQ25323 Hepatitis
C 266	20	100.0	552	2	AAQ79756	AaQ79756 Hepatitis	C 339	20	100.0	7911	2	AAQ32436	AaQ32436 HCV antiq
C 267	20	100.0	552	2	AAQ79756	AaQ79756 Hepatitis	C 340	20	100.0	7979	10	ADD93729	AdD93729 Hepatitis
C 268	20	100.0	556	2	AAQ79776	AaQ79776 Hepatitis	C 341	20	100.0	7979	10	ADD93730	AdD93730 Hepatitis
C 269	20	100.0	556	2	AAQ79776	AaQ79776 Hepatitis	C 342	20	100.0	7979	10	ADD93732	AdD93732 Hepatitis
C 270	20	100.0	556	2	AAQ79776	AaQ79776 Hepatitis	C 343	20	100.0	7979	10	ADD93731	AdD93731 Hepatitis
C 271	20	100.0	556	2	AAQ79776	AaQ79776 Hepatitis	C 344	20	100.0	7979	10	ADD93731	AdD93731 Hepatitis
C 272	20	100.0	556	2	AAQ79776	AaQ79776 Hepatitis	C 345	20	100.0	7980	10	ADD93725	AdD93725 Hepatitis
C 273	20	100.0	572	13	ADS34704	AdS34704 HCV J1 co	C 346	20	100.0	7983	10	ADD93727	AdD93727 Hepatitis
C 274	20	100.0	587	13	ADS34704	AdS34704 HCV J1 co	C 347	20	100.0	7987	6	AAQ25321	AaQ25321 Hepatitis
C 275	20	100.0	652	2	AAQ27966	AaQ27966 Hepatitis	C 348	20	100.0	7987	6	AAQ25321	AaQ25321 Hepatitis
C 276	20	100.0	665	3	AAQ27966	AaQ27966 Hepatitis	C 349	20	100.0	7987	6	AAQ25321	AaQ25321 Hepatitis
C 277	20	100.0	665	3	AAQ27966	AaQ27966 Hepatitis	C 350	20	100.0	7987	6	AAQ25321	AaQ25321 Hepatitis
C 278	20	100.0	665	3	AAQ27966	AaQ27966 Hepatitis	C 351	20	100.0	7987	6	AAQ25321	AaQ25321 Hepatitis
C 279	20	100.0	685	10	ADA49755	AdA49755 HCV 5' UTR	C 352	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 280	20	100.0	685	10	ADA49755	AdA49755 HCV 5' UTR	C 353	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 281	20	100.0	685	10	ADA49755	AdA49755 HCV 5' UTR	C 354	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 282	20	100.0	703	3	AAQ44921	AaQ44921 Hepatitis	C 355	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 283	20	100.0	713	3	AAQ44921	AaQ44921 Hepatitis	C 356	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 284	20	100.0	720	3	AAQ44921	AaQ44921 Hepatitis	C 357	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 285	20	100.0	780	3	AAQ44921	AaQ44921 Hepatitis	C 358	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 286	20	100.0	803	2	AAQ70436	AaQ70436 Recombina	C 359	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 287	20	100.0	803	2	AAQ70436	AaQ70436 Recombina	C 360	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 288	20	100.0	803	2	AAQ70436	AaQ70436 Recombina	C 361	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 289	20	100.0	803	2	AAQ70436	AaQ70436 Recombina	C 362	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 290	20	100.0	803	2	AAQ70436	AaQ70436 Recombina	C 363	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 291	20	100.0	803	2	AAQ70436	AaQ70436 Recombina	C 364	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 292	20	100.0	803	2	AAQ70436	AaQ70436 Recombina	C 365	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 293	20	100.0	817	13	ADS34705	AdS34705 siRNA-2 P	C 366	20	100.0	7989	6	AAQ25322	AaQ25322 Hepatitis
C 294	20	100.0	923	2	AAT28348	AaT28348 Hepatitis	C 367	20	100.0	7995	10	ADD93723	AdD93723 Hepatitis
C 295	20	100.0	1157	10	ADC64640	AdC64640 Hepatitis	C 368	20	100.0	7995	10	ADD93723	AdD93723 Hepatitis
C 296	20	100.0	1270	2	AAV60668	AaV60668 Fragment	C 369	20	100.0	8001	3	AAQ49867	AaQ49867 Hepatitis
C 297	20	100.0	1554	2	AAV60668	AaV60668 Fragment	C 370	20	100.0	8001	3	AAQ49867	AaQ49867 Hepatitis
C 298	20	100.0	1554	2	AAV60668	AaV60668 Fragment	C 371	20	100.0	8001	3	AAQ49867	AaQ49867 Hepatitis
C 299	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 372	20	100.0	8451	10	AAQ40436	AaQ40436 Hepatitis
C 300	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 373	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 301	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 374	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 302	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 375	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 303	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 376	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 304	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 377	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 305	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 378	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 306	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 379	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 307	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 380	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 308	20	100.0	1734	2	AAQ40436	AaQ40436 Hepatitis	C 381	20	100.0	8637	6	AAQ40436	AaQ40436 Hepatitis
C 309	20	100.0	1765	2	AAQ79141	AaQ79141 Hepatitis	C 382	20	100.0	8732	10	AAQ79141	AaQ79141 Hepatitis
C 310	20	100.0	1765	2	AAQ79141	AaQ79141 Hepatitis	C 383	20	100.0	9185	2	AAQ05956	AaQ05956 Sense str
C 311	20	100.0	1863	2	AAQ15363	AaQ15363 Fragment	C 384	20	100.0	9185	2	AAQ15363	AaQ15363 Fragment
C 312	20	100.0	1863	2	AAQ15363	AaQ15363 Fragment	C 385	20	100.0	9185	2	AAQ15363	AaQ15363 Fragment

C 386	20	100.0	9185	2	AAX00459	Aax00459	Hepatitis	C 459	20	100.0	9611	5	AAC86648	Aac86648	Nucleotid
C 387	20	100.0	9185	2	AAX26737	Aax26737	Nucleotid	C 460	20	100.0	9611	13	AD534713	Ad534713	Hepatitis
C 388	20	100.0	9185	2	ADF66068	Adf66068	Hepatitis	C 461	20	100.0	9618	11	ADN33102	Adn33102	Hepatitis
C 389	20	100.0	9185	3	AAW5297	Aaw5297	Sene Str	C 462	20	100.0	9622	10	AAW54424	Aaw54424	Hepatitis
C 390	20	100.0	9185	12	ADN35979	Adn35979	HCV cDNA	C 463	20	100.0	9646	2	AAV59361	Aav59361	Hepatitis
C 391	20	100.0	9365	6	AAW5518	Aaw5518	HCV cDNA	C 464	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 392	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 465	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 393	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 466	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 394	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 467	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 395	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 468	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 396	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 469	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 397	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 470	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 398	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 471	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 399	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 472	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 400	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 473	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 401	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 474	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 402	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 475	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 403	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 476	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 404	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 477	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 405	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 478	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 406	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 479	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 407	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 480	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 408	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 481	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 409	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 482	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 410	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 483	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 411	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 484	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 412	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 485	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 413	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis	C 486	20	100.0	9646	8	AAC62466	Aac62466	Hepatitis
C 414	20	100.0	9365	6	AAW5518	Aaw5518	Hepatitis</								



C 678	14	70.0	17	8	ACD56910	ACd56910 HCV DNAzy	C 751	13	65.0	13	8	ACD65999	ACd65999 Anti-HCV
C 679	14	70.0	17	8	ABZ24771	Abz24771 Locked nu	C 752	13	65.0	13	8	ACD65973	ACd65973 Anti-HCV
C 680	14	70.0	17	12	AD182810	Ad182810 HCV DNAzy	C 753	13	65.0	13	12	AD187542	Ad187542 Anti-HCV
C 681	14	70.0	18	4	AAC90038	Aac90038 Oligonuc1	C 754	13	65.0	13	12	AD187568	Ad187568 Anti-HCV
C 682	14	70.0	18	4	AAC92373	Aac92373 Oligonuc1	C 755	13	65.0	13	13	Az261843	Az261843 HCV 5' no
C 683	14	70.0	18	5	AAH23739	Aah23739 Oligonuc1	C 756	13	65.0	13	13	Az262401	Az262401 Substrate
C 684	14	70.0	19	2	AAQ70441	Aaq70441 Primer/pr	C 757	13	65.0	13	6	ABX03369	ABx03369 Hepatitis
C 685	14	70.0	19	10	ADF51571	Adf51571 Hepatitis	C 758	13	65.0	13	6	ABX00229	ABx00229 Hepatitis
C 686	14	70.0	19	10	ADF51587	Adf51587 Hepatitis	C 759	13	65.0	13	8	ACD65998	ACd65998 Anti-HCV
C 687	14	70.0	19	10	ADF52283	Adf52283 Hepatitis	C 760	13	65.0	13	12	AD187567	Ad187567 Anti-HCV
C 688	14	70.0	19	10	ADF52287	Adf52287 Hepatitis	C 761	13	65.0	13	16	AAT90601	Aat90601 Hepatitis
C 689	14	70.0	20	2	AAQ44885	Aaq44885 Antisense	C 762	13	65.0	13	3	AAI13418	Aai13418 Hepatitis
C 690	14	70.0	20	2	AAT01199	Aat01199 HCV gene	C 763	13	65.0	13	8	ABX74337	ABx74337 Hepatitis
C 691	14	70.0	20	2	AAT45057	Aat45057 CM14 cDNA	C 764	13	65.0	13	17	ACD56913	ACd56913 HCV DNAzy
C 692	14	70.0	20	2	AAT80241	Aat80241 Oligo HCV	C 765	13	65.0	13	17	AD182813	Ad182813 HCV DNAzy
C 693	14	70.0	20	3	AAA52568	Aaa52568 Oligo HCV	C 766	13	65.0	13	17	AD182813	Ad182813 HCV DNAzy
C 694	14	70.0	20	3	AAA52568	Aaa52568 Oligo HCV	C 767	13	65.0	13	18	AD182813	Ad182813 HCV DNAzy
C 695	14	70.0	20	6	AB565819	Ab565819 Inhibitor	C 768	13	65.0	13	18	AD182813	Ad182813 HCV DNAzy
C 696	14	70.0	20	6	AB565825	Ab565825 Inhibitor	C 769	13	65.0	13	18	AD182813	Ad182813 HCV DNAzy
C 697	14	70.0	20	12	ADP87810	Adp87810 Extended	C 770	13	65.0	13	18	AD182813	Ad182813 HCV DNAzy
C 698	14	70.0	23	12	AAQ53260	Aaq53260 Hepatitis	C 771	13	65.0	13	18	AD182813	Ad182813 HCV DNAzy
C 699	14	70.0	23	12	ADP87796	Adp87796 Extended	C 772	13	65.0	13	18	AD182813	Ad182813 HCV DNAzy
C 700	14	70.0	25	13	AAQ98285	Aaq98285 Hepatitis	C 773	13	65.0	13	19	AAH03051	Aah03051 Microorga
C 701	14	70.0	31	13	ADR82701	Adr82701 Peptide n	C 774	13	65.0	13	9	ADA27475	Ada27475 Microorga
C 702	14	70.0	31	13	ADR82701	Adr82701 Peptide n	C 775	13	65.0	13	19	ADP52263	Adp52263 Hepatitis
C 703	14	70.0	33	2	AAQ53258	Aaq53258 Hepatitis	C 776	13	65.0	13	19	ADP52271	Adp52271 Hepatitis
C 704	14	70.0	39	2	AAQ37633	Aaq37633 HCV detec	C 777	13	65.0	13	19	ADP51575	Adp51575 Hepatitis
C 705	14	70.0	42	2	AAV41501	Aav41501 Nucleotid	C 778	13	65.0	13	19	ADP51567	Adp51567 Hepatitis
C 706	14	70.0	43	2	AAV41501	Aav41501 Nucleotid	C 779	13	65.0	13	19	ADP51567	Adp51567 Hepatitis
C 707	14	70.0	46	2	AAV41499	Aav41499 Nucleotid	C 780	13	65.0	13	19	ADP51567	Adp51567 Hepatitis
C 708	14	70.0	47	2	AAV41517	Aav41517 Nucleotid	C 781	13	65.0	13	19	ADP51567	Adp51567 Hepatitis
C 709	14	70.0	53	2	AAQ98138	Aaq98138 Control 1	C 782	13	65.0	13	21	AAQ56956	Aaq56956 Human gen
C 710	14	70.0	57	2	AAQ63223	Aaq63223 Hepatitis	C 783	13	65.0	13	21	AAQ56956	Aaq56956 Human gen
C 711	14	70.0	64	2	AAQ98120	Aaq98120 Label ext	C 784	13	65.0	13	22	AAV72983	Aav72983 Hepatitis
C 712	14	70.0	180	2	AAQ31083	Aaq31083 HCV-1 gen	C 785	13	65.0	13	24	ADP87804	Adp87804 TEX on mi
C 713	14	70.0	182	10	ADQ02538	Adq02538 HCV-1 gen	C 786	13	65.0	13	24	ADP87804	Adp87804 TEX on mi
C 714	14	70.0	282	10	ADQ02538	Adq02538 HCV-1 gen	C 787	13	65.0	13	25	AAQ37583	Aaq37583 HCV conse
C 715	14	70.0	529	10	ABAI3309	Abai3309 Human ner	C 788	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 716	14	70.0	656	10	ACD97117	Ac97117 Human gol	C 789	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 717	14	70.0	924	8	ACA46928	Ac46928 Prokaryot	C 790	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 718	14	70.0	924	8	ACA46928	Ac46928 Prokaryot	C 791	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 719	14	70.0	927	4	AAH53169	Aah53169 S. epider	C 792	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 720	14	70.0	930	6	ABN90739	Abn90739 Staphyloc	C 793	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 721	14	70.0	930	13	ADSO2805	Adso2805 Staphyloc	C 794	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 722	14	70.0	1386	4	AAH87946	Aah87946 Bottom fe	C 795	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 723	14	70.0	1387	4	AAH87947	Aah87947 Saccharom	C 796	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 724	14	70.0	1482	11	ABD12849	Abd12849 Saccharom	C 797	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 725	14	70.0	1634	6	ABQ49122	Abq49122 Oligonuc1	C 798	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 726	14	70.0	1634	6	ABQ49122	Abq49122 Oligonuc1	C 799	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 727	14	70.0	2000	6	ABZ16777	Abz16777 Arabidops	C 800	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 728	14	70.0	2352	2	AAH63604	Aah63604 Dehiscenc	C 801	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 729	14	70.0	4069	4	AAH54612	Aah54612 S. epider	C 802	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 730	14	70.0	5020	8	ABZ10105	Abz10105 Haematopo	C 803	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 731	14	70.0	5506	6	ABN80229	Abn80229 Human che	C 804	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 732	14	70.0	5506	6	ABN80229	Abn80229 Human che	C 805	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 733	14	70.0	6175	6	ABL33306	Ab133306 Human imm	C 806	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 734	14	70.0	6224	6	ABL33306	Ab133306 Human imm	C 807	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 735	14	70.0	6224	6	ABL33306	Ab133306 Human imm	C 808	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 736	14	70.0	6224	6	ABL33306	Ab133306 Human imm	C 809	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 737	14	70.0	6380	4	ABL13596	Ab13596 Chemical1	C 810	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 738	14	70.0	8020	10	ADBE4209	Adbe4209 Human lym	C 811	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 739	14	70.0	8020	13	ADBS89617	Adbs89617 Oligonuc1	C 812	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 740	14	70.0	10717	6	ABL33694	Ab133694 Human imm	C 813	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 741	14	70.0	10717	6	ABL33694	Ab133694 Human imm	C 814	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 742	14	70.0	15600	10	ACF03818	Acf03818 Human che	C 815	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 743	14	70.0	15600	10	ACF03818	Acf03818 Human che	C 816	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 744	14	70.0	17959	6	ABL543575	Ab1543575 Chemical1	C 817	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 745	14	70.0	17959	6	ABL543575	Ab1543575 Chemical1	C 818	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 746	14	70.0	23683	6	ABL34622	Ab134622 Human met	C 819	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 747	14	70.0	23683	6	ABL34622	Ab134622 Human met	C 820	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 748	14	70.0	23683	7	ADBS9883	Adbs9883 Bistuphlt	C 821	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 749	14	70.0	90739	12	ADBS9883	Adbs9883 Bistuphlt	C 822	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse
C 750	13	65.0	13	5	ABC65137	Abc65137 Oligonuc1	C 823	13	65.0	13	25	AAQ37580	Aaq37580 HCV conse

824	13	65.0	712	6	ABQ23075	Abq23075 Oligonuc	897	13	65.0	2681	13	ACN43252	Acn43252 Human dia
825	13	65.0	712	6	ABQ23074	Abq23074 Oligonuc	898	13	65.0	2599	13	ACN43251	Acn43251 Human dia
826	13	65.0	786	11	ACH95552	Ach95552 Klebsiell	899	13	65.0	2706	10	ADG74697	Adg74697 Human kin
827	13	65.0	876	6	ABQ38784	Abq38784 Oligonuc	900	13	65.0	2801	3	ACF77062	Acf77062 Human ORP
828	13	65.0	876	6	ABQ38785	Abq38785 Oligonuc	901	13	65.0	3091	12	ADL27527	Adl27527 Genomic s
829	13	65.0	960	6	ACA44732	Ac444732 Prokaryot	902	13	65.0	3183	10	ADA52620	Ada52620 Human cod
830	13	65.0	963	10	ADF02210	Adf02210 Bacterial	903	13	65.0	3329	6	ABQ78455	Abq78455 Nucleotid
831	13	65.0	1162	6	ABO50240	Abq50240 Oligonuc	904	13	65.0	3329	6	ABA94918	Abq94918 Human met
832	13	65.0	1162	6	ABO50241	Abq50241 Oligonuc	905	13	65.0	3402	6	ABQ79786	Abq79786 Human met
833	13	65.0	1173	6	AB213078	Ab213078 Arabidops	906	13	65.0	3403	6	AD30515	Ad30515 Human 334
834	13	65.0	1239	6	ACF70523	Abq70523 Photoreph	907	13	65.0	3403	6	ABQ79785	Abq79785 Human met
835	13	65.0	1281	6	ABQ44106	Abq44106 Oligonuc	908	13	65.0	3403	6	ABQ78454	Abq78454 Nucleotid
836	13	65.0	1281	6	ABQ44107	Abq44107 Oligonuc	909	13	65.0	3403	6	ABA94914	Abq94914 Human met
837	13	65.0	1296	6	ACA29505	Ac29505 Prokaryot	910	13	65.0	3471	6	ABQ78456	Abq78456 Nucleotid
838	13	65.0	1419	12	AD102491	Ad102491 DNA encod	911	13	65.0	3471	6	ABA94916	Abq94916 Human met
839	13	65.0	1437	3	AC404857	Ac404857 Arabidops	912	13	65.0	3571	6	AB211529	Ab211529 Human pol
840	13	65.0	1446	6	ABL50838	Ab150838 Human Akt	913	13	65.0	3571	12	ADM44047	Adm44047 Novel hum
841	13	65.0	1560	12	ADM91317	Adm91317 DNA homol	914	13	65.0	3766	6	ABK85766	Abk85766 DNA encod
842	13	65.0	1593	12	ADQ84311	Adq84311 Human tum	915	13	65.0	3861	8	ABT19704	Abt19704 Aspergill
843	13	65.0	1593	12	ADQ84311	Adq84311 Human tum	916	13	65.0	3877	13	ADR07592	Adr07592 Full leng
844	13	65.0	1593	13	ADQ83643	Adq83643 Human tum	917	13	65.0	3897	13	ACN43263	Acn43263 Human dia
845	13	65.0	1593	13	ADQ85783	Adq85783 Human tum	918	13	65.0	4077	12	AD116376	Ad116376 Human pro
846	13	65.0	1593	13	ACN40577	Acn40577 Tumour-as	919	13	65.0	4253	6	ABS58376	Abs58376 Protein m
847	13	65.0	1599	2	AA711252	Aa711252 Mouse Akt	920	13	65.0	5433	4	ABL04331	Ab104331 Drosoephil
848	13	65.0	1599	3	AAA08448	Aaa08448 Human Akt	921	13	65.0	5433	4	ABL33540	Ab133540 Human imm
849	13	65.0	1599	3	AAZ60814	Aaz60814 Nucleotid	922	13	65.0	5878	6	ABL33733	Ab133733 Human imm
850	13	65.0	1599	11	ADC26887	Adc26887 DNA encod	923	13	65.0	5883	6	ABL33439	Ab133439 Human imm
851	13	65.0	1599	11	AD131678	Ad131678 Human CDN	924	13	65.0	6237	10	ADR82762	Adr82762 Human alp
852	13	65.0	1599	12	ADN71937	Adn71937 Human pro	925	13	65.0	6352	6	ABK31340	Abk31340 Signal tr
853	13	65.0	1617	12	ADL27528	Adl27528 CDNA sequ	926	13	65.0	6352	6	ABK70563	Ab1070563 Chemical
854	13	65.0	1701	10	ADB78667	Adb78667 Human nlc	927	13	65.0	6352	6	AA661235	Aa661235 Human gen
855	13	65.0	1715	6	ABV94263	Abv94263 Breast ca	928	13	65.0	6356	3	AAA51877	Aa51877 A. fumiga
856	13	65.0	1715	12	ADP48783	Adp48783 Human Akt	929	13	65.0	6381	4	AB116414	Ab116414 Drosoephil
857	13	65.0	1722	10	ADB07335	Adb07335 Novel cod	930	13	65.0	7002	4	ABL09667	Ab109667 Drosoephil
858	13	65.0	1771	6	AD26345	Ad26345 Human mut	931	13	65.0	7162	4	ABL16436	Ab116436 Drosoephil
859	13	65.0	1771	10	ADB78665	Adb78665 Human nlc	932	13	65.0	7297	5	ABA21079	Ab21079 Human ner
860	13	65.0	1771	10	ADB78665	Adb78665 Human nlc	933	13	65.0	7726	4	AB109666	Ab109666 Drosoephil
861	13	65.0	1771	10	ADB78665	Adb78665 Human nlc	934	13	65.0	10637	4	AB109666	Ab109666 Drosoephil
862	13	65.0	1771	10	ADB78675	Adb78675 Human nlc	935	13	65.0	11942	4	AB153542	Ab153542 Human CHR
863	13	65.0	1771	10	ADB78664	Adb78664 Human nlc	936	13	65.0	12046	6	AB133633	Ab133633 Human imm
864	13	65.0	1771	10	ADB78674	Adb78674 Human nlc	937	13	65.0	12222	4	AA654045	Aa654045 Human alp
865	13	65.0	1771	10	ADB78677	Adb78677 Human nlc	938	13	65.0	14756	10	ADC087364	Adc087364 Human GPC
866	13	65.0	1771	10	ADB78676	Adb78676 Human nlc	939	13	65.0	15954	6	ABK31494	Abk31494 Signal tr
867	13	65.0	1854	3	AA39548	Aa39548 Arabidops	940	13	65.0	15954	6	AB170467	Ab170467 Chemical
868	13	65.0	1947	4	ADA06387	Ada06387 Murine be	941	13	65.0	17131	6	AB133052	Ab133052 Human imm
869	13	65.0	1957	10	ADF81647	Adf81647 Human cod	942	13	65.0	25599	10	ACF65308	Acf65308 Human TBC
870	13	65.0	2040	10	ADP53081	Adp53081 Human cod	943	13	65.0	25599	10	ACF65308	Acf65308 Human TBC
871	13	65.0	2112	6	ABQ95955	Abq95955 Human cod	944	13	65.0	32328	4	ABL09994	Ab109994 Drosoephil
872	13	65.0	2125	13	ACN43262	Acn43262 Human dia	945	13	65.0	36471	3	AAA81453	Aa81453 N. mening
873	13	65.0	2125	13	ACN43262	Acn43262 Human dia	946	13	65.0	37030	10	ADB74276	Adb74276 Mycobacte
874	13	65.0	2199	13	ACN43261	Acn43261 Human dia	947	13	65.0	48829	11	ACN44868	Acn44868 Mouse gen
875	13	65.0	2272	13	ACN43260	Acn43260 Human dia	948	13	65.0	54732	13	ABD33335	Abd33335 Human can
876	13	65.0	2297	13	ACN43259	Acn43259 Human dia	949	13	65.0	55211	12	ADQ97266	Adq97266
877	13	65.0	2307	13	ACN43258	Acn43258 Human dia	950	13	65.0	58909	4	AA628543	Aa628543 Genomic f
878	13	65.0	2325	13	ACN43257	Acn43257 Human dia	951	13	65.0	59748	13	ABD33260	Abd33260 Human can
879	13	65.0	2345	13	ACN43256	Acn43256 Human dia	952	13	65.0	65186	10	ADH10017	Adh10017
880	13	65.0	2447	10	AD555029	Ad555029 Rat gene	953	13	65.0	68571	12	ADH56913	Adh56913 Human CAR
881	13	65.0	2447	10	AD555025	Ad555025 Rat gene	954	13	65.0	98300	12	ADO79403	Ado79403 KIA0783
882	13	65.0	2448	2	AAV112201	Aav112201 Human neu	955	13	65.0	104900	13	ABD32848	Abd32848 Human can
883	13	65.0	2448	2	AAV112201	Aav112201 Human neu	956	13	65.0	107280	13	ABD33169	Abd33169 Murine can
884	13	65.0	2448	2	AAV112201	Aav112201 Human neu	957	13	65.0	107280	13	ABD33169	Abd33169 Murine can
885	13	65.0	2448	2	AAV112201	Aav112201 Human neu	958	13	65.0	107280	13	ABD33169	Abd33169 Murine can
886	13	65.0	2448	2	AAV112201	Aav112201 Human neu	959	13	65.0	107280	13	ABD33169	Abd33169 Murine can
887	13	65.0	2448	2	AAV112201	Aav112201 Human neu	960	13	65.0	107280	13	ABD33169	Abd33169 Murine can
888	13	65.0	2448	2	AAV112201	Aav112201 Human neu	961	13	65.0	107280	13	ABD33169	Abd33169 Murine can
889	13	65.0	2448	2	AAV112201	Aav112201 Human neu	962	13	65.0	107280	13	ABD33169	Abd33169 Murine can
890	13	65.0	2448	2	AAV112201	Aav112201 Human neu	963	13	65.0	107280	13	ABD33169	Abd33169 Murine can
891	13	65.0	2448	2	AAV112201	Aav112201 Human neu	964	13	65.0	107280	13	ABD33169	Abd33169 Murine can
892	13	65.0	2448	2	AAV112201	Aav112201 Human neu	965	13	65.0	107280	13	ABD33169	Abd33169 Murine can
893	13	65.0	2448	2	AAV112201	Aav112201 Human neu	966	13	65.0	107280	13	ABD33169	Abd33169 Murine can
894	13	65.0	2448	2	AAV112201	Aav112201 Human neu	967	13	65.0	107280	13	ABD33169	Abd33169 Murine can
895	13	65.0	2448	2	AAV112201	Aav112201 Human neu	968	13	65.0	107280	13	ABD33169	Abd33169 Murine can
896	13	65.0	2448	2	AAV112201	Aav112201 Human neu	969	13	65.0	107280	13	ABD33169	Abd33169 Murine can

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C 970      12      60.0      13      5      ABC87844      Abc87844 Oligonucle
C 971      12      60.0      13      8      ACD65997      Acd65997 Anti-HCV
C 972      12      60.0      13      12      ADI87566      ADI87566 Anti-HCV
C 973      12      60.0      15      3      AAZ62399      Aaz62399 Substrate
C 974      12      60.0      15      6      ABX00256      Abx00256 Hepatitis
C 975      12      60.0      15      6      ABX01765      Abx01765 Hepatitis
C 976      12      60.0      15      8      ACD55975      Acd55975 Anti-HCV
C 977      12      60.0      17      8      ACD65756      Acd65756 HCV minus
C 978      12      60.0      17      8      ACD65756      Acd65756 HCV minus
C 979      12      60.0      17      12      ADI87250      ADI87250 HCV DNAzy
C 980      12      60.0      17      12      ADI87254      ADI87254 HCV DNAzy
C 981      12      60.0      17      12      ADP87811      ADP87811 Extension
C 982      12      60.0      17      12      ADP87811      ADP87811 Extension
C 983      12      60.0      18      8      ABZ10900      Abz10900 Haematopo
C 984      12      60.0      18      10      ABT23632      Abt23632 Stabilisi
C 985      12      60.0      19      10      ADP51577      Adp51577 Hepatitis
C 986      12      60.0      19      10      ADP51577      Adp51577 Hepatitis
C 987      12      60.0      19      10      ADP52294      Adp52294 Hepatitis
C 988      12      60.0      19      10      ADP51598      Adp51598 Hepatitis
C 989      12      60.0      19      10      ADP52273      Adp52273 Hepatitis
C 990      12      60.0      20      2      AAQ44916      Aaq44916 Antisense
C 991      12      60.0      20      2      AAQ44916      Aaq44916 Antisense
C 992      12      60.0      20      2      AAQ44916      Aaq44916 Antisense
C 993      12      60.0      25      9      ACI25526      Aci25526 Human mic
C 994      12      60.0      25      9      ACI25526      Aci25526 Human mic
C 995      12      60.0      25      9      ACI25526      Aci25526 Human mic
C 996      12      60.0      25      9      ACI25526      Aci25526 Human mic
C 997      12      60.0      25      9      ACI25526      Aci25526 Human mic
C 998      12      60.0      25      9      ACI25526      Aci25526 Human mic
C 999      12      60.0      25      9      ACI25526      Aci25526 Human mic
C 1000     12      60.0      25      9      ACI25526      Aci25526 Human mic

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## ALIGNMENTS

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RESULT 1
ID AAT80332 standard; RNA; 20 BP.
XX
XX AAT80332;
DT 16-OCT-1997 (first entry)
XX
XX Oligo HCV1 9x9, targeted to HCV mRNA position -67 to -86.
DE
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
OS
XX
XX Key
FH modified_base
FT 1..9
FT /tag= a
FT /note= "2'-OMe RNA"
FT modified_base
FT 10..11
FT /tag= b
FT /note= "Comprises phosphorothioate linkages"
FT modified_base
FT 12..20
FT /tag= c
FT /note= "2'-OMe RNA"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOF-) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
PA
PA

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XX
XX Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX
XX WPI, 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 1; Page 18; 100p; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma
XX
XX Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 0.061;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGGCGACCCACACTATC 20
DB 1 UUCGCGACCCACACTATC 20

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RESULT 2
ID AAT80337 standard; RNA; 20 BP.
XX
XX AAT80337;
DT 16-OCT-1997 (first entry)
XX
XX Oligo HCV1 9x5, targeted to HCV mRNA position -67 to -86.
DE
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
OS
XX
XX Key
FH modified_base
FT 1..9
FT /tag= a
FT /note= "2'-OMe RNA"
FT modified_base
FT 10..15
FT /tag= b
FT /note= "Comprises phosphorothioate linkages"
FT modified_base
FT 16..20
FT /tag= c
FT /note= "2'-OMe RNA"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOF-) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
PA
PA Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;

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XX DR WPI, 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX PS Claim 1, Page 18, 100pp; English.
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma.
XX SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGCGACCCCACTACTCTC 20
        |||||
DB      1 TTGCGACCCCACTACTCTC 20

RESULT 3
AAT80336
ID AAT80336 standard; RNA; 20 BP.
XX AC AAT80336;
XX DT 16-OCT-1997 (first entry)
XX DE Oligo HCV1 11x3, targeted to HCV mRNA position -67 to -86.
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX FH Key
XX FT modified_base      Location/Qualifiers
XX      1..11
XX      /*tag= a
XX      /note= "2'-Ome RNA"
XX FT modified_base      12..17
XX      /*tag= b
XX      /note= "Comprises phosphorothioate linkages"
XX FT modified_base      18..20
XX      /*tag= c
XX      /note= "2'-Ome RNA"
XX FT
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX PI Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX DR WPI, 1997-043122/04.

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PT PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
PT PS Claim 1, Page 18, 100pp; English.
PT CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
PT which are complementary to a portion of the 5' untranslated region (UTR)
PT of hepatitis C virus (HCV). These sequences may be used in a
PT pharmaceutical composition for the control or prevention of HCV
PT infection. They may be used to inhibit replication or expression of HCV
PT or for detecting the presence of HCV in a sample. They may be used to
PT inhibit HCV replication in a cell and are therefore useful in the
PT treatment of HCV infections such as chronic and acute hepatitis and
PT hepatocarcinoma.
PT SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGCGACCCCACTACTCTC 20
        |||||
DB      1 TTGCGACCCCACTACTCTC 20

RESULT 4
AAT80338
ID AAT80338 standard; RNA; 20 BP.
XX AC AAT80338;
XX DT 16-OCT-1997 (first entry)
XX DE Oligo HCV1 5x9, targeted to HCV mRNA position -67 to -86.
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX FH Key
XX FT modified_base      Location/Qualifiers
XX      1..5
XX      /*tag= a
XX      /note= "2'-Ome RNA"
XX FT modified_base      6..11
XX      /*tag= b
XX      /note= "Comprises phosphorothioate linkages"
XX FT modified_base      12..20
XX      /*tag= c
XX      /note= "2'-Ome RNA"
XX FT
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX PI Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX DR WPI, 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.

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The sequences given in AA180211-182 represent synthetic oligonucleotides which are complementary to a portion of the 5' untranslated region (UTR) of hepatitis C virus (HCV). These sequences may be used in a pharmaceutical composition for the control or prevention of HCV infection. They may be used to inhibit replication or expression of HCV or for detecting the presence of HCV in a sample. They may be used to inhibit HCV replication in a cell and are therefore useful in the treatment of HCV infections such as chronic and acute hepatitis and hepatocarcinoma.

Query Match	100.0%;	Score 20;	DB 2;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 0.061;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

RESULT 5	
AAT80329	
ID	AAT80329 standard; DNA; 20 BP.
XY	

DT	16-OCT-1997	(first entry)
XX		

complementary; 5' untranslated region; UTR; hepatitis C virus; HCV inhibition; replication; expression; detection; chronic hepatitis; acute hepatitis; hepatocarcinoma; ss.

Key	Location/Qualifiers
Modified base	1 30

FT	/note=	"Comprises phosphorothioate linkages"
FT	modified_base	17. .20

WO9639500-A2

04-JUN-1996; 96WO-EP002427.

(HOFER) HOFERMAN LA ROCHE & CO AG F.

Frank BL, Goodchild J, Hamlin HA, Kilbuckie RE, Roberts NA,  
Roberts PC, Walthers DM, Wolfe JL;

virgo:nucleotidase(s) complementary to HCV 5' untranslated region - used in the treatment and detection of HCV infection, esp. hepatitis and hepatocarcinoma.

The sequences given in AAT80211-382 represent synthetic oligonucleotides which are complementary to a portion of the 5' untranslated region (UTR) of hepatitis C virus (HCV). These sequences may be used in a

Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;

```

QY      1 TTGGGACCCCACTACTC 20
          |||||:|
Db      1 TTGGGACCCCACTACUC 20

```

RESULT 6	
AAT80330	
ID	AAT80330 standard; DNA; 20 BP
XX	

AC AAT80330;  
XX

DI 16-OCT-1997 (first entry)  
 XX

DE oligo HCV1 UX3, targetted to HCV mRNA position -67 to -86.  
XX

complementary; 3' untranslated region; UTR; hepatitis C virus; HCV; inhibition; replication; expression; detection; chronic hepatitis.

acute hepatitis; hepatocarcinoma; ss.

OS  
vv Synthetic

FH	Key	Location/Qualifiers
ET	modified base	1 30

ET

FT	modified_base
ET	

/note= "2'-OMe RNA"

PN WO9639500-A2  
 XY

PD 12-DEC-1996.  
XY

04-JUN-1996; 96WO-EP002427

06-JUN-1995; 95US-00471968

HYBRIDON INC (HYBR -) HOFFMANN LA ROCHE & CO AG F (HOFF -) EPA

Frank BT. Goodchilld

Roberts PC, Walthner DM, Wolfe JL;

WPT; 1997-043122/04.

Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in the treatment and detection of new infections.

carcinoma.

Claim 1; Page 18; 100pp; English

which are complementary to a portion of the 5' untranslated region (UTR) of the mRNA. The sequences given in AAT80211-382 represent synthetic oligonucleotides

of hepatitis C virus (HCV). These sequences may be used in a pharmaceutical composition for the control or prevention of

or for detecting the presence of HCV in a sample. They may be used to inhibit replication or expression of HCV infection. They may be used to inhibit replication or expression of HCV infection.

inhibit HCV replication in a cell and are therefore useful in the treatment of HCV infections such as hepatitis C.

hepatocarcinoma



Sequence	20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;
Query Match	100.0%; Score 20; DB 2; Length 20;
Best Local Similarity	95.0%; Pred. No. 0.061;
Matches	19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 TTGGGACCCCAACTACTC 20
DB	1 TTGGGACCCCAACTACTC 20
RESULT 7	
AAT80333	
ID	AAT80333 standard; RNA; 20 BP.
XX	
AC	AAT80333;
XX	
DT	16-OCT-1997 (first entry)
XX	
DE	Oligo HCV1 8x8, targeted to HCV mRNA position -67 to -86.
XX	
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	inhibition; replication; expression; detection; chronic hepatitis;
KW	acute hepatitis; hepatocarcinoma; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..8
FT	/*tag= a
FT	/note= "2'-Ome RNA"
FT	9..12
FT	/*tag= b
FT	/note= "Comprises phosphorothioate linkages"
FT	13..20
FT	/*tag= c
FT	/note= "2'-Ome RNA"
XX	
PN	W09639500-A2.
XX	
PD	12-DEC-1996.
XX	
PF	04-JUN-1996; 96WO-EP002427.
XX	
PR	06-JUN-1995; 95US-00471968.
XX	
PA	(HOF) HOFMANN LA ROCHE & CO AG F.
PA	(HYBR-) HYBRIDON INC.
XX	
PI	Frank BL, Goodchild J, Hamlin HA, Kilkuakie RE, Roberts NA;
PI	Roberts PC, Walther DM, Wolte JL;
XX	
DR	WPI; 1997-043122/04.
XX	
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
XX	
PS	Claim 1; Page 18; 100pp; English.
XX	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmaceutical composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma
XX	
QO	Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;

```

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 0.061;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0
Cy              1 TTGCGACCCCAACTACTCTC 20
                ::::::::::::::::::::|
Db              1 UUCGGAGCCCAACACUACUC 20

RESULT 8
AAT80339
ID AAT80339 standard; RNA; 20 BP.
XX
AC AAT80339;
XX
DT 16-OCT-1997 (first entry)
XX
DE Oligo HCV1 3x11, targeted to HCV mRNA position -67 to -86.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KM inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..3
FT /*tag= a
FT /note= "2'-OME RNA"
FT modified_base 4..9
FT /*tag= b
FT /note= "Comprises phosphorothioate linkages"
FT modified_base 10..20
FT /*tag= c
FT /note= "2'-OME RNA"
FN W09639500-A2.
PN
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EPO02427.
XX
PR 06-JUN-1995; 95US-00471968.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
PI Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX
DR WPI; 1997-041122/04.
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
PS Claim 1; Page 18; 100pp; English.
XX
The sequences given in AAT80211-382 represent synthetic oligonucleotides
which are complementary to a portion of the 5' untranslated region (UTR)
of hepatitis C virus (HCV). These sequences may be used in a
pharmaceutical composition for the control or prevention of HCV
infection. They may be used to inhibit replication or expression of HCV
or for detecting the presence of HCV in a sample. They may be used to
inhibit HCV replication in a cell and are therefor useful in the
treatment of HCV infections such as chronic and acute hepatitis and
hepatocarcinoma
Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 TTGGGACCCCAACTACTC 20  
DB 1 TTGGGACCCCAACTACTC 20

## RESULT 9

AAT80340  
ID AAT80340 standard; RNA; 20 BP.

AC AAT80340;

DT 16-OCT-1997 (first entry)

DE Oligo HCV1 0x14, targeted to HCV mRNA position -67 to -86.

OS  
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.

XX Synthetic.

FT Key Location/Qualifiers

FT modified\_base 1..6

FT /tag= a

FT /note= "Comprises phosphorothioate linkages"

FT modified\_base 7..20

FT /tag= b

FT /note= "2'-OME RNA"

PN WO9639500-A2.

PD 12-DEC-1996.

PF 04-JUN-1996; 96WO-EP002427.

PR 06-JUN-1995; 95US-00471968.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA (HYBR-) HYBRIDON INC.

PI Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;

PI Roberts PC, Walther DM, Wolfe JL;

DR WPI; 1997-043122/04.

PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.

PS Claim 1; Page 18; 100pp; English.

XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
XX which are complementary to a portion of the 5' untranslated region (UTR)  
XX of hepatitis C virus (HCV). These sequences may be used in a  
XX pharmaceutical composition for the control or prevention of HCV  
XX infection. They may be used to inhibit replication or expression of HCV  
XX or for detecting the presence of HCV in a sample. They may be used to  
XX inhibit HCV replication in a cell and are therefore useful in the  
XX treatment of HCV infections such as chronic and acute hepatitis and  
XX hepatocarcinoma

SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.061;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 1 TTGGGACCCCAACTACTC 20

RESULT 10  
AAT80238  
ID AAT80238 standard; DNA; 20 BP.

AC AAT80238;

DT 15-OCT-1997 (first entry)

DE Oligo HCV1, targeted to HCV mRNA RNase sensitive region C.

OS  
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.

XX Synthetic.

FT Key Location/Qualifiers

FT modified\_base 1..20

FT /tag= a

FT /note= "Comprises phosphorothioate linkages"

PN WO9639500-A2.

PD 12-DEC-1996.

PF 04-JUN-1996; 96WO-EP002427.

PR 06-JUN-1995; 95US-00471968.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA (HYBR-) HYBRIDON INC.

PI Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;

PI Roberts PC, Walther DM, Wolfe JL;

DR WPI; 1997-043122/04.

PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.

PS Claim 1; Page 25; 100pp; English.

XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
XX which are complementary to a portion of the 5' untranslated region (UTR)  
XX of hepatitis C virus (HCV). These sequences may be used in a  
XX pharmaceutical composition for the control or prevention of HCV  
XX infection. They may be used to inhibit replication or expression of HCV  
XX or for detecting the presence of HCV in a sample. They may be used to  
XX inhibit HCV replication in a cell and are therefore useful in the  
XX treatment of HCV infections such as chronic and acute hepatitis and  
XX hepatocarcinoma. This oligo was used in an RNase H assay to determine  
XX whether it binds successfully to its target. Three regions of HCV mRNA  
XX were investigated as RNase sensitive sites. This oligo binds to position  
XX -67 to -86

SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.061;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 1 TTGGGACCCCAACTACTC 20

## RESULT 11

AAT80334  
ID AAT80334 standard; RNA; 20 BP.

AC AAT80334;

XX

```

DT 16-OCT-1997 (first entry)
XX
XX Oligo HCV1 7x7, targeted to HCV mRNA position -67 to -86.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH modified_base 1..7
FT /tag= a
FT /note= "2'-OME RNA"
FT modified_base 8..13
FT /tag= b
FT /note= "Comprises phosphorothioate linkages"
FT modified_base 14..20
FT /tag= c
FT /note= "2'-OME RNA"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 1; Page 18; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma
XX
XX Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 2; Length 20;
XX Best Local Similarity 80.0%; Pred. No. 0.061;
XX Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGGGACCCCAACTACTC 20
DB 1 UUCGGACCCCAACUACUC 20

```

```

XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH modified_base 1..6
FT /tag= a
FT /note= "2'-OME RNA"
FT modified_base 7..14
FT /tag= b
FT /note= "Comprises phosphorothioate linkages"
FT modified_base 15..20
FT /tag= c
FT /note= "2'-OME RNA"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 1; Page 18; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma
XX
XX Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 2; Length 20;
XX Best Local Similarity 80.0%; Pred. No. 0.061;
XX Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGGGACCCCAACTACTC 20
DB 1 UUCGGACCCCAACUACUC 20

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RESULT 12
AAT80335
ID AAT80335 standard; RNA; 20 BP.
XX
XX AAT80335;
XX
XX 16-OCT-1997 (first entry)
DT
XX Oligo HCV1 6x6, targeted to HCV mRNA position -67 to -86.
DE

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```

RESULT 13
AAT80331
ID AAT80331 standard; DNA; 20 BP.
XX
XX AAT80331;
XX
XX 16-OCT-1997 (first entry)
DT
XX Oligo HCV1 0X2, targeted to HCV mRNA position -67 to -86.
DE
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX

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```

XX PD 27-JUN-2002.
XX XX
XX PF 02-JUL-1997; 97US-00887505.
XX PR 06-JUN-1995; 95US-00471968.
XX PR 02-JUL-1996; 96US-0021104P.
PA PA (KILK/) KILKUSKIE R L.
PA PA (FRAN/) FRANK B L..
PA PA (GOOD/) GOODCHILD J.
PA PA (WOLF/) WOLFE J L..
PA PA (ROBE/) ROBERTS P C.
PA PA (HAML/) HAMLIN H A.
PA PA (ROBE/) ROBERTS N A.
PA PA (WALT/) WALTHER D M.
PT PT Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,
PI PI Hamlin HA, Roberts NA, Walther DW;
XX XX
XX DR WPI; 2002-537132/57.
XX XX
XX PT Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
XX treating HCV infections and hepatocellular carcinoma.
XX PS Claim 1; Page 6; 74pp; English.
XX CC The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC creating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 0.061;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 TTGCGACCCCAACTACTC 20
DB 1 TTGCGACCCCAACTACTC 20
| | | | | | | | | | | | | | | | | |
RESULT 15
ID ABS65918
ABR65918 standard; DNA; 20 BP.
XX ABRS65918;
XX AC
XX XT 15-NOV-2002 (first entry)
XX DT
XX DE Inhibitory oligonucleotide specific for hepatitis C virus #124.
KW Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;
KM non-B hepatitis; acute hepatitis; chronic hepatitis;
KM hepatocellular carcinoma; viraemia; cytostatic; antineoplastic therapy;
gene therapy; ss; DNA-RNA hybrid.
XX XX
XX OS Synthetic.
XX XX
XX PN US2002081577-A1.
XX DN 27-JUN-2002.

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XX 02-JUL-1997; 97US-00887505.
PR 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
DR WPI, 2002-537132/57.
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX Claim 1; Page 6; 74pp; English.
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 0.061;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
DB 1 TTCCGACCCCAACTACTC 20
1 TTCCGACCCCAACTACTC 20
RESULT 16
ABS65924
ID ABS65924 standard; DNA; 20 BP.
XX
AC ABS65924;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #130.
XX
KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
XX
OS Synthetic.
XX
PN US2002081577-A1.
XX
PD 27-JUN-2002.
XX
PR 02-JUL-1997; 97US-00887505.

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XX 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
DR WPI, 2002-537132/57.
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX Claim 1; Page 6; 74pp; English.
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
DB 1 TTCCGACCCCAACTACTC 20
1 TTCCGACCCCAACTACTC 20
RESULT 17
ABS65920
ID ABS65920 standard; DNA; 20 BP.
XX
AC ABS65920;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #126.
XX
KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
XX
OS Synthetic.
XX
PN US2002081577-A1.
XX
PD 27-JUN-2002.
XX
PR 02-JUL-1997; 97US-00887505.
XX
PR 06-JUN-1995; 95US-00471968.

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PR 02-JUL-1996; 96US-0021104P.
XX
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,
PI Hamlin HA, Roberts NA, Walther DM;
XX WPI; 2002-537132/57.
XX
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
XX Claim 1; Page 6; 74pp; English.
XX
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis. HCV has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGGAGCCCACTACTC 20
Db 1 TTGGGAGCCCACTACTC 20
RESULT 18
ABS65917
ID ABS65917 standard; DNA; 20 BP.
XX
XX ABS65917;
AC
XX
XX 15-NOV-2002 (first entry)
DT
XX
XX Inhibitory oligonucleotide specific for hepatitis C virus #123.
DE
XX
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; vironcide; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
XX
XX Synthetic.
OS
XX
XX US2002081577-A1.
PN
XX
XX 27-JUN-2002.
PD
XX
XX 02-JUL-1997; 97US-00887505.
PF
XX
XX 06-JUN-1995; 95US-00471968.
PR
XX
XX 02-JUL-1996; 96US-0021104P.
PR
XX

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```

PA (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,
PI Hamlin HA, Roberts NA, Walther DM;
XX WPI; 2002-537132/57.
XX
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
XX Claim 1; Page 6; 74pp; English.
XX
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis. HCV has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 0.061;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGGAGCCCACTACTC 20
Db 1 TTGGGAGCCCACTACTC 20
RESULT 19
ABS65923
ID ABS65923 standard; DNA; 20 BP.
XX
XX ABS65923;
AC
XX
XX 15-NOV-2002 (first entry)
DT
XX
XX Inhibitory oligonucleotide specific for hepatitis C virus #129.
DE
XX
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; vironcide; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
XX
XX Synthetic.
OS
XX
XX US2002081577-A1.
PN
XX
XX 27-JUN-2002.
PD
XX
XX 02-JUL-1997; 97US-00887505.
PF
XX
XX 06-JUN-1995; 95US-00471968.
PR
XX
XX 02-JUL-1996; 96US-0021104P.
PR
XX
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA

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PA (GOOD/) GOODCHILD J.  
 PA (WOLFE/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI: 2002-537132/57.  
 XX  
 XX Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 1: Page 6, 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGGACCCCAACTACTC 20  
 Db 1 TTGGGACCCCAACTACTC 20  
 RESULT 20  
 ABS65921  
 ID ABS65921 standard; DNA; 20 BP.  
 XX  
 AC ABS65921;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #127.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; vironcide; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.  
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 PA (WALT/) WALTHER D M.  
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 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
 PI Hamlin HA, Roberts NA, Walther DM;  
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 DR WPI: 2002-537132/57.  
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 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGGACCCCAACTACTC 20  
 Db 1 TTGGGACCCCAACTACTC 20  
 RESULT 21  
 ABS65913  
 ID ABS65913 standard; DNA; 20 BP.  
 XX  
 AC ABS65913;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #119.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; vironcide; cytostatic; antisense therapy;  
 KW gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.

PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walthers DM;  
 XX  
 DR WPI, 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
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 PS Claim 1; Page 6; 74pp; English.  
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 CC The invention describes synthetic oligonucleotides complementary to a  
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 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
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 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis. HCV has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV  
 XX  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 0.061;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACACTACTC 20  
 Db 1 TTGCGACCCCAACACTACTC 20  
 XX  
 RESULT 22  
 ABS65916  
 ID ABS65916 standard; DNA; 20 BP.  
 XX  
 AC ABS65916;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #122.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.

XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walthers DM;  
 XX  
 DR WPI, 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 1; Page 6; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis. HCV has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 0.061;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACACTACTC 20  
 Db 1 TTGCGACCCCAACACTACTC 20  
 XX  
 RESULT 23  
 ABS65919  
 ID ABS65919 standard; DNA; 20 BP.  
 XX  
 AC ABS65919;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #125.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;



PI Hamlin HA, Roberts NA, Walther DM;  
XX  
XX WPI, 2002-537132/57.  
DR  
XX Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
XX Claim 1, Page 6; 74pp; English.  
PS  
XX The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV  
XX  
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.061;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGGGACCCCAACTACTC 20  
1 TTTGGGACCCCAACTACTC 20  
DB 1 UUCGGACCCCAACTACTC 20  
RESULT 24  
ABS65914  
ID ABS65914 standard; DNA; 20 BP.  
XX  
AC ABS65914;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #120.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KW gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
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PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX

DR WPI, 2002-537132/57.  
XX  
XX Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
XX Claim 1, Page 6; 74pp; English.  
PS  
XX The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV  
XX  
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 95.0%; Pred. No. 0.061;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGGGACCCCAACTACTC 20  
1 TTTGGGACCCCAACTACTC 20  
DB 1 TTGGGACCCCAACTACTC 20  
RESULT 25  
ABS65915  
ID ABS65915 standard; DNA; 20 BP.  
XX  
AC ABS65915;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #121.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KW gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
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PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
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PA (WALT/) WALTHER D M.  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
XX WPI, 2002-537132/57.  
XX

PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
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 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
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 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis. HCV has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV

SQ Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;

Query Match  
 Best Local Similarity 100.0%; Score 20; DB 6; Length 20;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
 Db 1 TTGCGACCCACACTACTC 20

RESULT 26  
 ABS65822  
 ID ABS65822 standard; DNA; 20 BP.

AC ABS65822;

DT 15-NOV-2002 (first entry)

DE Inhibitory oligonucleotide specific for hepatitis C virus #28.

KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss.

OS Synthetic.

PN US2002081577-A1.

PD 27-JUN-2002.

PF 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

PR 02-JUL-1996; 96US-0021104P.

PA (KILK/) KILKUSKIE R. L.

PA (FRANK/) FRANK B. L.

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PA (ROBE/) ROBERTS P. C.

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PA (ROBE/) ROBERTS N. A.

PA (WALT/) WALTHER D. M.

PI Kilkuskie R. L., Frank B. L., Goodchild J., Wolfe J. L., Roberts P. C.,

PI Hamlin H. A., Roberts N. A., Walther D. M.

DR WPI; 2002-537132/57.

XX Synthetic oligonucleotides complementary to a portion of the 5'  
 XX untranslated region of hepatitis C virus (HCV), useful for diagnosing and

PT treating HCV infections and hepatocellular carcinoma.  
 XX Claim 1, Page 9, 74pp; English.

CC The invention describes synthetic oligonucleotides complementary to a  
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 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis. HCV has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV

SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match  
 Best Local Similarity 100.0%; Score 20; DB 6; Length 20;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
 Db 1 TTGCGACCCACACTACTC 20

RESULT 27

AAT80285  
 ID AAT80285 standard; DNA; 24 BP.

AC AAT80285;

DT 15-OCT-1997 (first entry)

DE Oligo HCV34, targeted to HCV RNA RNase sensitive region.

KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KW inhibition; replication; expression; detection; chronic hepatitis;  
 KW acute hepatitis; hepatocarcinoma; ss.

OS Synthetic.

PN WO9639500-A2.

PD 12-DEC-1996.

PF 04-JUN-1996; 96WO-EP002427.

PR 06-JUN-1995; 95US-00471968.

PA (HOFF/) HOFFMANN LA ROCHE & CO AG F.

PA (HYBR-) HYBRIDON INC.

PA (ROBE/) ROBERTS P. C.

PA (HAML/) HAMLIN H. A.

PA (ROBE/) ROBERTS N. A.

PA (WALT/) WALTHER D. M.

PI Kilkuskie R. L., Frank B. L., Goodchild J., Wolfe J. L., Roberts P. C.,

PI Hamlin H. A., Roberts N. A., Walther D. M.

DR WPI; 1997-043122/04.

XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in

XX the treatment and detection of HCV infection, esp. hepatitis and hepato-

XX carcinoma.  
 XX Claim 1, Page 26, 100pp; English.

XX The sequences given in AAT80211-382 represent synthetic oligonucleotides

CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This oligo was used in an RNase H assay to determine  
 CC whether it binds successfully to its target. Three regions of HCV mRNA  
 CC were investigated as RNase sensitive sites. This oligo binds to position  
 CC -88 to -65

XX Sequence 24 BP; 5 A; 10 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.061;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTGCGAGCCCAACACTACTC 20  
 3 TTGCGAGCCCAACACTACTC 22

RESULT 28  
 ABS65869

ID ABS65869 standard; DNA; 24 BP.

AC ABS65869;

DT 15-NOV-2002 (first entry)

XX Inhibitory oligonucleotide specific for hepatitis C virus #75.

XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

XX non-B hepatitis; acute hepatitis; chronic hepatitis;

XX hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX gene therapy; ss.

XX Synthetic.

XX US2002081577-A1.

XX 27-JUN-2002.

XX 02-JUL-1997; 97US-00887505.

XX 06-JUN-1995; 95US-00471968.

XX 02-JUL-1996; 96US-0021104P.

XX (KILIK/) KILIKUSKIE R L.

XX (FRANK/) FRANK B L.

XX (GOOD/) GOODCHILD J.

XX (WOLF/) WOLFE J L.

XX (ROBE/) ROBERTS P C.

XX (HAML/) HAMLIN H A.

XX (ROBE/) ROBERTS N A.

XX (WALT/) WALTHER D M.

XX KILUSKIE RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,

XX Hamlin HA, Roberts NA, Walther DM;

XX MPI; 2002-537132/57.

PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.

PS Claim 1; Page 9; 74pp; English.

CC The invention describes synthetic oligonucleotides complementary to a  
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 CC treating hepatitis C virus infection, in antisense technology and gene

CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV

XX Sequence 24 BP; 5 A; 10 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.061;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTGCGAGCCCAACACTACTC 20  
 3 TTGCGAGCCCAACACTACTC 22

RESULT 29  
 AAA74631

ID AAA74631 standard; DNA; 25 BP.

AC AAA74631;

DT 08-JAN-2001 (first entry)

XX HCV probe C252-25-PRB.

XX Hepatitis C virus; HCV; HCV detection; probe; ss.

XX Hepatitis C virus.

XX EP1026262-A2.

XX 09-AUG-2000.

XX 01-FEB-2000; 2000EP-00300763.

XX 03-FEB-1999; 99US-0118497P.

XX (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.

XX Linnen JM, Gorman KM;

XX MPI; 2000-507254/46.

PT Detecting hepatitis C virus in biological sample involves amplifying  
 PT reverse transcribed products of virus RNA using amplification primers  
 PT whose sequences correspond to 5' or 3' non-coding region of the virus  
 PT RNA.

PS Claim 30; Page 27; 28pp; English.

CC The present sequence is a probe used in a method for detecting hepatitis  
 CC C virus (HCV) RNA in biological samples. The HCV RNA is reverse  
 CC transcribed to generate cDNA. This is then amplified with primers  
 CC corresponding to the 5' or 3' non-coding region of HCV. The product was  
 CC captured by hybridization to oligonucleotide probes, including the  
 CC present sequence, which were covalently attached to latex particles and  
 CC deposited on the surface of a flow through membrane. The probe/product  
 CC complex was reacted with streptavidin-horseradish peroxidase conjugate,  
 CC which catalyzes the oxidative conversion of a dye precursor to a blue  
 CC dye. The method is useful for the diagnosis of HCV infection in patients,  
 CC in testing the efficacy of anti-HCV therapeutic regimens, and in screening  
 CC blood for HCV-infected samples. The method provides an improved single-  
 CC round, reverse transcription/amplification assay which detects low copy  
 CC levels of HCV RNA. The primers and assay system are designed to allow the  
 CC co-amplification of multiple regions of the HCV genome, multiple viral  
 CC species, and an internal positive control (IPC) RNA (or DNA).  
 CC Simultaneous amplification/detection of multiple regions of the HCV

CC genome increases assay sensitivity and the co-amplification of an IPC  
CC decreases the likelihood of false negative results because of PCR  
CC inhibition

SQ Sequence 25 BP; 5 A; 10 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGAGCCCACTACTC 20  
2 TTGCGAGCCCACTACTC 21

Db 2 TTGCGAGCCCACTACTC 21

RESULT 30  
AAT80341  
ID AAT80341 standard; DNA; 26 BP.  
XX  
AC AAT80341;  
XX  
DT 16-OCT-1997 (first entry)  
XX  
DE Oligo HCV-1ss1, targeted to HCV mRNA position -67 to -86.  
XX  
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /tag= a  
FT /note= "Comprises phosphorothioate linkages"  
FT stem\_loop 10..26  
FT /tag= b  
FT misc\_feature 21..26  
FT /tag= c  
FT /note= "Nucleotides included for the purpose of base  
FT pairing, not complementary to the target sequence"  
XX  
PN WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 1; Page 19; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma

XX SQ Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.06;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGAGCCCACTACTC 20  
1 TTGCGAGCCCACTACTC 20

Db 1 TTGCGAGCCCACTACTC 20

RESULT 31  
ABS65925  
ID ABS65925 standard; DNA; 26 BP.  
XX  
AC ABS65925;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #131.  
XX  
KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KW gene therapy; ss.  
XX  
OS Synthetic.  
XX  
FN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILK) KILUSKIE R L.  
PA (FRAN) FRANK B L.  
PA (GOOD) GOODCHILD J.  
PA (WOLF) WOLFE J L.  
PA (ROBE) ROBERTS P C.  
PA (HAML) HAMLIN H A.  
PA (ROBE) ROBERTS N A.  
PA (WALT) WALTHER D M.  
XX  
PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
DR WPI; 2002-537132/57.  
XX  
PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
PS Claim 1; Page 6; 74pp; English.  
XX  
CC The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC B, acute and chronic hepatitis. HCV has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic oligonucleotide used for inhibiting HCV  
CC replication and expression of HCV  
XX  
SQ Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
 |||||  
 DB 1 TTGGGACCCCACTACTC 20

RESULT 32  
 AAA96562  
 ID AAA96562 standard; DNA; 27 BP.  
 AC AAA96562;  
 XX 08-FEB-2001 (first entry)  
 DE Nucleotide sequence of a probe specific for HCV.  
 KM HCV; HIV; viral detection; probe; ss.  
 XX  
 XX  
 OS Hepatitis C virus.  
 XX CA2296044-A1.  
 PN 03-AUG-2000.  
 PD 01-FEB-2000; 2000CA-02296044.  
 PF 03-FEB-1999; 99US-0118498P.  
 PR (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 PA Linen JM, Song K, Patterson DR, Gorman KM;  
 PI WPI; 2000-594741/57.  
 DR  
 XX  
 XX  
 PT New methods for the simultaneous detection of hepatitis C virus and human  
 immunodeficiency virus in biological samples from humans.  
 CC  
 XX  
 PS Claim 7; Page 23; 45pp; English.  
 CC The specification describes a method for co-detecting Hepatitis C virus  
 (HCV) RNA and human immunodeficiency virus (HIV) RNA in a biological  
 sample. The method uses HCV and HIV specific reverse transcription  
 primers, either separately or in combination. The reverse transcribed  
 products are then amplified using primers specific for the 5' noncoding  
 region of HCV and/or HIV. The presence of specific products indicates the  
 presence of the appropriate RNA in the sample. The method is used for the  
 simultaneous detection of the presence of HCV RNA and HIV RNA in a  
 sample. The present sequence represents a probe specific for HCV  
 CC  
 XX  
 SQ Sequence 27 BP; 5 A; 12 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
 |||||  
 DB 4 TTGGGACCCCACTACTC 23

RESULT 33  
 AAA91665/C  
 ID AAA91665 standard; RNA; 27 BP.  
 AC AAA91665;  
 XX 03-JAN-2001 (first entry)  
 DT HCV(-)RNA oligonucleotide.  
 XX

XX  
 KM Hepatitis C virus; HCV; HCV RNA replication inhibitor; ribozyme;  
 KM antiviral; ss.  
 XX  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US6107028-A.  
 PD 22-AUG-2000.  
 XX  
 XX  
 PF 15-MAY-1996; 96US-00648272.  
 PR 14-DEC-1994; 94US-00357508.  
 PR 07-JUN-1995; 95US-00476257.  
 PR 11-SEP-1995; 95US-00534220.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Lieber A, Kay MA;  
 DR WPI; 2000-578530/54.  
 XX  
 XX  
 PT Inhibiting hepatitis C viral RNA replication in an infected cell for  
 treating or preventing viral infection, comprises introducing ribozymes  
 specific for a minus strand of the viral 5' non-coding sequence.  
 PT  
 XX  
 PS Example 2; Col 17; 28pp; English.  
 XX  
 XX  
 CC The present sequence is an oligonucleotide which was used for in solution  
 hybridization to quantitate hepatitis C virus (HCV) RNA following  
 ribozyme expression. Ribozymes were identified that can specifically  
 cleave HCV RNA in a HCV 5' non-coding sequence, the capsid sequence, the  
 NS-5 sequence or any other conserved region of the hepatitis C RNA.  
 CC Ribozymes may be introduced into a cell infected with HCV in order to  
 inhibit HCV RNA replication or expression. Unlike prior art compositions  
 and methods, compositions comprising these ribozymes effectively reduce  
 CC and eradicate HCV from the infected cells and significantly impair the  
 CC ability of the virus to replicate, thus preventing further dissemination  
 CC of the disease. The composition is inherently specific for HCV and has  
 CC negligible toxicity  
 XX  
 SQ Sequence 27 BP; 6 A; 4 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
 |||||  
 DB 24 TTGGGACCCCACTACTC 5

RESULT 34  
 AAA74630  
 ID AAA74630 standard; DNA; 27 BP.  
 AC AAA74630;  
 XX 08-JAN-2001 (first entry)  
 DT HCV probe C252-27-PRB.  
 XX  
 DE HCV probe C252-27-PRB.  
 XX  
 XX  
 KM Hepatitis C virus; HCV; HCV detection; probe; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN EP1026262-A2.  
 PD 09-AUG-2000.  
 PF 01-FEB-2000; 2000EP-00300763.  
 PR 03-FEB-1999; 99US-0118497P.  
 XX

```

XX PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX FT
XX FI Linmen JM, Gorman KM;
XX DR WPI; 2000-507254/46.
XX PT Detecting hepatitis C virus in biological sample involves amplifying
XX FT reverse transcribed products of virus RNA using amplification primers
XX PT whose sequences correspond to 5' or 3' non-coding region of the virus
XX FT RNA.
XX PS Claim 30; Page 27; 28pp; English.
XX CC
XX CC The present sequence is a probe used in a method for detecting hepatitis
XX CC C virus (HCV) RNA in biological samples. The HCV RNA is reverse
XX CC transcribed to generate cDNA. This is then amplified with primers
XX CC corresponding to the 5' or 3' non-coding region of HCV. The product was
XX CC captured by hybridisation to oligonucleotide probes, including the
XX CC present sequence, which were covalently attached to latex particles and
XX CC deposited on the surface of a flow through membrane. The probe/product
XX CC complex was reacted with streptavidin-horse radish peroxidase conjugate,
XX CC which catalyses the oxidative conversion of a dye precursor to a blue
XX CC dye. The method is useful for the diagnosis of HCV infection in patients,
XX CC in testing the efficacy of anti-HCV therapeutic regimes, and in screening
XX CC blood for HCV-infected samples. The method provides an improved single-
XX CC round, reverse transcription/amplification assay which detects low copy
XX CC levels of HCV RNA. The primers and assay system are designed to allow the
XX CC co-amplification of multiple regions of the HCV genome, multiple viral
XX CC species, and an internal positive control (IPC) RNA (or DNA).
XX CC Simultaneous amplification/detection of multiple regions of the HCV
XX CC genome increases assay sensitivity and the co-amplification of an IPC
XX CC decreases the likelihood of false negative results because of PCR
XX CC inhibition
XX SQ Sequence 27 BP; 5 A; 12 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCAACTACTC 20
DB 4 TTGCGACCCCAACTACTC 23
RESULT 35
ABA9710/c
ID ABA9710 standard; RNA; 27 BP.
XX AC
XX AC ABA9710;
XX DT
XX DT 07-AUG-2003 (revised)
XX DT 06-JUN-2002 (first entry)
XX DE HCV sub-domain IIId polymorphic fragment IIId_gc.pdb.
XX XX
XX KW Sub-domain IIId; screening; internal ribosome entry site; IRES; virucide;
XX KW molecular modelling; hepatitis C infection; protein co-ordinate data; ss.
XX OS Hepatitis C virus.
XX XX
XX FH Key Location/Qualifiers
XX FH stem_loop 1..27
XX FT /*tag= a
XX FT misc_binding 1..3
XX FT /*tag= b
XX FT /bound_moiety= "IIId_gc.pdb"
XX FT /note= "This region binds to nucleotides 27 to 25,
XX FT forming a stem loop structure"
XX FT 9..11
XX FT /*tag= c
XX FT /bound_moiety= "IIId_gc.pdb"

```

```

FT FT /note= "This region binds to nucleotides 20 to 18,
FT FT forming a stem loop structure"
FT FT misc_binding 18..20
FT FT /*tag= d
FT FT /bound_moiety= "IIId_gc.pdb"
FT FT /note= "This region binds to nucleotides 11 to 9, forming
FT FT a stem loop structure"
FT FT misc_binding 25..27
FT FT /*tag= e
FT FT /bound_moiety= "IIId_gc.pdb"
FT FT /note= "This region binds to nucleotides 3 to 1, forming
FT FT a stem loop structure"
XX FT
XX FN WO200181627-A2.
XX XX
XX XX 01-NOV-2001.
XX PD
XX XX
XX XX 26-APR-2001; 2001WO-GB001871.
XX PF
XX XX 26-APR-2000; 2000GB-00010173.
XX PR
XX XX 26-APR-2000; 2000US-0199773P.
XX XX
XX PA (RIBO-) RIBOTARGETS LTD.
XX XX
XX PI Kinick R, Walker S, Afshar M, Collier A, Aboul-Ela F, Westhof E;
XX XX WPI; 2002-062037/08.
XX DR
XX XX
XX PT Identifying compound that interacts with hepatitis C virus internal
XX PT ribosome entry site sub-domain IIId, comprises providing atomic co-
XX PT ordinates of domain in computer storage medium, applying molecular
XX PT modeling techniques.
XX XX
XX PS Disclosure; Fig 6; 56pp; English.
XX XX
XX CC This invention describes a novel in silico method, for identifying a
XX CC compound that interacts with sub-domain IIId of the hepatitis C virus
XX CC (HCV) internal ribosome entry site (IRES). The method comprises providing
XX CC atomic co-ordinates of the sub-domain IIId in a storage medium on a
XX CC computer, and using the computer to apply molecular modelling techniques
XX CC to the co-ordinates. The compounds identified by the method of the
XX CC invention are useful in an assay for displacement from a fragment of the
XX CC HCV IRES, by contacting the compound with the HCV IRES and assaying the
XX CC interaction between them. The products of the invention also have
XX CC manufacture of a medicament for treating hepatitis C infection, and for
XX CC treating hepatitis C infection. This sequence represents the Hepatitis c
XX CC virus IRES sub-domain IIId fragment IIId_gc.pdb which is used to
XX CC illustrate the method of the invention. (Updated on 07-AUG-2003 to
XX CC correct OS field.)
XX XX
XX SQ Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCAACTACTC 20
DB 23 TTGCGACCCCAACTACTC 4
RESULT 36
ABA9715/c
ID ABA9715 standard; RNA; 27 BP.
XX AC
XX AC ABA9715;
XX DT
XX DT 07-AUG-2003 (revised)
XX DT 06-JUN-2002 (first entry)
XX XX
XX XX HCV sub-domain IIId loop fragment RNA.

```

KW	Sub-domain IIId; screening; internal ribosome entry site; IRES; virucide;
XV	molecular modelling; hepatitis C infection; protein co-ordinate data; ss.
XX	Hepatitis C virus.
OS	
XX	
FT	Key
FT	Location/Qualifiers
FT	stem_loop
FT	1..27
FT	/tag= a
FT	1..3
FT	/tag= b
FT	/bound_moiety= "HCY Loop IIID"
FT	/note= "This region binds to nucleotides 27 to 25,
FT	forming a stem loop structure"
FT	9..11
FT	/tag= c
FT	/bound_moiety= "HCY Loop IIID"
FT	/note= "This region binds to nucleotides 20 to 18,
FT	forming a stem loop structure"
FT	18..20
FT	/tag= d
FT	/bound_moiety= "HCY Loop IIID"
FT	/note= "This region binds to nucleotides 11 to 9, forming
FT	a stem loop structure"
FT	25..27
FT	/tag= e
FT	/bound_moiety= "HCY Loop IIID"
FT	/note= "This region binds to nucleotides 3 to 1, forming
FT	a stem loop structure"
XX	
PN	WO200181627-A2.
PD	
XX	
PF	01-NOV-2001.
XX	
PR	26-APR-2001; 2001WO-GB001871.
PR	26-APR-2000; 2000GB-00010173.
PA	26-APR-2000; 2000US-0195773P.
XX	(RIBO-) RIBOTARGETS LTD.
PI	
XX	Klinck R, Walker S, Afshar M, Collier A, Aboul-Ela F, Westhof E;
DR	WPI; 2002-062037/08.
PT	
PT	Identifying compound that interacts with hepatitis C virus internal
PT	ribosome entry site sub-domain IIId, comprises providing atomic co-
PT	ordinates of domain in computer storage medium, applying molecular
PT	modelling techniques.
XX	
PS	Disclosure; Fig 3C; 56pp; English.
XX	
CC	This invention describes a novel in silico method, for identifying a
CC	compound that interacts with sub-domain IIId of the hepatitis C virus
CC	(HCV) Internal ribosome entry site (IRES). The method comprises providing
CC	atomic co-ordinates of the sub-domain IIId in a storage medium on a
CC	computer, and using the computer to apply molecular modelling techniques
CC	to the co-ordinates. The compounds identified by the method of the
CC	invention are useful in an assay for displacement from a fragment of the
CC	HCY IRES, by contacting the compound with the HCY IRES and assaying the
CC	interaction between them. The products of the invention also have
CC	vinucleic activity and are also useful as pharmaceuticals, for the
CC	manufacture of a medicament for treating hepatitis C infection, and for
CC	treating hepatitis C infection. This sequence represents the Hepatitis C
CC	virus IRES sub-domain IIId loop fragment which is used to illustrate the
CC	method of the invention. (Updated on 07-AUG-2003 to correct OS field.)
XX	
SQ	Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;
	Query Match 100.0%; Score 20; DB 6; Length 27;
	Best Local Similarity 100.0%; Pred.No. 0.06;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
by	1 TTGGGACCAACTACTC 20

```

Db      23 TTGGGACCCAACTACTC 4
|||||
RESULT 37
ID AAL53726/c
AAL53726 standard; RNA; 27 BP.
XX
XX AAL53726;
XX
XX 27-OCT-2003 (revised)
DT 07-FEB-2003 (first entry)
XX
DE Hepatitis C Virus target motif SEQ ID No 20.
XX
XX Target RNA: target RNA:support-attached test compound; flow cytometry;
KW mass spectrometry; high-throughput screening; RNA motif; ss.
XX
XX Hepatitis C virus; Virus.
OS
XX WO200283837-A1.
XX
XX PD 24-OCT-2002.
XX
XX PF 11-APR-2002; 2002MO-US011758.
XX
XX PR 11-APR-2001; 2001US-0282966P.
XX
XX PA (PTCT-) PTC THERAPEUTICS INC.
XX
XX Alimstead NG;
PI
XX WP1; 2003-075534/07.
XX
XX PT Identifying a test compound that binds to a target RNA molecule by
PT separating the detectably labeled target RNA:support-attached test
PT compound complex from uncomplexed target RNA molecules and test compounds
PT by flow cytometry.
XX
XX Example; Page 60; 131pp; English.
PS
XX The invention relates to a novel method for identifying a test compound
XX that binds to a target RNA molecule comprising separating the detectably
XX labeled target RNA:support-attached test compound complex from
XX uncomplexed target RNA molecules and test compounds. The separating
XX process is carried out by flow cytometry and determining a structure of
XX the type of test compound of the RNA:support-attached test compound
XX complex by mass spectrometry. The method is useful for high-throughput
XX screening of libraries of compounds to identify pharmaceutical leads.
XX This polynucleotide sequence represents one of the target RNA motifs/
XX regions of the invention. (Updated on 27-Oct-2003 to standardise OS
XX field)
XX
XX Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY 1 TTGGGACCCAACTACTC 20
|||
DB 23 TTGGGACCCAACTACTC 4
|||
RESULT 38
AAD49658/c
AAD49658 standard; RNA; 27 BP.
XX
XX AAD49658;
XX
XX AC
XX ADT 24-MAR-2003 (first entry)
XX
XX Hepatitis C virus internal ribosome entry site subdomain IIId RNA.

```

XX Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;  
 KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;  
 KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;  
 KW neurodegenerative disorder; Parkinson's disease; gene therapy; virucide;  
 KW haemostatic; antibacterial; nootropic; neuroprotective; cyostatic; HCV;  
 KW fungicide; Hepatitis C virus; internal ribosome entry site; IRES; ss.  
 XX Hepatitis C virus.  
 OS  
 XX WO200283953-A1.  
 XX  
 XX 24-OCT-2002.  
 XX  
 XX 11-APR-2002; 2002WO-US011757.  
 XX  
 XX 11-APR-2001; 2001US-0282965P.  
 XX  
 XX (PTCT-) PTC THERAPEUTICS INC.  
 XX  
 XX Rando R, Welch E;  
 XX  
 XX WPI; 2003-075561/07.  
 XX  
 XX  
 XX PT Identifying a test compound that binds to a target RNA molecule for  
 PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,  
 PT diabetes, by contacting a detectably labeled target RNA molecule with a  
 PT library of test compounds.  
 XX  
 XX  
 XX Example; Page 69; 152pp; English.  
 XX  
 XX The invention relates to a method for identifying a test compound that  
 CC binds to a target RNA molecule, which comprises contacting a detectably  
 CC labelled target RNA molecule with a library of test compounds under  
 CC conditions that permit direct binding of the labelled target RNA to a  
 CC member of the library of test compounds so that a detectably labeled  
 CC target RNA-test compound complex is formed. The method is useful for  
 CC screening libraries of compounds for those that are selectively bind to a  
 CC pre-selected target RNA. The compounds are useful for inhibiting the  
 CC formation of a specific bound RNA-host cell factor complexes in vivo.  
 CC They are also useful for treating or preventing diseases associated with  
 CC overproduction or decreased protein function, such as amyloidosis,  
 CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,  
 CC dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,  
 CC inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative  
 CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).  
 CC The invention is also used in gene therapy. The present sequence is  
 CC Hepatitis C virus (HCV) internal ribosome entry site (IRES) subdomain  
 CC I11d RNA. This sequence is used to illustrate the method of the invention  
 SQ  
 SQ Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 8; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCAACTACTC 20  
 Db 23 TTGCGACCAACTACTC 4  
 RESULT 39  
 ADE85926/c  
 ID ADE85926 standard; RNA; 27 BP.  
 XX  
 XX ADE85926;  
 XX  
 XX 29-JAN-2004 (first entry)  
 XX  
 XX Stem-loop forming RNA from HCV subdomain I11d.  
 XX  
 XX TOLL-like receptor; immunostimulant; antimicrobial; antiallergic;  
 KM cyostatic; vaccine; HCV; ss.

XX Hepatitis C virus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH stem\_loop 1..27  
 FT /\*tag= a  
 XX  
 XX WO2003086280-A2.  
 XX  
 XX 23-OCT-2003.  
 XX  
 XX 04-APR-2003; 2003WO-US010406.  
 XX  
 XX 04-APR-2002; 2002US-0370515P.  
 XX  
 XX 29-OCT-2002; 2002US-0421966P.  
 XX  
 XX (COLE-) COLEY PHARM GMBH.  
 XX  
 XX Lipford G, Bauer S;  
 XX  
 XX WPI; 2003-845251/78.  
 XX  
 XX  
 XX PT New immunostimulatory composition, useful in inducing an immune response  
 PT against microbial or cancer antigen or allergen.  
 XX  
 XX Disclosure; SEQ ID NO 4; 220pp; English.  
 XX  
 XX The present sequence is that of a stem-loop forming 27-mer from hepatitis  
 CC C virus (HCV) subdomain I11d. This sequence has been reported to be  
 CC critical in HCV internal ribosome entry site (IRES)-mediated translation.  
 CC The invention relates to immunostimulatory RNA oligomers that contain at  
 CC least one guanine and at least one uracil. Such immunostimulatory RNAs  
 CC are known to occur in the context of an IRES. Claimed immunostimulatory  
 CC RNA oligomers are thought to signal through an MyD88-dependent pathway,  
 CC probably through Toll-like receptor (TLR) 7 or TLR8, and are believed to  
 CC be ligands of TLR7 or TLR8. Claimed immunostimulatory compositions  
 CC comprise a G-U-containing RNA oligomer and optionally an antigen,  
 CC especially an allergen, cancer antigen or microbial antigen. Methods are  
 CC provided for activating an immune cell, inducing an immune response,  
 CC stimulating TLR8 or TLR7 signalling, and supplementing a TLR8- or TLR7-  
 CC mediated immune response. The methods and compositions are useful for  
 CC activating immune cells in vivo, in vitro and ex vivo, treating  
 CC infection, treating cancer, identifying a target receptor, and screening  
 CC for additional immunostimulatory compounds.  
 SQ  
 SQ Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCAACTACTC 20  
 Db 23 TTGCGACCAACTACTC 4  
 RESULT 40  
 AAT80278  
 ID AAT80278 standard; DNA; 28 BP.  
 XX  
 XX AAT80278;  
 XX  
 XX 15-OCT-1997 (first entry)  
 XX  
 XX Oligo HCV36, targeted to HCV mRNA RNase sensitive region.  
 XX  
 XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 XX acute hepatitis; hepatocarcinoma; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH



```

FT modified_base 1..28
FT /tag= a
FT /note= "Comprises phosphorothioate linkages"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 1; Page 26; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This oligo was used in an RNase H assay to determine
XX whether it binds successfully to its target. Three regions of HCV mRNA
XX were investigated as RNase sensitive sites. This oligo binds to position
XX -94 to -67
XX
XX Sequence 28 BP; 7 A; 11 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGCGACCCCAACTACTC 20
XX |||||
XX 1 TTGCGACCCCAACTACTC 20
XX
XX Db
XX
XX RESULT 41
XX AAT80284
XX ID AAT80284 standard; DNA; 28 BP.
XX
XX AC AAT80284;
XX
XX DT 15-OCT-1997 (first entry)
XX
XX DE Oligo HCV35, targeted to HCV mRNA RNase sensitive region.
XX
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..28
XX /tag= a
XX /note= "Comprises phosphorothioate linkages"
XX
XX WO9639500-A2.
XX

```

```

PD 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 1; Page 26; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This oligo was used in an RNase H assay to determine
XX whether it binds successfully to its target. Three regions of HCV mRNA
XX were investigated as RNase sensitive sites. This oligo binds to position
XX -90 to -63
XX
XX Sequence 28 BP; 5 A; 12 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGCGACCCCAACTACTC 20
XX |||||
XX 5 TTGCGACCCCAACTACTC 24
XX
XX Db
XX
XX RESULT 42
XX ABS65862
XX ID ABS65862 standard; DNA; 28 BP.
XX
XX AC ABS65862;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Inhibitory oligonucleotide specific for hepatitis C virus #68.
XX
XX KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
XX non-B hepatitis; acute hepatitis; chronic hepatitis;
XX hepatocellular carcinoma; virucide; cytostatic; antitense therapy;
XX gene therapy; ss.
XX
XX OS Synthetic.
XX
XX US2002081577-A1.
XX
XX PD 27-JUN-2002.
XX
XX PF 02-JUL-1997; 97US-00887505.
XX
XX 06-JUN-1995; 95US-00471968.
XX 02-JUL-1996; 96US-0021104P.
XX
XX (KILK/) KILKUSKIE R L.
XX (FRAN/) FRANK B L.
XX (GOOD/) GOODCHILD J.
XX

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PA (WOLFE/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walthers DM;  
 XX WPI: 2002-537132/57.  
 DR  
 XX  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 1; Page 9; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV  
 XX  
 SQ Sequence 28 BP; 7 A; 11 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 1 TTGCGACCCCAACTACTC 20  
 RESULT 43  
 AB865868  
 ID AB865868 standard; DNA; 28 BP.  
 XX  
 AC AB865868;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #74.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 XX (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLFE/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walthers DM;  
 XX WPI: 2002-537132/57.  
 DR  
 XX  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 1; Page 9; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV  
 XX  
 SQ Sequence 28 BP; 5 A; 12 C; 5 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 5 TTGCGACCCCAACTACTC 24  
 RESULT 44  
 ABK15311/c  
 ID ABK15311 standard; RNA; 29 BP.  
 XX  
 AC ABK15311;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Hepatitis C virus IRES element domain IIId RNA sequence.  
 XX  
 KW Hepatitis C virus; HCV; internal ribosome entry site element; IRES; ss;  
 KW 40S ribosome subunit; domain IIId; domain IIIE.  
 XX  
 OS Hepatitis C virus.  
 XX  
 FH Key  
 FT stem\_loop  
 FT 1..29  
 FT /tag= a  
 FT 5..88  
 FT /tag= c  
 FT /note= "Forms characteristic S turn in backbone"  
 FT 5..25  
 FT /tag= b  
 FT /note= "Form sheared base pair"  
 FT 6..24  
 FT /tag= d  
 FT /note= "Form parallel base pair"  
 FT 7  
 FT /tag= e  
 FT /note= "Bulged residue; forms a base triple with reversed  
 FT Hoogsteen pair (residues 8 and 23)"  
 FT 8..23  
 FT /tag= f

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FT FT misc_feature /note= "Form reverse Hoogsteen base pair"
FT FT          9..22
FT FT      /*tag= h
FT FT      /note= "Form sheared base pair"
FT FT          9
FT FT      /*tag= g
FT FT      /note= "Minor groove exposed Watson-Crick face"
FT FT          13..18
FT FT      /*tag= i
FT FT      /note= "Hairpin loop"
FT FT          23
FT FT      /*tag= j
FT FT      /note= "Minor groove exposed Watson-Crick face"
FT FT          24
FT FT      /*tag= k
FT FT      /note= "Minor groove exposed Watson-Crick face"
FT FT          25
FT FT      /*tag= l
FT FT      /note= "Minor groove exposed Watson-Crick face"
XX XX
XX XX WO200203919-A2.
XX XX
XX XX 17-JAN-2002.
XX XX
XX XX 10-JUL-2001; 2001WO-US021871.
XX XX
XX XX 10-JUL-2000; 2000US-0217673P.
XX XX
XX XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX XX
XX XX Puglisi JD;
XX XX
XX XX WPI; 2002-179655/23.
XX XX
XX XX Computer for producing a three dimensional representation of a molecule
PT PT hepatitis C virus entry site element comprises a machine-readable device,
PT PT data storage medium, working memory, central processing unit and display.
XX XX
PS PS Claim 3; Fig 1c; 39pp; English.
XX XX
XX XX The present invention relates to a new computer for producing three
CC CC dimensional representation of a molecule. The computer of the invention
CC CC comprises a machine-readable data storage medium, a working memory for
CC CC storing instructions, a central processing unit coupled to the working
CC CC memory and machine-readable data storage medium and a display coupled to
CC CC the central processing unit. The molecule comprises a hepatitis C virus
CC CC (HCV) internal ribosomal entry site (IRES) element. The invention is
CC CC useful for producing a three dimensional representation of a molecule
CC CC comprising hepatitis B virus C IRES element, for identifying potential
CC CC inhibitors of hepatitis B virus translation and for modelling
CC CC interactions of the IRES with its binding partner, the 40S ribosome
CC CC subunit. The computer generates the three-dimensional graphical
CC CC representations of molecules or their portions from a set of structure co-
CC CC ordinates and displays graphical three-dimensional representation of the
CC CC HCV IRES stem loops in at least one of domain IId or IIle. The
CC CC structural data permits the identification of atoms that are important
CC CC for 40S ribosomal subunit binding. The present nucleic acid sequence
CC CC represents the hepatitis C virus internal ribosome entry site element
CC CC domain IId of the invention. This sequence represents residues 252-280
CC CC of ABK15309
XX XX
XX XX Sequence 29 BP; 5 A; 6 C; 13 G; 0 T; 5 U; 0 Other;
SQ SQ
Query Match 100.0%; Score 20; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY 1 TTCGGACCAACTACTC 20
DB 24 TTCGGACCAACTACTC 5

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ADCS4069/C
ID ADC54069 standard; DNA; 29 BP.
XX
XX
AC ADC54069;
XX
XX 18-DEC-2003 (first entry)
XX
XX HCV 5'UTR signal amplification probe, SEQ ID NO:20.
DE
XX HCV; hepatitis C virus; classification; interferon therapy; 5'UTR;
KW signal amplification; probe; ss.
XX
XX Hepatitis C virus.
OS
XX JP2002345467-A.
PN
XX 03-DEC-2002.
PD
XX 17-APR-2001; 2001JP-00118810.
PF
XX 23-OCT-2000; 2000JP-00322567.
PR
XX (SRLS-) SRL KK.
PA
XX WPI; 2003-460879/44.
DR
XX
XX Probe and method for classification of hepatitis C virus (HCV) types used
PT for forecast of therapeutic effect of interferon administration.
PT
XX
XX Disclosure; SEQ ID NO 20; 15pp; Japanese.
PS
XX The invention relates to a nucleic acid probe for the classification of
CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1mi
CC (type 1), MH2mi (type 2) and MH3G3C+MHG3C' (type 3). The probe can be
CC used to classify HCV type to enable prediction of the success or
CC otherwise of interferon therapy in a patient. Sequences ADC54068-ADC54073
CC represent HCV 5'UTR signal amplification probes. Note: The present
CC sequence is given in the sequence listing, but is not further referred to
CC in the specification.
XX
XX Sequence 29 BP; 6 A; 5 C; 12 G; 6 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 TTCCGACCCCAACTACTC 20
DB 26 TTCCGACCCCAACTACTC 7
RESULT 46
AAQ31157
ID AAQ31157 standard; DNA; 33 BP.
XX
XX AAQ31157;
XX
XX 25-MAR-2003 (revised)
DT 24-MAR-1993 (first entry)
DT
XX Probe 126 for genotyping analysis of HCV-1.
XX
XX Hepatitis C virus; non-A, non-B hepatitis; polymerase chain reaction;
KW amplified solution phase nucleic acid sandwich assay;
KW genotyping analysis; capture probe; detection probe; ss.
XX
XX Synthetic.
OS
XX WO9219743-A2.
PN
XX 12-NOV-1992.
PD
XX 08-MAY-1992; 92WO-US004036.
PF

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```

XX 08-MAY-1991; 91US-00697326.
XX (CHIR ) CHIRON CORP.
XX Cha T, Beall E, Irvine B, Kolberg J, Urdea MS,
XX WPI; 1992-398869/48.
XX
XX Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX related to HCV-1, useful for treating and detecting HCV-1 infections and
XX as a vaccine.
XX
XX Claim 63; Page 140; 106pp; English.
XX
XX A sandwich hybridisation assay can be used for HCV-1 genotyping analysis.
XX One example uses nucleotide sequences which correspond to sequences in
XX the C gene and the 5' UT region of HCV isolates as either capture or
XX detection probes. Probe 126 is preferably used as a labelled probe.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTGGGACCCCAACTACTC 20
XX 10 TTGGGACCCCAACTACTC 29
XX
XX Db
XX
XX RESULT 47
XX AAQ46463
XX ID AAQ46463 standard; DNA; 33 BP.
XX
XX AAQ46463;
XX
XX 25-MAR-2003 (revised)
XX 13-DEC-1993 (first entry)
XX
XX Hepatitis C virus RNA assay label probe HCV.33.8.
XX
XX Detection; HCV; reduced background signal; improved reproducibility;
XX hybridisation; 5'-untranslated region; C gene; ss.
XX
XX Synthetic.
XX
XX WO9313224-A1.
XX
XX 08-JUL-1993.
XX
XX 22-DEC-1992; 92WO-US011343.
XX
XX 23-DEC-1991; 91US-00813338.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Sheridan P, Chang C, Running J;
XX
XX WPI; 1993-227338/28.
XX
XX Immobilising nucleic acid probe on styreneI, useful for HCV sequence
XX detection - by using intermediate passively adsorbed polymer having
XX functional gps. for covalently bonding to probe via its base-stable
XX linkages.
XX
XX Example; Fig 3.1; 34pp; English.
XX
XX The sequence is that of a synthetic label probe which is complementary to
XX nucleotide sequences in the hepatitis C virus C gene and the 5'-
XX untranslated region. It may be used in an assay for the detection of HCV
XX RNA. (Updated on 25-MAR-2003 to correct PN field.)

```

```

XX Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTGGGACCCCAACTACTC 20
XX 10 TTGGGACCCCAACTACTC 29
XX
XX Db
XX
XX RESULT 48
XX AAQ07837
XX ID AAQ07837 standard; DNA; 33 BP.
XX
XX AAQ07837;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 10-DEC-1998 (first entry)
XX
XX HCV.33.8 amplifier probe.
XX
XX Comb-type branched polynucleotide; amplification multimer; analyte;
XX hybridisation assay; hepatitis C virus; HCV; amplifier probe; ss.
XX
XX Synthetic.
XX
XX Hepatitis C virus.
XX
XX US5710264-A.
XX
XX 20-JAN-1998.
XX
XX 07-JUN-1995; 95US-00478085.
XX
XX 27-JUL-1990; 90US-00558897.
XX 23-DEC-1991; 91US-00813588.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chang C, Fultz TJ, Warner B, Urdea MS, Horn T;
XX
XX WPI; 1998-109872/10.
XX
XX New large comb-type branched polynucleotides - useful as amplification
XX multimers in nucleic acid hybridisation assays.
XX
XX Example 6; Col 25; 33pp; English.
XX
XX The invention relates to a large comb-type branched polynucleotide of
XX formula 3'-A-S-(S'-X')m-S'-5'; where X' is a branched site joined to -
XX (R)n-S'-E-L; A = an oligonucleotide complementary to an analyte nucleic
XX acid sequence; S = a first spacer segment of 1-50 linked monomers where
XX each monomer is selected from nucleotides and a cleavable linker R; S' =
XX a branching site spacer segment of 0-15 linked monomers where each of the
XX monomers is selected from nucleotides and cleavable linker R; X' = a
XX multifunctional nucleotide that provides a branch site; m = 1-100; S' =
XX a second spacer segment of 0-10 linked monomers where each of the
XX monomers is selected from nucleotides and cleavable linker R; R = a
XX cleavable linker molecule; n = 0 or 1; S'' = a third spacer segment of 0
XX -10 linked monomers where each of the monomers is selected from
XX nucleotides and cleavable linker R; E = an oligonucleotide segment of 5-
XX 10 nucleotides; L = an oligonucleotide containing 2-10 iterations of a
XX nucleotide sequence complementary to a labelled nucleic acid probe. The
XX invention also relates to a branched nucleic acid polymer. The poly-
XX nucleotides are useful as amplification multimers in nucleic acid
XX hybridisation assays used for genetic research, biomedical research and
XX clinical diagnostics. Since the polynucleotide multimers include a large
XX number (at least 20) iterations of a sequence that are available for
XX specific hybridisation, they permit a greater degree of amplification and
XX decrease the threshold level of a detectable analyte. The present
XX sequence represents a hepatitis C virus (HCV) amplifier probe. (Updated

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CC on 25-MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct  
CC OS field.)

Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.06;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
10 TTGGGACCCCAACTACTC 29

Db 10 TTGGGACCCCAACTACTC 29

RESULT 49

AAV83065  
ID AAV83065 standard; DNA; 33 BP.

AC AAV83065;

DT 24-FEB-1999 (first entry)

DE Amplifier probe HCV.33.8.

XX Comb-type branched polynucleotide; amplifier probe;

KW multifunctional nucleotide; pendant polynucleotide sidechain;  
KW hybridisation assay; amplification multimer; sandwich assay; ss.

OS Synthetic.

OS Hepatitis C virus.

PN US5849481-A.

PD 15-DEC-1998.

PF 05-JUN-1995; 95US-00470124.

PR 27-JUL-1990; 90US-00558897.

PR 23-DEC-1991; 91US-00813586.

PA (CHIR ) CHIRON CORP.

PI Warner B, Horn T, Fultz TJ, Urdea MS, Chang C;

DR WPI, 1999-069715/06.

PT Improved nucleic acid hybridisation assays - using large comb-type  
PT polypeptide(s).

PS Example 6; Col 24; 31pp; English.

XX Oligonucleotides AAV83063-80 represent amplifier probes, used in a  
CC sandwich hybridisation assay for Hepatitis C virus (HCV) DNA. The

CC sandwich hybridisation assay utilises the comb-type branched  
CC polynucleotide amplification multimer of the invention. This large comb-

CC type branched polynucleotide comprises a polynucleotide backbone having  
CC at least 15 multifunctional nucleotides each defining a sidechain site

CC and pendant polynucleotide sidechains extending from the multifunctional  
CC nucleotides, each comprising iterations of a single stranded

CC oligonucleotide unit capable of binding specifically to a second single-  
CC stranded polynucleotide sequence. The total number of iterations in all

CC sidechains is at least 20. The first single-stranded polynucleotide  
CC sequence is a labelled polynucleotide, directly or indirectly linked to a

CC nucleic acid analyte. In the nucleic acid hybridisation assay of the  
CC invention, the labelled nucleic acid probe is hybridised to the branched

CC polymeric nucleotide via the second single-stranded oligonucleotide unit.  
CC The comb-type branched polynucleotides are used as amplification

CC multimers in nucleic acid hybridisation assays and other assays such as  
CC direct, indirect and sandwich assays

XX Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 0.06;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
10 TTGGGACCCCAACTACTC 29

Db 10 TTGGGACCCCAACTACTC 29

RESULT 50

AAA86970/C  
ID AAA86970 standard; DNA; 40 BP.

AC AAA86970;

DT 15-JAN-2001 (first entry)

DE Probe for Hepatitis C.

XX Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;

KW single nucleotide polymorphism; identification; viral load; probe;

KW genotyping; medical marker diagnostic; primer; target; mutation;

XX genetic disease; ss.

OS Hepatitis C virus.

PN WO200049180-A1.

PD 24-AUG-2000.

PF 18-FEB-2000; 2000MO-US004242.

PR 18-FEB-1999; 99US-00252436.

PR 21-JUL-1999; 99US-00358972.

PR 25-AUG-1999; 99US-00383316.

PA (PROM-) PROMEGA CORP.

PI Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;

PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;

DR WPI, 2000-565377/52.

PT Determining presence or absence of a predetermined endogenous nucleic  
PT acid sequence by using an enzyme that depolymerizes the 3' end of an

PT oligonucleotide probe hybridized to a target sequence to release  
PT identifier nucleotides.

PS Example; Page 349; 389pp; English.

XX The present invention describes a method (M1) for determining the  
CC presence or absence of a predetermined endogenous nucleic acid target

CC sequence (ENMT). The method comprises hybridising a probe having an  
CC identifier nucleotide (IN) with ENMT which is treated with an enzyme that

CC depolymerises the 3' end of hybridised NA to release the INs. M1 is used  
CC for determining the number of known sequence repeats present in a nucleic

CC acid target sequence in a nucleic acid sample. The method is also useful  
CC for determining whether a nucleic acid target sequence in a sample is an

CC allele from a homozygous or heterozygous locus. The method is also useful  
CC for detection of mutations, translocations and SNPs in nucleic acids

CC (including those associated with genetic disease), determination of viral  
CC load, species identification, sample contamination, and analysis of

CC forensic samples. AAA86971 to AAA87079 and AAA812817 represent sequence  
CC which are used in the exemplification of the present invention. N.B.

CC There is a discrepancy between the SEQ ID NO: and sequences given in the  
CC examples, and the SEQ ID NO: and sequences given in the sequence listing

XX Sequence 40 BP; 6 A; 8 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCAACTACTC 20  
 ID |||||  
 Db 29 TTGCGACCAACTACTC 10

RESULT 51  
 ID AAA93199/c  
 AC AAA93199 standard; DNA; 40 BP.  
 XX  
 AC AAA93199;  
 XX  
 DT 11-JAN-2001 (first entry)  
 XX  
 DE Hepatitis C virus RNA interrogation probe HCV1.  
 XX  
 KW Hepatitis C virus; HCV; nucleic acid detection; genomic typing;  
 KM mutation detection; viral load determination; species identification;  
 XX forensic analysis; probe; ss..  
 OS Hepatitis C virus.  
 XX  
 PN WO200049179-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-US004176.  
 XX  
 PR 18-FEB-1999; 99US-00252436.  
 PR 21-JUL-1999; 99US-00358972.  
 PR 27-SEP-1999; 99US-00406147.  
 XX  
 PA (PROM-) PROMEGA CORP.  
 XX  
 PI Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB,  
 PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;  
 XX  
 DR WPI; 2000-549282/50.

PT Detecting the presence of predetermined exogenous nucleic acid target  
 PT sequence useful for e.g. genotyping, comprises depolymerizing the 3' end  
 PT of an oligonucleotide probe hybridized to a nucleic acid target sequence.  
 XX  
 PS Claim 47; Page 185; 230pp; English.

CC The present sequence is a probe which was used to interrogate hepatitis C  
 CC virus (HCV) RNA isolated from infected or uninfected human serum samples.  
 CC The probe was used to determine the viral load of the samples. This was  
 CC performed as part of a method for determining the presence of a known  
 CC exogenous nucleic acid target sequence in a nucleic acid sample. The  
 CC method comprises admixing a treated sample with a depolymerizing enzyme  
 CC which releases one or more nucleotides from the 3'-end of a hybridised  
 CC nucleic acid probe. The method is used for assaying nucleic acids for a  
 CC particular native or mutant sequence, and for genomic typing. It is  
 CC useful for detecting mutations, translocations, and single nucleotide  
 CC polymorphisms, determination of viral load, species identification,  
 CC detection of sample contamination, and analysis of forensic samples.  
 CC Compared with previous methods of detecting nucleic acid hybrids, the new  
 CC method has higher sensitivity without the need for radiochemicals or  
 CC electrophoresis. It is quantitative, highly reproducible and can be  
 CC automated. The method can reliably detect as few as 10 copies of a virus  
 CC in a sample, and is capable of providing multiple analyses in a single  
 CC assay (multiplex assay)  
 CC  
 XX

Sequence 40 BP; 6 A; 8 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.059;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCAACTACTC 20  
 ID |||||  
 Db 29 TTGCGACCAACTACTC 10

RESULT 52  
 ID ADC46968  
 AC ADC46968 standard; DNA; 40 BP.  
 XX  
 AC ADC46968;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Synthesised bridge probe #SEQ ID 4.  
 XX  
 KW Oligonucleotide; amplification; gene detection; self-assembly; probe; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003040367-A1.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 30-OCT-2002; 2002WO-JP011321.  
 XX  
 PR 08-NOV-2001; 2001JP-00342709.  
 PR 08-MAY-2002; 2002JP-00132402.  
 XX  
 PA (SANK-) SANKO JUNYAKU CO LTD.  
 XX  
 PI Usui M, Mitsuoka M, Haki C;  
 XX  
 DR WPI; 2003-441572/41.  
 XX  
 PT Self-assembly formed from amplified target gene and probe pairs for  
 PT sample and accurate detection of the target gene.  
 XX  
 PS Example Examples; Page 35; 123pp; Japanese.

CC The invention relates to a method for forming an oligonucleotide self-  
 CC assembly, in which oligonucleotides containing a target gene sequence are  
 CC first amplified by a conventional gene amplification method, and the  
 CC amplification product is then incorporated into the self-assembly by  
 CC reaction with one or more oligonucleotide probe pairs. Also disclosed is  
 CC the detection of a specific gene using the novel method. The  
 CC oligonucleotide probe pairs (which may consist of one pair, or two or  
 CC more different pairs) consist of at least three distinct hybridising  
 CC regions which are each complementary to a region on the other probe of  
 CC the pair, or to a region on the target oligonucleotide. Preferably each  
 CC complementary region includes at least one G-C coupling. The regions  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe sequence. The self-assembly  
 CC is formed by first forming a dimer of the probe pair, by hybridisation of  
 CC the central complementary regions of the probes. This dimer is then  
 CC hybridised with the target oligonucleotides, each 3' or 5' terminal  
 CC portion of the probe dimer hybridizing to a different region on one or  
 CC other strand of the target oligonucleotide sequence. The probes may be  
 CC DNA, RNA, PNA or LNA. The 3' and/or 5' terminals of the probes may be  
 CC methylated. The oligonucleotides may be synthesised in the initial  
 CC amplification reaction from single or double stranded DNA or RNA and the  
 CC synthesis may include ligation of a target sequence to sequences  
 CC complementary to the probe pairs. They may be enzymatically cleavable by  
 CC exonuclease, kinase H or restriction enzymes. This method is an accurate  
 CC specific and sensitive method for the detection of a target gene sequence  
 CC at low cost and without complicated procedures or apparatus. The current  
 CC sequence represents a synthesised bridge probe utilised in an example  
 CC from the invention.  
 CC  
 XX

Sequence 40 BP; 7 A; 14 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.059;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCAACTACTC 20  
 ID |||||  
 Db 29 TTGCGACCAACTACTC 10

Db 3 TTCGGACCCACACTACTC 22

## RESULT 53

ADP87787/c  
ID ADP87787 standard; DNA; 40 BP.

AC ADP87787;

DT 09-SEP-2004 (first entry)

DE TEX on microarray template M3.

TEX; thermodynamic equilibrium extension of primers; template; ss.

OS Synthetic.

PN US2004115643-A1.

PD 17-JUN-2004 .

PF 12-DEC-2002; 2002US-00318416.

PR 12-DEC-2002; 2002US-00318416.

PA (LIZA/) LIZARDI P M.  
PA (GRIB/) GRIBANOV O G.

PI Lizardi PM, Gribanov OG;

DR WPI; 2004-468050/44.

PT Amplifying nucleic acid for detecting nucleic acid, by extension of one or more primers using target templates having replication terminating feature, dissociation of primer from templates to produce multiple extended primers.

PS Example; SEQ ID NO 19; 75pp; English.

The invention relates to amplifying (M1) a nucleic acid, involving (TT) contacting one or more extension primers (EP) and target templates (CC) and incubating under conditions to promote interaction of (EP) and templates, extension of (EP) using the interacting (TT), and dissociation of the extended (EP) from (TT), to produce multiple extended (EP) from at least one (TT), where each (TT) comprise a replication terminating feature. In (M1), (EP) and target templates are incubated under isothermal conditions or single set of conditions. The target templates are nucleic acid sequences of interest. Each of (EP) comprises or consists of a target complement portion, preferably nucleotides, where the nucleotides consist of the target complement portion. Each (EP) further comprises non-target complement portion. The method is known as TmX (thermodynamic equilibrium extension of primers). The method is useful for amplifying nucleic acid and for detecting nucleic acid sequences which involves performing (M1), and detecting one or more of the extended (EP). In (M1), only those sequences targeted by (EP) are amplified, thus allowing specific sequences to be targeted for amplification. Flexibility in the location of replication terminating feature allows flexibility in targeting sequences. If a targeted sequence is not present, the sequence will not be amplified. Multiple sequences can be amplified in the same reaction by targeting multiple sequences with (EP). Simultaneous amplification and detection is facilitated using detection probes associated with a substrate. Multiplex detection can be facilitate by an array of detection probes with different detection probes at different locations of a substrate. The present sequence is a synthetic template sequence used to demonstrate the method of the invention.

**SQ** Sequence 40 BP; 7 A; 9 C; 15 G; 9 T; 0 U; 0 Other;

Query Match	100.0%	Score 20;	DB 12;	Length 40;
Best Local Similarity	100.0%;	Pred. No. 0.059;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
|||||  
Db . 31 TTGCGACCCACACTACTC 12

## RESULT 54

ADP87774/c  
ID ADP87774 standard; DNA; 40 BP.

AC ADP87774;

DT 09-SEP-2004 (first entry)

DE TEX control template sequence.

KW TEX; thermodynamic equilibrium extension of primers; ss; target.

OS Synthetic.

PN US2004115643-A1.

PD 17-JUN-2004.

PF 12-DEC-2002; 2002US-00318416.

PR 12-DEC-2002; 2002US-00318416.

PA (LIZA/) LIZARDI P M.  
PA (GRIB/) GRIBANOV O G.

PI Lizardi PM, Gribanov OG;

DR WPI; 2004-468050/44.

PT Amplifying nucleic acid for detecting nucleic acid, by extension of one  
PT or more primers using target templates having replication terminating  
PT feature, dissociation of primer from templates to produce multiple  
PT extended primers.

PS Example; SEQ ID NO 6; 75pp; English.

CC The invention relates to amplifying (M) a nucleic acid, involving  
CC contacting one or more extension primers (EP) and target templates (TT)  
CC and incubating under conditions to promote interaction of (EP) and  
CC templates, extension of (EP) using the interacting (TT), and dissociation  
CC of the extended (EP) from (TT), to produce multiple extended (EP) from at  
CC least one (TT), where each (TT) comprise a replication terminating  
CC feature. In (M1), (EP) and target templates are incubated under  
CC isothermal conditions or single set of conditions. The target templates  
CC are nucleic acid sequences of interest. Each of (EP) comprises or  
CC consists of a target complement portion, preferably nucleotides, where  
CC the nucleotides consist of the target complement portion. Each (EP)  
CC further comprises non-target complement portion. The method is known as  
CC TTX (thermodynamic equilibrium extension of primers). The method is  
CC useful for amplifying nucleic acid and for detecting nucleic acid  
CC sequences which involves performing (M1), and detecting one or more of  
CC the extended (EP). In (M1), only those sequences targeted by (EP) are  
CC amplified, thus allowing specific sequences to be targeted for  
CC amplification. Flexibility in the location of replication terminating  
CC feature allows flexibility in targeting sequences. If a targeted sequence  
CC is not present, the sequence will not be amplified. Multiple sequences  
CC can be amplified in the same reaction by targeting multiple sequences  
CC with (EP). Simultaneous amplification and detection is facilitated using  
CC detection probes associated with a substrate. Multiplex detection can be  
CC facilitate by an array of detection probes with different detection  
CC probes at different locations of a substrate. The present sequence is a  
CC control target sequence used in an example demonstrating the method of  
CC the invention.

SQ Sequence 40 BP; 7 A; 8 C; 15 G; 10 T; 0 U; 0 Other;

```
Query Match      100.0%; Score 20; DB 12; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.059;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGGACCCAACTACTC 20  
 |||||  
 Db 31 TTTCGGACCCAACTACTC 12

RESULT 55  
 ADP87786/c  
 ID ADP87786 standard; DNA; 40 BP.

AC ADP87786;

DT 09-SEP-2004 (first entry)

DE TEX synthetic spacer C3 #1.

XX TEX; thermodynamic equilibrium extension of primers; template; ss.

OS Synthetic.

PN US2004115643-A1.

PD 17-JUN-2004.

PF 12-DEC-2002; 2002US-00318416.

PR 12-DEC-2002; 2002US-00318416.

PA (LIZA/) LIZARDI P M.

PI (GRIB/) GRIBANOV O G.

PI Lizardi PM, Grihanov OG;

PI MPI; 2004-468050/44.

PT Amplifying nucleic acid for detecting nucleic acid, by extension of one  
 PT or more primers using target templates having replication terminating  
 PT feature, dissociation of primer from templates to produce multiple  
 PT extended primers.

PS Example; SEQ ID NO 18; 75bp; English.

CC The invention relates to amplifying (M1) a nucleic acid, involving  
 CC contacting one or more extension primers (EP) and target templates (TT)  
 CC and incubating under conditions to promote interaction of (EP) and  
 CC templates, extension of (EP) using the interacting (TT), and dissociation  
 CC of the extended (EP) from (TT), to produce multiple extended (EP) from at  
 CC least one (TT), where each (TT) comprise a replication terminating  
 CC feature. In (M1), (EP) and target templates are incubated under  
 CC isothermal conditions or single set of conditions. The target templates  
 CC are nucleic acid sequences of interest. Each of (EP) comprises or  
 CC consists of a target complement portion, preferably nucleotides, where  
 CC the nucleotides consist of the target complement portion. Each (EP)  
 CC further comprises non-target complement portion. The method is known as  
 CC TEX (thermodynamic equilibrium extension of primers). The method is  
 CC useful for amplifying nucleic acid and for detecting nucleic acid  
 CC sequences which involve performing (M1), and detecting one or more of  
 CC the extended (EP). In (M1), only those sequences targeted by (EP) are  
 CC amplified, thus allowing specific sequences to be targeted for  
 CC amplification. Flexibility in the location of replication terminating  
 CC feature allows flexibility in targeting sequences. If a targeted sequence  
 CC is not present, the sequence will not be amplified. Multiple sequences  
 CC can be amplified in the same reaction by targeting multiple sequences  
 CC with (EP). Simultaneous amplification and detection is facilitated using  
 CC detection probes associated with a substrate. Multiplex detection can be  
 CC facilitate by an array of detection probes with different detection  
 CC probes at different locations of a substrate. The present sequence is a  
 CC synthetic template sequence used to demonstrate the method of the  
 CC invention.

Sequence 40 BP; 7 A; 8 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.059;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGGACCCAACTACTC 20  
 |||||  
 Db 31 TTTCGGACCCAACTACTC 12.

RESULT 56

AAQ98098  
 ID AAQ98098 standard; DNA; 46 BP.

AC AAQ98098;

DT 05-FEB-1996 (first entry)

DE Capture extender probe used in an improved sandwich hybridisation assay.

XX Probe; nucleotide; solution phase sandwich hybridisation assay;

KM competitive; analyte binding sequence; background signal reduction; ss.

OS Synthetic.

PN Key

PD misc\_binding

PF Location/Qualifiers

PT 34..46

PT /\*tag= a

PT /note= "binds to immobilised capture probe"

PA WO9516055-A1.

PI 15-JUN-1995.

PF 07-DEC-1994; 94WO-US014119.

PR 08-DEC-1993; 93US-00164388.

PA (CHIR ) CHIRON CORP.

PI Urdea MG, Fultz T, Warner BD, Collins M;

PI MPI; 1995-224335/29.

PT Soln. phase sandwich hybridisation assays for nucleic acid(s) - with  
 PT capture extender molecules or competitive oligo:nucleotide(s) to minimise  
 PT background signal, increasing sensitivity and selectivity.  
 PS Example 1; Page 33; 86bp; English.  
 CC AAQ98098-098099 are capture extender probes (CEs) used in a new improved  
 CC method of solution phase sandwich hybridisation assays. The capture  
 CC extender probes contain an analyte binding sequence (ABS) and a support  
 CC binding sequence (SBS) which hybridise to a sequence present in a capture  
 CC probe when immobilised on a solid support. The analyte binding sequences  
 CC are different in each capture extender probe and the capture probes  
 CC contain two CE-binding sequences, so that two different CE can bind to a  
 CC single capture probe. The new method minimises background signals (caused  
 CC by non-specific hybridisation), this improves both sensitivity and  
 CC selectivity of the assay without increasing cost or time

Sequence 46 BP; 9 A; 17 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.059;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGGACCCAACTACTC 20  
 |||||  
 Db 10 TTTCGGACCCAACTACTC 29

RESULT 57  
 ADQ54055/c



ID ADC54055 standard; cDNA; 57 BP.  
XX  
AC ADC54055;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Genotype 3 HCV 5' non-coding region fragment, SEQ ID NO:6.  
XX  
XX HCV, hepatitis C virus; classification; interferon therapy; genotype 3;  
KM MHCG3C; MHCG3C'; 5' non-coding region; ss.  
XX  
XX Hepatitis C virus.  
OS  
PN JP2002345467-A.  
XX  
PD 03-DEC-2002.  
XX  
PF 17-APR-2001; 2001JP-00118810.  
XX  
PR 23-OCT-2000; 2000JP-00322567.  
XX  
XX (SRLS-) SRL KK.  
PA  
XX WPI; 2003-460879/44.  
DR  
XX  
XX Probe and method for classification of hepatitis C virus (HCV) types used  
PT for forecast of therapeutic effect of interferon administration.  
XX  
XX  
PS Claim 10; SEQ ID NO 6; 15pp; Japanese.  
XX  
CC The invention relates to a nucleic acid probe for the classification of  
CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1am  
CC (type 1), MH2am (type 2) and MHCG3C/MHCG3C' (type 3). The probe can be  
CC used to classify HCV type to enable prediction of the success or  
CC otherwise of interferon therapy in a patient. The present sequence  
CC represents a specifically claimed HCV genotype 3 5' non-coding region  
CC fragment.  
XX  
XX Sequence 57 BP; 10 A; 15 C; 22 G; 10 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 20; DB 10; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.058;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCGGACCCCAACTACTC 20  
DB 46 TTCGGACCCCAACTACTC 27  
RESULT 59  
ACC80000/c  
ID ACC80000 standard; DNA; 60 BP.  
XX  
AC ACC80000;  
XX  
XX 12-SEP-2003 (first entry)  
DT  
XX Hepatitis C virus 60-mer oligonucleotide HCV0188 SEQ ID NO:1.  
DE  
XX Hepatitis C virus; HCV; HCV0188; control feature; polynucleotide array;  
KM diagnostic; screening; gene expression analysis; polymorphism detection;  
KM splice variant; ss.  
XX  
XX Hepatitis C virus.  
OS  
PN EP1262566-A2.  
XX  
PD 04-DEC-2002.  
XX  
PF 29-MAY-2002; 2002EP-00253745.  
XX  
PR 30-MAY-2001; 2001US-00870939.  
XX

PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
XX Amorese DA, Shannon KM, Collins PJ, Wolber PK;  
PI  
XX WPI; 2003-543475/52.  
DR  
XX  
XX Polynucleotide array for genetic applications, has two sets of multiple  
PT features, with features of first set having longer polynucleotide  
PT molecules (400 nucleotides) than features of second set with 100  
PT nucleotides.  
XX  
XX  
PS Disclosure; Page 9; 18pp; English.  
XX  
XX The present invention describes a polynucleotide array (1), which  
CC comprises a first set of multiple features, where each feature  
CC independently has first polynucleotide molecules (PM1) of at least 400  
CC nucleotides in length, and a second set of features, where each feature  
CC independently has second polynucleotide molecules (PM2) of no more than  
CC 100 nucleotides in length. Also described: (1) a kit comprising (1) and  
CC polynucleotide controls which are, or their complements are, at least 70%  
CC complementary to sequences of respective second polynucleotides; and (2)  
CC fabricating (M) a polynucleotide array, by forming a first set of  
CC multiple features on a substrate, with each feature independently having  
CC PM1 and forming a second set of features on the substrate, with each  
CC feature independently having PM2. (1) is useful in a method involving  
CC exposing (1) to control targets, such that the control targets hybridise  
CC at least 100 times more efficiently to respective second features than  
CC they do to any of the first features, and simultaneously exposing (1) to  
CC a sample, where the second set of features hybridise more efficiently  
CC with control targets than any of the first set features hybridise to any  
CC control targets. The method further involves reading the array to obtain  
CC an image representing the amount of polynucleotides which have bound to  
CC first and second set features, and evaluating locations of first features  
CC in the image using the locations of second features in the image. (1) is  
CC useful in diagnostic, screening, gene expression analysis, and other  
CC applications. (1) is also useful for detecting polymorphisms or splice  
CC variants. The present sequence represents a Hepatitis C virus control  
CC features related 60-mer oligonucleotide, designated HCV0188, which is  
CC given in the exemplification of the present invention  
XX  
SQ Sequence 60 BP; 10 A; 11 C; 24 G; 15 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 9; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0.058;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCGGACCCCAACTACTC 20  
DB 24 TTCGGACCCCAACTACTC 5  
RESULT 59  
ADC46965/c  
ID ADC46965 standard; DNA; 80 BP.  
XX  
AC ADC46965;  
XX  
XX 18-DEC-2003 (first entry)  
DT  
XX Synthesised bridge probe #SEQ ID 1.  
DE  
XX Oligonucleotide; amplification; gene detection; self-assembly; probe; ss.  
KM  
XX Synthetic.  
OS  
PN WO2003040367-A1.  
XX  
PD 15-MAY-2003.  
XX  
PF 30-OCT-2002; 2002WO-JP011321.  
XX  
PR 08-NOV-2001; 2001JP-00342709.  
XX  
XX 08-MAY-2002; 2002JP-00132402.  
XX

XX (SANKO) SANKO JUNYAKU CO LTD.  
 PA Usui M, Mitsuoka M, Haki C;  
 XX  
 PI  
 XX  
 DR WPI, 2003-441572/41.  
 XX

PT Self-assembly formed from amplified target gene and probe pairs for  
 XX simple and accurate detection of the target gene.  
 PS

XX Example Examples; Page 34; 123pp; Japanese.

XX The invention relates to a method for forming an oligonucleotide self-  
 CC assembly, in which oligonucleotides containing a target gene sequence are  
 CC first amplified by a conventional gene amplification method, and the  
 CC amplification product is then incorporated into the self-assembly by  
 CC reaction with one or more oligonucleotide probe pairs. Also disclosed is  
 CC the detection of a specific gene using the novel method. The  
 CC oligonucleotide probe pairs (which may consist of one pair, or two or  
 CC more different pairs) consist of at least three distinct hybridising  
 CC regions which are each complementary to a region on the other probe of  
 CC the pair, or to a region on the target oligonucleotide. Preferably each  
 CC complementary region includes at least one G-C coupling. The regions  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe pair may be in the internal part  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe pair, by hybridisation of  
 CC hybridised with the target oligonucleotides, each 3' or 5' terminal  
 CC portion of the probe dimer hybridizing to a different region on one or  
 CC other strand of the target oligonucleotide sequence. The probes may be  
 CC DNA, RNA, PNA or LNA. The 3' and/or 5' terminals of the probes may be  
 CC methylated. The oligonucleotides may be synthesised in the initial  
 CC amplification reaction from single or double stranded DNA or RNA and the  
 CC complementary may include ligation of a target sequence to sequences  
 CC complementary to the probe pairs. They may be enzymatically cleavable by  
 CC exonuclease, RNase H or restriction enzymes. This method is an accurate,  
 CC specific and sensitive method for the detection of a target gene sequence  
 CC at low cost and without complicated procedures or apparatus. The current  
 CC sequence represents a synthesised bridge probe utilised in an example  
 CC from the invention.  
 CC

SO Sequence 80 BP; 16 A; 21 C; 26 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
 |||||  
 DB 78 TTGGGACCCCACTACTC 59

RESULT 60  
 ADC46966  
 ID ADC46966 standard; DNA; 80 BP.  
 AC  
 XX ADC46966;  
 XX

DT 18-DEC-2003 (first entry)  
 XX  
 DE Synthesised bridge probe #SEQ ID 2.  
 XX

KM Oligonucleotide; amplification; gene detection; self-assembly; probe; ss.  
 XX

OS Synthetic.  
 XX

PN W02003040367-A1.  
 XX

XX 15-MAY-2003.  
 PD

PF 30-OCT-2002; 2002MO-JP011321.  
 XX

PR 08-NOV-2001; 2001JP-00342709.  
 PR 08-MAY-2002; 2002JP-00132402.  
 XX

XX (SANKO) SANKO JUNYAKU CO LTD.  
 PA Usui M, Mitsuoka M, Haki C;  
 XX

PI Usui M, Mitsuoka M, Haki C;  
 XX  
 DR WPI, 2003-441572/41.  
 XX

PT Self-assembly formed from amplified target gene and probe pairs for  
 XX simple and accurate detection of the target gene.  
 PS

XX Example Examples; Page 34-35; 123pp; Japanese.

XX The invention relates to a method for forming an oligonucleotide self-  
 CC assembly, in which oligonucleotides containing a target gene sequence are  
 CC first amplified by a conventional gene amplification method, and the  
 CC amplification product is then incorporated into the self-assembly by  
 CC reaction with one or more oligonucleotide probe pairs. Also disclosed is  
 CC the detection of a specific gene using the novel method. The  
 CC oligonucleotide probe pairs (which may consist of one pair, or two or  
 CC more different pairs) consist of at least three distinct hybridising  
 CC regions which are each complementary to a region on the other probe of  
 CC the pair, or to a region on the target oligonucleotide. Preferably each  
 CC complementary region includes at least one G-C coupling. The regions  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe pair may be in the internal part  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe pair, by hybridisation of  
 CC hybridised with the target oligonucleotides, each 3' or 5' terminal  
 CC portion of the probe dimer hybridizing to a different region on one or  
 CC other strand of the target oligonucleotide sequence. The probes may be  
 CC DNA, RNA, PNA or LNA. The 3' and/or 5' terminals of the probes may be  
 CC methylated. The oligonucleotides may be synthesised in the initial  
 CC amplification reaction from single or double stranded DNA or RNA and the  
 CC complementary may include ligation of a target sequence to sequences  
 CC complementary to the probe pairs. They may be enzymatically cleavable by  
 CC exonuclease, RNase H or restriction enzymes. This method is an accurate,  
 CC specific and sensitive method for the detection of a target gene sequence  
 CC at low cost and without complicated procedures or apparatus. The current  
 CC sequence represents a synthesised bridge probe utilised in an example  
 CC from the invention.  
 CC

SO Sequence 80 BP; 17 A; 26 C; 21 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
 |||||  
 DB 3 TTGGGACCCCACTACTC 22

RESULT 61  
 AD080850  
 ID AD080850 standard; DNA; 100 BP.  
 AC  
 XX AD080850;  
 XX

DT 29-JUL-2004 (first entry)  
 XX

DE Hepatitis C virus reference DNA with partial homology to target Seqid 3.  
 XX

KM competitive PCR; quantitative; virus; viral infection; viraemia; ds.  
 XX

OS Hepatitis C virus.  
 XX

PN JP2004113194-A.  
 XX

PD 15-APR-2004.  
 XX

```

PF 27-SEP-2002; 2002JP-00284452.
XX
PR 27-SEP-2002; 2002JP-00284452.
XX
PA (TOKE ) TOSHIBA KK.
XX
XX WPI; 2004-360137/34.
XX
DR Quantitating target nucleic acid involves competitively amplifying target
PT nucleic acid and reference sequences containing homologous sequences with
PT respect to target, and determining amplified product obtained for the
PT sequences.
XX
PS Claim 6; SEQ ID NO 3; 26pp; Japanese.
XX
CC This invention relates to a novel method for quantitating the amount of
CC target nucleic acid molecules present in a sample. Specifically, it
CC refers to competitively amplifying (using the same primer set) the target
CC oligonucleotides and a number of reference sequences that are partially
CC homologous to the target, where the concentration for each set is equal
CC and amplified product obtained for each type of sequence can be
CC determined and measured. The present invention describes this method as
CC useful for quantitating target nucleic acids such as those derived from a
CC viral genome or mRNA, in order to establish the presence and identity of
CC a viral infection, as well as the degree of viremia. Accordingly, the
CC method also enables measurement of the degree of responsiveness following
CC treatment with a medicament by measuring target mRNA in the subject. This
CC polynucleotide sequence is reference DNA from the hepatitis C virus that
CC shares partial homology with the target nucleic acid of the invention.
XX
SQ Sequence 100 BP; 21 A; 36 C; 25 G; 18 T; 0 U; 0 Other;
XX
QY Query Match 100.0%; Score 20; DB 12; Length 100;
DB Beat Local Similarity 100.0%; Pred.No. 0.056;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
69 TTGCGAGCCCAACTACTC 20
|||||
69 TTGCGAGCCCAACTACTC 88
RESULT 62
AAT09185
ID AAT09185 standard; DNA; 108 BP.
XX
XX AAT09185;
XX
XX 21-OCT-2004 (revised)
DT 21-OCT-2004 (revised)
DT 14-AUG-1996 (first entry)
XX
XX Hepatitis C virus specific amp-probe-2 (HCV C).
DE
XX
XX Ligase dependent polymerase chain reaction; LD-PCR; probe; hybridisation;
KM ligand binding pair; ligase; paramagnetic bead; primer; amplification;
KM hepatitis; untranslated region; UTR; rRNA; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_binding 1..26
FT /*tag= a
FT /bound_moiety
FT /note="complementary to a fragment of the hepatitis C
FT virus 5' untranslated region"
FT misc_binding 83..108
FT /*tag= b
FT /bound_moiety
FT /note="complementary to a fragment of the hepatitis C
FT virus 5' untranslated region"
XX
XX W09535390-A1.
XX
XX 28-DEC-1995.
XX
XX

```

XX	PF	14-JUN-1995;	95WO-US007671.
XX	PR	22-JUN-1994;	94US-00263937.
XX	PA	(MOUNT ) MOUNT SINAI SCHOOL MEDICINE.	
XX	P1	Zhang DY;	
XX	DR	WPI, 1996-058427/06.	
PT	PT	Ligation dependent polymerase chain reaction - for the detection of	
XX	PS	Infectious pathogens and abnormal human genes, e.g. HIV and neoplasia.	
XX	XX	Example 8; Page 62; 100P; English.	
CC	CC	A novel method of detecting a target nucleic acid (TNA) sequence involves	
CC	CC	use of the ligase dependent polymerase chain reaction method (LD-PCR). In	
CC	CC	this method, two probes are provided. The first probe contains a region	
CC	CC	at the 5' end which is complementary and will hybridise with the TNA, the	
CC	CC	3' end of the first probe is generic and is bound to one half of a ligand	
CC	CC	binding pair (LBP). The second probe contains a region at the 5' end	
CC	CC	which is complementary to a region in the TNA which is immediately	
CC	CC	adjacent to the complementary region of the first probe. When the probes	
CC	CC	are bound to the TNA, they can be ligated together using a conventional	
CC	CC	ligase. The TNA:ligated probe complex can be isolated by binding the	
CC	CC	first probe to a paramagnetic bead to which is attached the second half	
CC	CC	of the LBP. The TNA can be dissociated from the ligated probe complex	
CC	CC	which can then be detected either by a label attached to the second	
CC	CC	probe, by using an external probe or by PCR using the ligated probes as a	
CC	CC	template. The capture probes AAT09176-7 are used to isolate a region of	
CC	CC	the Hepatitis C virus 5' untranslated region. This probe can be used to	
CC	CC	detect this region by hybridisation such that the 5' and 3' ends of the	
CC	CC	probe lie adjacent to each other when hybridised to the TNA, resulting in	
CC	CC	closed circular mol. after ligation. The ligated sequence can	
CC	CC	subsequently be detected by PCR amplification with the primers AAT09181-2	
CC	CC		
CC	CC		
CC	CC		
XX	SQ	Revised record issued on 21-OCT-2004 : Correction to Feature Table Key	
XX	SQ	Sequence 108 BP; 28 A; 34 C; 21 G; 25 T; 0 U; 0 Other:	
		Query Match 100.0%; Score 20; DB 2; Length 108;	
		Best Local Similarity 100.0%; Pred. No. 0.056;	
		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY		1 TTTCGGACCCCAACTACTC 20	
Db		4 TTTCGGACCCCAACTACTC 23	
<hr/>			
RESULT 63			
ID	AAV20727	AAV20727 standard; DNA; 108 BP.	
XX	AAV20727;		
XX	AC		
XX	DT	17-JUL-1998 (first entry)	
XX	DE	Hepatitis C virus probe SEQ ID NO:31.	
XX	KM	Hepatitis C virus; HCV; HIV; probe; detection; capture; amplification;	
XX	KX	paramagnetic particle; ligation; ss.	
OS	OS	Synthetic.	
XX	OS	Hepatitis C virus.	
XX	PN	MO9804745-A1.	
XX	PD	05-FEB-1998.	
XX	PF	30-JUL-1997; 97WO-US013390.	
XX	RR	31-JUL-1996; 96US-00690495.	

XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 XX  
 XX  
 PI Zhang DY, Brandwein M;  
 XX  
 XX  
 DR WPI, 1998-159153/14.

XX  
 XX  
 PT Detection of target nucleic acids in samples - using capture and  
 PT amplification probes, paramagnetic particles and ligation to form a  
 XX nucleotide sequence which can be detected.  
 XX

XX Example 8; Page 70; 136pp; English.

XX The present sequence represents a probe used in an example of the present  
 CC invention for the detection of HCV RNA in a sample. The present invention  
 CC describes methods for: (A) detecting a target nucleic acid (NA) in a  
 CC sample; (B) in situ detection of a target NA in a sample; (C) detecting  
 CC an antigen in a sample; and (D) detecting an antibody in a sample. The  
 CC methods can be used for the rapid automated detection and monitoring of  
 CC pathogenic organisms, as well as the detection of abnormal genes in an  
 CC individual. The methods allow for isolation, amplification and detection  
 CC of NA sequences corresponding to the target NA to be carried out in the  
 CC same receptacle, e.g. tube or micro-well plate. The method also allows  
 CC for standardisation of conditions, because only a pair of generic  
 CC amplification probes may be utilised in the present method for detecting  
 CC a variety of target NAs, thus allowing efficient multiplex amplification.  
 CC The method also allows the direct detection of RNA by probe amplification.  
 CC without the need for DNA template production. The amplification probes,  
 CC which may be covalently joined end to end, form a contiguous ligated  
 CC amplification sequence. The assembly of the amplifiable DNA by ligation  
 CC increase specificity, and makes possible the detection of a single  
 CC mutation in a target  
 XX

SO Sequence 108 BP; 28 A; 34 C; 21 G; 25 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.056;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 |||||  
 Db 4 TTGGGACCCCAACTACTC 23

RESULT 64  
 AAV22777

ID AAV22777 standard; DNA; 108 BP.

AC AAV22777;

XX 27-AUG-2003 (revised)

DT 22-JUL-1998 (first entry)

DE Amp-probe-2 (HCV C) for detecting Hepatitis C virus 5' UTR RNA.

KM Probe; Amp-probe-2 (HCV C); automated detection; Mycobacteria;  
 KM nucleic acid; monitoring; pathogenic organism; abnormal gene; ss.

OS Synthetic.  
 OS Hepatitis C virus.

XX W09804746-A1.

XX 05-FEB-1998.

XX 30-JUL-1997; 97MO-US013391.

XX 31-JUL-1996; 96US-00690494.

PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.

PI Zhang DY, Brandwein M, Hsu H TCH;

DR WPI, 1998-159154/14.

XX  
 XX  
 PT Detection of target nucleic acids in samples - using capture and  
 PT amplification probes, paramagnetic particles and ligation to form a  
 XX nucleotide sequence which is amplified.  
 XX

PS Example 8; Page 67; 142pp; English.

XX The present sequence represents a probe, designated Amp-probe-2 (HCV C),  
 CC used for detecting the 5' untranslated region (5' UTR) of Hepatitis C  
 CC virus RNA. Nucleotides 1-26 at the 5' end of the probe are complementary  
 CC to a portion of the 5'UTR of the HCV genome. The probe is used to  
 CC exemplify the method of the invention, which describes the detection of a  
 CC target nucleic acid in a sample. The method comprises contacting the  
 CC paramagnetic particles coated with a ligand binding moiety. Each  
 CC capture/amplification probe has a ligand bound to its non-complementary  
 CC sequence that is capable of binding to and forming an affinity pair with  
 CC the ligand binding moiety coated onto the paramagnetic particles. The  
 CC oligonucleotide probes also comprise a probe that can be circularised, by  
 CC having the 3' and 5' ends ligated together. The circularised probe is  
 CC amplified with a DNA polymerase having strand displacement activity under  
 CC conditions whereby an extension primer is extended around the circle for  
 CC multiple revolutions to form a single stranded DNA of repeating units  
 CC complementary to the sequence of the circular probe, and multiple copies  
 CC of a second extension primer hybridise to complementary regions of the  
 CC single stranded DNA and are extended by the DNA polymerase to provide  
 CC extension products. The extension products of the second extension primer  
 CC displace downstream copies of the second extension primer and  
 CC corresponding extension products to provide displaced single strands to  
 CC which multiple copies of the first extension primer bind and are extended  
 CC by the DNA polymerase. The amplified DNA is detected. The method can be  
 CC used for the rapid automated detection and monitoring of pathogenic  
 CC organisms as well as the detection of abnormal genes in an individual.  
 CC (Updated on 27-AUG-2003 to correct 05 field.)  
 XX

SO Sequence 108 BP; 28 A; 34 C; 21 G; 25 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.056;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 |||||  
 Db 4 TTGGGACCCCAACTACTC 23

RESULT 65

ABK86847

ID ABK86847 standard; DNA; 108 BP.

XX ABK86847;

DT 24-SEP-2002 (first entry)

DE Hepatitis C virus C amp-probe-2.

KM Hepatitis C; RNA detection; ss; probe; nucleic acid detection;  
 KM infectious disease.

XX Hepatitis C virus.

XX W0200244339-A2.

XX 06-JUN-2002.

XX 03-DEC-2001; 2001MO-US045822.

XX 01-DEC-2000; 2000US-00728265.

PA (ZHAN/) ZHANG D Y.  
 PA (BRAN/) BRANDWEIN M.  
 PA (HSU/) HSU H T C H.



CC oligonucleotide probe under conditions that allow hybridisation between  
 CC complementary sequences in the target nucleic acid and the circular  
 CC oligonucleotide probe, adding at least one forward primer comprising a  
 CC sequence complementary to a portion of the circular oligonucleotide  
 CC probe, adding an oligonucleotide primer pair comprising a first primer  
 CC and a second primer where the first primer of the pair comprises a first  
 CC sequence that is substantially identical to a portion of the circular  
 CC oligonucleotide probe, a second sequence that is complementary to the  
 CC second primer of the pair, and a signal generating moiety, the second  
 CC primer of the pair comprises a sequence that is complementary to the  
 CC first primer and a moiety capable of quenching, masking or inhibiting the  
 CC activity of the signal generating moiety, and when the first primer and  
 CC the second primer are bound to one another, the signal is inhibited,  
 CC adding at least one reverse primer comprising a sequence that is  
 CC substantially identical to a portion of the circular oligonucleotide  
 CC probe, adding a DNA polymerase, and amplifying the circular  
 CC oligonucleotide probe and separating the signal generating moiety and the  
 CC quenching, masking or inhibitory moiety to generate a signal, where  
 CC the detection of signal indicates the presence of the target nucleic acid in  
 CC the sample. Also included are a kit for (M1) and amplifying (M2) a  
 CC circular nucleic acid sequence. In (M1), the circular oligonucleotide  
 CC probe is formed by ligating the 3' and 5' ends of linear oligonucleotide  
 CC sequences, comprising 3' and 5' ends regions complementary to adjacent  
 CC hybridisation between complementary sequences in the target nucleic acid  
 CC and the linear oligonucleotide probe. The circular probe is amplified  
 CC using an amplification method chosen from polymerase chain reaction,  
 CC strand displacement amplification, transcription mediated amplification,  
 CC ramification-extension amplification method (RAM) and primer extension.  
 CC (M1) is useful for detecting a target nucleic acid in a sample. (M2) is  
 CC useful for amplification of genomic DNA and total mRNAs expressed in  
 CC cells and for analysing differential mRNA expression. (M1) is useful for  
 CC detecting genetic variations in nucleic acids in sample from patients  
 CC with genetic diseases or neoplasia. The DNA and/or mRNA amplified by (M2)  
 CC is used in techniques developed for detection of infectious agents, and  
 CC detection of normal and abnormal genes. (M1) is used in clinical assays  
 CC as to detect and monitor pathogenic microorganisms in a test sample, as well  
 CC as to detect abnormal genes in an individual. (M1) is useful for routine  
 CC diagnostic testing in a clinical laboratory setting. The present sequence  
 CC is an amplification probe used to demonstrate the above methods.

SQ Sequence 108 BP; 28 A; 34 C; 21 G; 25 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.056;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTCTC 20  
 |||||  
 DB 4 TTGGGACCCCACTACTCTC 23

RESULT 68  
 ADC54054/C

ID . ADC54054 standard; cDNA; 126 BP.

AC ADC54054;

DT 18-DEC-2003 (first entry)

XX Genotype 3 HCV 5' non-coding region fragment, SEQ ID NO:5.

KW HCV; hepatitis C virus; classification; interferon therapy; genotype 3;

OS Hepatitis C virus.

PN JP2002345467-A.

PD 03-DEC-2002.

PF 17-APR-2001; 2001JP-00118810.

PR 23-OCT-2000; 2000JP-00322567.

PA (SRUS-) SRL KK.

DR WPI; 2003-460879/44.

PT Probe and method for classification of hepatitis C virus (HCV) types used  
 for forecast of therapeutic effect of interferon administration.

PS Claim 10; SEQ ID NO 5; 15bp; Japanese.

CC The invention relates to a nucleic acid probe for the classification of  
 CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are 1H1am1  
 CC (type 1), MH2am1 (type 2) and MHG3C+MHG3C' (type 3). The probe can be  
 CC used to classify HCV type to enable prediction of the success or  
 CC otherwise of interferon therapy in a patient. The present sequence  
 CC represents a specifically claimed HCV genotype 3 5' non-coding region  
 CC fragment.

SQ Sequence 126 BP; 26 A; 34 C; 40 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 0.056;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTCTC 20  
 |||||  
 DB 115 TTGGGACCCCACTACTCTC 96

RESULT 69

AA510487/C

ID AA510487 standard; RNA; 163 BP.

AC AA510487;

DT 24-OCT-2001 (first entry)

DE HCV 5'-UTR domain IIRdel1 EMSA RNA probe.

KW HCV 5'-UTR; minimal IRES; mIRES; internal ribosome entry site; eIF3;

KM RNA electrophoretic gel mobility shift assay; EMSA; mutant; ss.

OS Hepatitis C virus; strain Ia M67463.

XX Synthetic.

Key

misc\_binding

misc\_binding

misc\_binding

misc\_binding

stem\_loop

misc\_binding

misc\_binding

misc\_binding

misc\_binding

Location/Qualifiers  
 1..5  
 /tag= a  
 /bound\_moiety= "Forms double stranded region with bases  
 159-163"  
 7..10  
 /tag= b  
 /bound\_moiety= "Forms double stranded region with bases  
 157-154"  
 11..19  
 /tag= c  
 /bound\_moiety= "Forms double stranded region with bases  
 122-114"  
 20..23  
 /tag= d  
 /bound\_moiety= "Forms double stranded region with bases  
 112-109"  
 26..41  
 /tag= e  
 /note= "Designated as IIRa"  
 42..51  
 /tag= f  
 /bound\_moiety= "Forms double stranded region with bases  
 97-88"  
 54..55  
 /tag= g

FT	/bound_moiety= "Forms double stranded region' with bases
FT	82-82"
FT	57. .80
FT	/*tag= h
FT	/note= "Designated as IIID"
FT	82. .83
FT	/*tag= i
FT	/bound_moiety= "Forms double stranded region with bases
FT	55-54"
FT	88. .97
FT	/*tag= j
FT	/bound_moiety= "Forms double stranded region with bases
FT	51-42"
FT	99. .108
FT	/*tag= k
FT	/note= "Designated as IIIC"
FT	109. .112
FT	/*tag= l
FT	/bound_moiety= "Forms double stranded region with bases
FT	23-20"
FT	114. .122
FT	/*tag= m
FT	/bound_moiety= "Forms double stranded region with bases
FT	19-11"
FT	123. .126
FT	/*tag= n
FT	/bound_moiety= "Forms double stranded region with bases
FT	149-146"
FT	129. .144
FT	/*tag= o
FT	/note= "Designated as IIIA"
FT	146. .149
FT	/*tag= p
FT	/bound_moiety= "Forms double stranded region with bases
FT	126-123"
FT	154. .157
FT	/*tag= q
FT	/bound_moiety= "Forms double stranded region with bases
FT	10-7"
FT	159. .163
FT	/*tag= r
FT	/bound_moiety= "Forms double stranded region with bases 5
FT	-1"
XX	
PN	WO200144266-A2.
PN	
PD	21-JUN-2001.
XX	
PF	18-DEC-2000; 2000WO-GB004862.
PR	
PR	16-DEC-1999; 99GB-00029820.
PR	22-DEC-1999; 99US-0171804P.
PA	(RIBO-) RIBOTARGETS LTD.
XX	
P1	Karn J, Walker S;
DR	WPI, 2001-465050/50.
XX	
PT	Nucleotide sequences derived from Hepatitis C virus, useful for
PT	identifying candidate antiviral compounds.
PS	Disclosure, Fig 5B; 48pp; English.
XX	
CC	The present sequence represents Hepatitis C virus (HCV) 5'-UTR domain
CC	Iridelation RNA probe used in a RNA electrophoretic gel mobility shift
CC	assay (EMSA). The present sequence is described in an invention relating
CC	to a novel compound comprising nucleotide sequences capable of annealing
CC	and which is derived from a 5'-untranslated region (UTR) of HCV which is
CC	essential for binding of eIF3 (eukaryotic initiation factor 3). The
CC	invention particularly relates to a sub-region of the HCV 5'-UTR referred
CC	to as the minimal internal ribosome entry site (MIREIS) which can be used
CC	to identify drugs which inhibit HCV translation initiation. The compounds

[illegible]

Db 179 TTGGGACCCCAACTACTC 160

RESULT 71  
AAQ43068/c  
ID AAQ43068 standard; cDNA; 184 BP.

XX AAQ43068;

XX 25-MAR-2003 (revised)  
XX 23-SEP-1993 (first entry)

XX -255 to -62 region of 5' non-coding region of HCV from donor E-b17.

XX Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
XX NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.

XX Hepatitis C virus.

XX WO9310239-A2.

XX 27-MAY-1993.

XX 20-NOV-1992; 92MO-GB002143.

XX 21-NOV-1991; 91GB-00024696.

XX 24-JUN-1992; 92GB-00013362.

XX (COMM-) COMMON SERVICES AGENCY.

XX Simmonds P, Chan S, Yap PL;

XX WPI; 1993-182554/22.

XX DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for  
XX diagnosing and treating HCV infection, screening blood samples and  
XX identifying different HCV types.

XX Disclosure; Fig 1; 120pp; English.

XX The sequences given in AAQ43058-75 show the -255 to -62 non-coding region  
XX of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
XX variants. Analysis of this region revealed the existence of three  
XX distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
XX the groups identified were similar to those of HCV variants termed type 1  
XX and 2, whilst the third appeared to represent a novel virus type.  
XX Comparison of other regions of the genome, eg. the NS-5 region (see also  
XX AAR37923-26), showed a high degree of sequence diversity with type 3  
XX being phylogenetically different to type 1 and 2. The same degree  
XX of differentiation was noted in the NS-3 (see AAR37927-30) and core region  
XX (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
XX 2003 to correct PN field.)

XX Sequence 184 BP; 34 A; 55 C; 59 G; 36 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 2; Length 184;  
XX Best Local Similarity 100.0%; Pred. No. 0.055;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 179 TTGGGACCCCAACTACTC 160

RESULT 72  
AAQ43060/c  
ID AAQ43060 standard; cDNA; 184 BP.

XX AAQ43060;

XX 25-MAR-2003 (revised)  
XX 23-SEP-1993 (first entry)

XX -255 to -62 portion of 5' non-coding region of HCV from donors E-b7.

XX Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
XX NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.

XX Hepatitis C virus.

XX WO9310239-A2.

XX 27-MAY-1993.

XX 20-NOV-1992; 92MO-GB002143.

XX 21-NOV-1991; 91GB-00024696.

XX 24-JUN-1992; 92GB-00013362.

XX (COMM-) COMMON SERVICES AGENCY.

XX Simmonds P, Chan S, Yap PL;

XX WPI; 1993-182554/22.

XX DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for  
XX diagnosing and treating HCV infection, screening blood samples and  
XX identifying different HCV types.

XX Disclosure; Fig 1; 120pp; English.

XX The sequences given in AAQ43058-75 show the -255 to -62 non-coding region  
XX of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
XX variants. Analysis of this region revealed the existence of three  
XX distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
XX the groups identified were similar to those of HCV variants termed type 1  
XX and 2, whilst the third appeared to represent a novel virus type.  
XX Comparison of other regions of the genome, eg. the NS-5 region (see also  
XX AAR37923-26), showed a high degree of sequence diversity with type 3  
XX being phylogenetically different to type 1 and 2. The same degree  
XX of differentiation was noted in the NS-3 (see AAR37927-30) and core region  
XX (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
XX 2003 to correct PN field.)

XX Sequence 184 BP; 35 A; 59 C; 58 G; 32 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 2; Length 184;  
XX Best Local Similarity 100.0%; Pred. No. 0.055;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 179 TTGGGACCCCAACTACTC 160

RESULT 73  
AAQ43067/c  
ID AAQ43067 standard; cDNA; 184 BP.

XX AAQ43067;

XX 25-MAR-2003 (revised)  
XX 23-SEP-1993 (first entry)

XX -255 to -62 region of 5' non-coding region of HCV from donor E-b16.

XX Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
XX NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.

XX Hepatitis C virus.

XX WO9310239-A2.

XX 27-MAY-1993.



```

PF 20-NOV-1992; 92WO-GB002143.
XX
PR 21-NOV-1991; 91GB-00024696.
PR 24-JUN-1992; 92GB-00013362.
XX
PA (COMM-) COMMON SERVICES AGENCY.
XX
PI Simmonds P, Chan S, Yap PL;
XX
DR WPI; 1993-182554/22.
XX
PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
PT diagnosing and treating HCV infection, screening blood samples and
PT identifying different HCV types.
XX
PS Disclosure; Fig 1; 120pp; English.
XX
CC The sequences given in AAQ43058-75 show the -255 to -62 non-coding region
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV
CC variants. Analysis of this region revealed the existence of three
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of
CC the groups identified were similar to those of HCV variants termed type 1
CC and 2, whilst the third appeared to represent a novel virus type.
CC Comparison of other regions of the genome, eg. the NS-5 region (see also
CC AAR37923-26), showed a high degree of sequence diversity with type 3
CC being phylogenetically different to type 1 and 2. The same degree
CC differentiation was noted in the NS-3 (see AAR37927-30) and core region
CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 184 BP; 34 A; 55 C; 59 G; 36 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCCGCGACCAACTACTC 20
Db 179 TTCCGCGACCAACTACTC 160
XX
RESULT 74
AAT11272
ID AAT11272 standard; RNA; 186 BP.
XX
AC AAT11272;
XX
DT 26-JUN-1996 (first entry)
XX
DE Hepatitis C virus partial 5'-UTR antisense RNA AS15.
XX
KW Antisense; therapy; complementary; HCV; 5'-untranslated region;
KW hepatitis C virus; inhibition; infection; treatment; stem-loop;
KW clone 2-1; ss.
XX
OS Hepatitis C virus.
XX
PN JP07303485-A.
XX
PD 21-NOV-1995.
XX
PF 13-MAY-1994; 94JP-00124609.
XX
PR 13-MAY-1994; 94JP-00124609.
XX
PA (TOFU) TONEN CORP.
XX
DR WPI; 1996-035187/04.
XX
PT Hepatitis C virus (HCV) anti-sense RNA - inhibits HCV structural gene
PT expression in vivo for treatment of HCV infection.
XX
PS Claim 2; Page 10; 12pp; Japanese.

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XX
CC The present sequence is a specifically claimed example of RNA that is
CC complementary (i.e. antisense) to part of the 5'-untranslated region of
CC the hepatitis C virus genome sequence contained in clone 2-1. The 5'-UTR
CC includes several stem-loop sequences. The antisense RNA is useful for
CC inhibiting expression of HCV structural genes and thereby inhibiting
CC viral replication in vivo. The antisense therapy can be used in addition
CC to conventional interferon treatment of HCV infections
XX
SQ Sequence 186 BP; 41 A; 65 C; 48 G; 0 T; 32 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 186;
Best Local Similarity 80.0%; Pred. No. 0.055;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCCGCGACCAACTACTC 20
Db 43 TTCCGCGACCAACTACTC 62
XX
RESULT 75
AAQ43059/C
ID AAQ43059 standard; cDNA; 187 BP.
XX
AC AAQ43059;
XX
DT 25-MAR-2003 (revised)
DT 23-SEP-1993 (first entry)
XX
DE -255 to -62 portion of 5' non-coding region of HCV from donors E-b2-6.
XX
KW Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;
KW NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.
XX
OS Hepatitis C virus.
XX
PN WO9310239-A2.
XX
PD 27-MAY-1993.
XX
PF 20-NOV-1992; 92WO-GB002143.
XX
PR 21-NOV-1991; 91GB-00024696.
XX
PR 24-JUN-1992; 92GB-00013362.
XX
PA (COMM-) COMMON SERVICES AGENCY.
XX
PI Simmonds P, Chan S, Yap PL;
XX
DR WPI; 1993-182554/22.
XX
PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
PT diagnosing and treating HCV infection, screening blood samples and
PT identifying different HCV types.
XX
PS Disclosure; Fig 1; 120pp; English.
XX
CC The sequences given in AAQ43058-75 show the -255 to -62 non-coding region
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV
CC variants. Analysis of this region revealed the existence of three
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of
CC the groups identified were similar to those of HCV variants termed type 1
CC and 2, whilst the third appeared to represent a novel virus type.
CC Comparison of other regions of the genome, eg. the NS-5 region (see also
CC AAR37923-26), showed a high degree of sequence diversity with type 3
CC being phylogenetically different to type 1 and 2. The same degree
CC differentiation was noted in the NS-3 (see AAR37927-30) and core region
CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 187 BP; 36 A; 57 C; 60 G; 34 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 187;

```

Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
182 TTCCGACCCCACTACTC 163

RESULT 76

AA10486/C  
ID AA10486 standard; RNA; 187 BP.

AA10486;

11-SEP-2003 (revised)  
24-OCT-2001 (first entry)

HCV 5'-UTR domain III EMSA RNA probe.

HCV 5'-UTR; minimal IRES; MIREs; internal ribosome entry site; eIF3,  
eukaryotic initiation factor 3; HCV translation initiation; antiviral;  
RNA electrophoretic gel mobility shift assay; EMSA; ss.

Hepatitis C virus; strain Ia M67463.

Location/Qualifiers

Key

1..3  
/\*tag= a

/\*tag= a  
/\*tag= a  
/\*tag= b  
/\*tag= b  
/\*tag= c  
/\*tag= c  
/\*tag= d  
/\*tag= d  
/\*tag= e  
/\*tag= e  
/\*tag= f  
/\*tag= f  
/\*tag= g  
/\*tag= g  
/\*tag= h  
/\*tag= h  
/\*tag= i  
/\*tag= i  
/\*tag= j  
/\*tag= j  
/\*tag= k  
/\*tag= k  
/\*tag= l  
/\*tag= l  
/\*tag= m  
/\*tag= m

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

FT /bound\_moiety= "Forms double stranded region with bases

FT misc\_feature

FT 112..114  
/\*tag= n  
/note= "eIF3 toeprint"

FT misc\_binding

FT 114..122  
/\*tag= o  
/bound\_moiety= "Forms double stranded region with bases

FT misc\_binding

FT 123..126  
/\*tag= p  
/bound\_moiety= "Forms double stranded region with bases

FT stem\_loop

FT 129..144  
/\*tag= q  
/note= "Designated as IIId"

FT misc\_binding

FT 146..149  
/\*tag= r  
/bound\_moiety= "Forms double stranded region with bases

FT misc\_binding

FT 154..157  
/\*tag= s  
/bound\_moiety= "Forms double stranded region with bases

FT misc\_binding

FT 159..160  
/\*tag= t  
/bound\_moiety= "Forms double stranded region with bases

FT misc\_binding

FT 161..172  
/\*tag= u  
/note= "Designated as IIId"

FT stem\_loop

FT 173..184  
/\*tag= v  
/tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT misc\_binding

FT 185..187  
/\*tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT stem\_loop

FT 161..172  
/\*tag= u  
/note= "Designated as IIId"

FT stem\_loop

FT 173..184  
/\*tag= v  
/tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT misc\_binding

FT 185..187  
/\*tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT stem\_loop

FT 161..172  
/\*tag= u  
/note= "Designated as IIId"

FT stem\_loop

FT 173..184  
/\*tag= v  
/tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT misc\_binding

FT 185..187  
/\*tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT stem\_loop

FT 161..172  
/\*tag= u  
/note= "Designated as IIId"

FT stem\_loop

FT 173..184  
/\*tag= v  
/tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT misc\_binding

FT 185..187  
/\*tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT stem\_loop

FT 161..172  
/\*tag= u  
/note= "Designated as IIId"

FT stem\_loop

FT 173..184  
/\*tag= v  
/tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT misc\_binding

FT 185..187  
/\*tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT stem\_loop

FT 161..172  
/\*tag= u  
/note= "Designated as IIId"

FT stem\_loop

FT 173..184  
/\*tag= v  
/tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT misc\_binding

FT 185..187  
/\*tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT stem\_loop

FT 161..172  
/\*tag= u  
/note= "Designated as IIId"

FT stem\_loop

FT 173..184  
/\*tag= v  
/tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT misc\_binding

FT 185..187  
/\*tag= w  
/bound\_moiety= "Forms double stranded region with bases 3

FT stem\_loop

The present sequence represents Hepatitis C virus (HCV) 5'-UTR domain III RNA probe used in a RNA electrophoretic gel mobility shift assay (EMSA). The present sequence is described in an invention relating to a novel compound comprising nucleotide sequences capable of annealing and which is derived from a 5'-untranslated region (UTR) of HCV which is essential for binding of eIF3 (eukaryotic initiation factor 3). The invention particularly relates to a sub-region of the HCV 5'-UTR referred to as the minimal internal ribosome entry site (IRES) which can be used to identify drugs which inhibit HCV translation initiation. The compounds of the invention may be used to screen for potential HCV antiviral compounds. Assays based on the IRES enable potential antivirals to be screened in a cheaper and easier way. It allows rapid assaying with a small volume of material and are suitable to parallel processing.

(Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 187 BP; 35 A; 48 C; 64 G; 0 T; 40 U; 0 Other;  
Query Match 100.0%; Score 20; DB 4; Length 187;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCGGACCCCAACTACTC 20  
DB 146 TTCGGACCCCAACTACTC 127

RESULT 77  
AAQ43073/C  
ID AAQ43073 standard; cDNA; 194 BP.  
XX AAQ43073;  
AC  
XX 25-MAR-2003 (revised)  
DT 23-SEP-1993 (first entry)  
XX  
DE -255 to -62 region of 5' non-coding region of HCV S1.  
XX  
XX Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
KM NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.  
XX  
XX Hepatitis C virus.  
OS  
XX WO9310239-A2.  
FN  
XX 27-MAY-1993.  
PD  
XX 20-NOV-1992; 92MO-GB002143.  
PF  
XX 21-NOV-1991; 91GB-00024696.  
PR 24-JUN-1992; 92GB-00013362.  
XX  
XX (COMM-) COMMON SERVICES AGENCY.  
PA  
XX Simmonds P, Chan S, Yap PL;  
FI  
XX WPI; 1993-182554/22.  
DR  
XX DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for  
PT diagnosing and treating HCV infection, screening blood samples and  
PT identifying different HCV types.  
PT  
XX  
XX Disclosure; Fig 1; 120pp; English.  
PS  
XX The sequences given in AAQ43058-75 show the -255 to -62 non-coding region  
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
CC variants. Analysis of this region revealed the existence of three  
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
CC the groups identified were similar to those of HCV variants termed type 1  
CC and 2, whilst the third appeared to represent a novel virus type.  
CC Comparison of other regions of the genome, eg. the NS-5 region (see also  
CC AA37923-26), showed a high degree of sequence diversity with type 3  
CC being phylogenetically different to type 1 and 2. The same degree  
CC differentiation was noted in the NS-3 (see AA37927-30) and core region  
CC (see AA37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 194 BP; 37 A; 55 C; 63 G; 39 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 2; Length 194;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCGGACCCCAACTACTC 20  
DB 189 TTCGGACCCCAACTACTC 170

RESULT 76

AAQ43074/C  
ID AAQ43074 standard; cDNA; 194 BP.  
XX  
XX AAQ43074;  
AC  
XX 25-MAR-2003 (revised)  
DT 23-SEP-1993 (first entry)  
XX  
DE -255 to -62 region of 5' non-coding region of HCV HCV-J.  
XX  
XX Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
KM NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.  
XX  
XX Hepatitis C virus.  
OS  
XX WO9310239-A2.  
FN  
XX 27-MAY-1993.  
PD  
XX 20-NOV-1992; 92MO-GB002143.  
PF  
XX 21-NOV-1991; 91GB-00024696.  
PR 24-JUN-1992; 92GB-00013362.  
XX  
XX (COMM-) COMMON SERVICES AGENCY.  
PA  
XX Simmonds P, Chan S, Yap PL;  
FI  
XX WPI; 1993-182554/22.  
DR  
XX DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for  
PT diagnosing and treating HCV infection, screening blood samples and  
PT identifying different HCV types.  
PT  
XX  
XX Disclosure; Fig 1; 120pp; English.  
PS  
XX The sequences given in AAQ43058-75 show the -255 to -62 non-coding region  
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
CC variants. Analysis of this region revealed the existence of three  
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
CC the groups identified were similar to those of HCV variants termed type 1  
CC and 2, whilst the third appeared to represent a novel virus type.  
CC Comparison of other regions of the genome, eg. the NS-5 region (see also  
CC AA37923-26), showed a high degree of sequence diversity with type 3  
CC being phylogenetically different to type 1 and 2. The same degree  
CC differentiation was noted in the NS-3 (see AA37927-30) and core region  
CC (see AA37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 194 BP; 35 A; 56 C; 64 G; 39 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 2; Length 194;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCGGACCCCAACTACTC 20  
DB 189 TTCGGACCCCAACTACTC 170

RESULT 79  
AAQ43072/C  
ID AAQ43072 standard; cDNA; 194 BP.  
XX  
XX AAQ43072;  
AC  
XX 25-MAR-2003 (revised)  
DT 23-SEP-1993 (first entry)  
XX  
DE -255 to -62 region of 5' non-coding region of HCV A1.  
XX  
XX Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
KM NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.

```

XX OS Hepatitis C virus.
XX XX
XX PN W09310239-A2.
XX XX
XX PD 27-MAY-1993.
XX XX
XX PF 20-NOV-1992; 92WO-GB002143.
XX XX
XX PR 21-NOV-1991; 91GB-00024696.
XX PR 24-JUN-1992; 92GB-00013362.
XX XX
XX PA (COMM-) COMMON SERVICES AGENCY.
XX XX
XX PI Simmonds P, Chan S, Yap PL;
XX XX
XX DR WPI; 1993-182554/22.
XX XX
XX PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
XX PT diagnosing and treating HCV infection, screening blood samples and
XX PT identifying different HCV types.
XX XX
XX PS Disclosure; Fig 1; 120pp; English.
XX XX
XX CC The sequences given in AA043058-75 show the -255 to -62 non-coding region
XX CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV
XX CC variants. Analysis of this region revealed the existence of three
XX CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of
XX CC the groups identified were similar to those of HCV variants termed type 1
XX CC and 2, whilst the third appeared to represent a novel virus type.
XX CC Comparison of other regions of the genome, eg. the NS-5 region (see also
XX CC AAR37923-26), showed a high degree of sequence diversity with type 3
XX CC being phylogenetically different to type 1 and 2. The same degree
XX CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region
XX CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX XX
SQ Sequence 194 BP; 37 A; 56 C; 64 G; 37 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20
DB 189 TTGCGACCCCAACTACTC 170

RESULT 80
AA043058/C
ID AA043058 standard; cDNA; 194 BP.
XX XX
XX AC AA043058;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 23-SEP-1993 (first entry)
XX XX
XX DE -255 to -62 portion of 5' non-coding region of HCV from donor E-D1.
XX XX
XX KW Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;
XX KW NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.
XX XX
XX OS Hepatitis C virus.
XX XX
XX PN W09310239-A2.
XX XX
XX PD 27-MAY-1993.
XX XX
XX PF 20-NOV-1992; 92WO-GB002143.
XX XX
XX PR 21-NOV-1991; 91GB-00024696.
XX PR 24-JUN-1992; 92GB-00013362.
XX XX

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XX PA (COMM-) COMMON SERVICES AGENCY.
XX XX
XX PI Simmonds P, Chan S, Yap PL;
XX XX
XX DR WPI; 1993-182554/22.
XX XX
XX XX
XX PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
XX PT diagnosing and treating HCV infection, screening blood samples and
XX PT identifying different HCV types.
XX XX
XX PS Disclosure; Fig 1; 120pp; English.
XX XX
XX CC The sequences given in AA043058-75 show the -255 to -62 non-coding region
XX CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV
XX CC variants. Analysis of this region revealed the existence of three
XX CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of
XX CC the groups identified were similar to those of HCV variants termed type 1
XX CC and 2, whilst the third appeared to represent a novel virus type.
XX CC Comparison of other regions of the genome, eg. the NS-5 region (see also
XX CC AAR37923-26), showed a high degree of sequence diversity with type 3
XX CC being phylogenetically different to type 1 and 2. The same degree
XX CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region
XX CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX XX
SQ Sequence 194 BP; 37 A; 57 C; 63 G; 37 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20
DB 189 TTGCGACCCCAACTACTC 170

RESULT 81
AA043070/C
ID AA043070 standard; cDNA; 194 BP.
XX XX
XX AC AA043070;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 23-SEP-1993 (first entry)
XX XX
XX DE -255 to -62 region of 5' non-coding region of HCV H-90.
XX XX
XX KW Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;
XX KW NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.
XX XX
XX OS Hepatitis C virus.
XX XX
XX PN W09310239-A2.
XX XX
XX PD 27-MAY-1993.
XX XX
XX PF 20-NOV-1992; 92WO-GB002143.
XX XX
XX PR 21-NOV-1991; 91GB-00024696.
XX PR 24-JUN-1992; 92GB-00013362.
XX XX
XX PA (COMM-) COMMON SERVICES AGENCY.
XX XX
XX PI Simmonds P, Chan S, Yap PL;
XX XX
XX DR WPI; 1993-182554/22.
XX XX
XX PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
XX PT diagnosing and treating HCV infection, screening blood samples and
XX PT identifying different HCV types.
XX PS Disclosure; Fig 1; 120pp; English.
XX XX

```

CC The sequences given in AA043058-75 show the -255 to -62 non-coding region  
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
CC variants. Analysis of this region revealed the existence of three  
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
CC the groups identified were similar to those of HCV variants termed type 1  
CC and 2, whilst the third appeared to represent a novel virus type.  
CC Comparison of other regions of the genome, eg. the NS-5 region (see also  
CC AAR37923-26), showed a high degree of sequence diversity with type 3  
CC being phylogenetically different to type 1 and 2. The same degree  
CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region  
CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 194 BP; 38 A; 56 C; 62 G; 38 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 2; Length 194;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGAGCCCAACTACTC 20  
DB 189 TTCCGGAGCCCAACTACTC 170  
RESULT 82  
AA043075/c  
ID AA043075 standard; cDNA; 194 BP.  
XX  
AC AA043075;  
XX  
DT 25-MAR-2003 (revised)  
DT 23-SEP-1993 (first entry)  
XX  
DE -255 to -62 region of 5' non-coding region of HCV HCV-J1.  
XX  
KM Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
KM NS-5; phylogeny; differentiation; NS-3; core region; type 3; 88.  
XX  
OS Hepatitis C virus.  
XX  
PN WO9310239-A2.  
XX  
PD 27-MAY-1993.  
XX  
PF 20-NOV-1992; 92MO-GB002143.  
XX  
PR 21-NOV-1991; 91GB-00024696.  
PR 24-JUN-1992; 92GB-00013362.  
XX  
PS (COMM-) COMMON SERVICES AGENCY.  
XX  
PI Simmonds P, Chan S, Yap PL;  
PI WPI, 1993-182554/22.  
XX  
PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for  
PT diagnosing and treating HCV infection, screening blood samples and  
PT identifying different HCV types.  
XX  
PS Disclosure; Fig 1; 120pp; English.  
XX  
CC The sequences given in AA043058-75 show the -255 to -62 non-coding region  
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
CC variants. Analysis of this region revealed the existence of three  
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
CC the groups identified were similar to those of HCV variants termed type 1  
CC and 2, whilst the third appeared to represent a novel virus type.  
CC Comparison of other regions of the genome, eg. the NS-5 region (see also  
CC AAR37923-26), showed a high degree of sequence diversity with type 3  
CC being phylogenetically different to type 1 and 2. The same degree  
CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region  
CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

XX  
SQ Sequence 194 BP; 37 A; 57 C; 63 G; 37 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 2; Length 194;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGAGCCCAACTACTC 20  
DB 189 TTCCGGAGCCCAACTACTC 170  
RESULT 83  
ADS34710/c  
ID ADS34710 standard; DNA; 197 BP.  
XX  
AC ADS34710;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE siRNA-7 PCR product, seq id 53.  
XX  
KM Virucide; antiinflammatory; hepatotropic; hepatitis C virus; HCV;  
KM proliferation; siRNA; short interfering RNA; RNA interference;  
KM gene silencing; ds.  
XX  
OS Unidentified.  
XX  
PN WO2004078974-A1.  
XX  
PD 16-SEP-2004.  
XX  
PF 23-JAN-2004; 2004WO-JP000605.  
XX  
PR 24-JAN-2003; 2003JP-00016750.  
XX  
PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.  
PA (CHUS) CHUGAI SEIYAKU KK.  
XX  
PI Kohara M, Watanabe T, Taira K, Miyagishi M, Sudo M;  
PI WPI, 2004-662428/64.  
XX  
DR  
XX  
PT New oligo ribonucleotide or peptide nucleic acid capable of sequence-  
PT specifically binding with RNA of hepatitis C virus, useful for inhibiting  
PT proliferation of hepatitis C virus and useful as hepatitis C virus  
PT therapeutic agent.  
XX  
PS Example 6; SEQ ID NO 53; 80pp; Japanese.  
XX  
CC The invention relates to an oligo ribonucleotide or peptide nucleic acid  
CC (I) capable of sequence-specifically binding with RNA of hepatitis C  
CC virus (HCV), and comprising a sequence hybridising under stringent  
CC conditions with RNA of HCV. The method of the invention relates to the  
CC inhibition of the proliferation of HCV. The oligo ribonucleotide or  
CC peptide nucleic acid of the invention is useful for inhibiting the  
CC proliferation of HCV which involves contacting (I) with RNA of HCV. (1)  
CC is useful as a therapeutic agent of hepatitis C. The current sequence  
CC represents a PCR product from an example of the invention.  
XX  
SQ Sequence 197 BP; 48 A; 57 C; 56 G; 36 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 13; Length 197;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGAGCCCAACTACTC 20  
DB 77 TTCCGGAGCCCAACTACTC 58  
RESULT 84  
ABL41919/c

```

ID ABL41919 standard; RNA; 209 BP.
XX
XX ABL41919;
AC
XX
XX 11-JUN-2002 (first entry)
DT
XX
XX DNA comprising consensus endodogmatic sequence/exodogmatic sequence.
DE
XX
XX cellular organism; pathogen; retroviral particle; probe; ss.
KM
XX
XX Synthetic.
OS
XX
XX Key
FH Location/Qualifiers
FT 5..49
FT stem_loop
FT
FT misc_structure
FT 5..17
FT /tag= a
FT /note= "these bases bind to bases 47-49"
FT
FT misc_structure
FT 10..14
FT /tag= b
FT /note= "these bases bind to bases 39-43"
FT
FT misc_structure
FT 39..43
FT /tag= c
FT /note= "these bases bind to bases 10-14"
FT
FT stem_loop
FT 92..104
FT /tag= d
FT /note= "these bases bind to bases 10-14"
FT
FT misc_structure
FT 92..96
FT /tag= e
FT /note= "these bases bind to bases 100-104"
FT
FT misc_structure
FT 100..104
FT /tag= f
FT /note= "these bases bind to bases 92-96"
FT
FT stem_loop
FT 105..118
FT /tag= g
FT /note= "these bases bind to bases 115-118"
FT
FT misc_structure
FT 116..118
FT /tag= h
FT /note= "these bases bind to bases 105-108"
FT
FT stem_loop
FT 153..208
FT /tag= i
FT /note= "these bases bind to bases 153-157"
FT
FT misc_structure
FT 153..157
FT /tag= j
FT /note= "these bases bind to bases 204-208"
FT
FT misc_structure
FT 158..160
FT /tag= k
FT /note= "these bases bind to bases 193-195"
FT
FT misc_structure
FT 162..167
FT /tag= l
FT /note= "these bases bind to bases 186-191"
FT
FT misc_structure
FT 171..173
FT /tag= m
FT /note= "these bases bind to bases 182-184"
FT
FT misc_structure
FT 182..184
FT /tag= n
FT /note= "these bases bind to bases 171-173"
FT
FT misc_structure
FT 186..191
FT /tag= o
FT /note= "these bases bind to bases 162-167"
FT
FT misc_structure
FT 193..195
FT /tag= p
FT /note= "these bases bind to bases 158-160"
FT
FT misc_structure
FT 204..208
FT /tag= q
FT /note= "theses bases bind to bases 204-208"
FT
XX
XX WO200202803-A2.
XX
XX 10-JAN-2002.
XX
XX 18-JUN-2001; 2001WO-CH000381.
XX

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PR 03-JUL-2000; 2000CH-00001311.
XX
XX (HAFN/) HAFNER W A.
PA (MEMO/) MENOUD P.
XX
XX Hafner WA, Menoud P;
XX
XX WPI, 2002-148020/19.
DR
XX
XX Formulating molecular probes, useful for diagnosis and therapy, by
PT analyzing the forms of presentation of targets in organisms.
XX
XX Disclosure; Fig 1; 25pp; French.
XX
XX The specification describes a process for formulating and selecting non-
CC contagious molecular probes which are used for detecting nucleic acids.
CC The process that takes account of the forms of presentation of cellular
CC organisms during the life cycle, or where these forms depend on different
CC chemical, biological and physical states of the organism. The process is
CC a contamination free diagnostic method for direct quantitative and
CC qualitative analysis and gene typing of infectious agents without prior
CC DNA or RNA extraction. The probes enable detection of nucleic acids in
CC sections of living or immobilised, frozen or fixed tissues. Probes of the
CC invention are useful for detecting viral (including oncogenic),
CC bacterial, animal and plant nucleic acid, e.g. in situ hybridization for
CC detecting presence of (pathogenic) microbes and/or determination of
CC genotype, as primers for polymerase chain reaction amplification and
CC therapeutically for blocking replication of pathogens, e.g. as ribozymes.
CC Particularly, the probes are used to detect retroviral particles
CC circulating in body fluids or present in cells. The present sequence
CC represents a sequence comprising a consensus endodogmatic
CC sequence/consensus exodogmatic sequence
XX
XX SQ Sequence 209 BP; 48 A; 59 C; 64 G; 0 T; 38 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 6; Length 209;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGGCGACCCACACTACTC 20
XX Db 45 TTGGCGACCCACACTACTC 26
XX
XX RESULT 85
XX ADA93664/C
XX ID ADA93664 standard; DNA; 209 BP.
XX
XX ADA93664;
XX AC
XX 20-NOV-2003 (first entry)
XX DT
XX Competitor DNA KF-2.
XX DE
XX detection; detector complex; prion protein; lectin; murine; IGC; ds.
XX KW
XX Unidentified.
XX OS
XX EPI270738-A1.
XX PN
XX 02-JAN-2003.
XX PD
XX 18-JUN-2001; 2001EP-00114562.
XX PF
XX 18-JUN-2001; 2001EP-00114562.
XX PR
XX (CHIM-) CHIMERA BIOTEC GMBH.
XX PA
XX Niemeyer CM, Macker R, Adler M;
XX PI
XX WPI; 2003-315784/31.
XX DR
XX
XX Detecting a substance in a liquid sample, using detector nucleic acid
PT

```

PT which is amplified and detected, is more sensitive than a comparable  
PT ELISA and is useful to detect prion protein or lectin.  
XX  
PS Example 2; Page 35; 44pp; German.  
XX  
CC This invention describes a novel method of detecting a substance in a  
CC test sample. The method comprises forming a detector complex, in which  
CC the substance is bound to a connection agent conjugated to a detector  
CC nucleic acid which is replicated with a replication agent. A competitor  
CC nucleic acid which competes for the replication agent is also added and  
CC replication of the detector and competitor nucleic acids is determined.  
CC Preferably two or more binding reagents and/or two or more detector  
CC nucleic acids are used. The detected substance is preferably immobilised  
CC on a solid surface. Preferably the substance is bound to an immobilised  
CC binding reagent connected to a first immobilised nucleic acid, which is  
CC hybridised to a second nucleic acid bound to a solid surface. A negative  
CC control is preferably also performed using the detector and competitor  
CC nucleic acids in the absence of the substance and the mix of replicated  
CC detector and competitor nucleic acids in the sample test compared to the  
CC negative control test. The method is useful for detecting a substance,  
CC particularly a prion protein or a lectin in a liquid and is more  
CC sensitive than a comparable ELISA. This sequence represents  
CC polynucleotide fragment KF-2 which is a competitive inhibitor of murine  
CC IGG designated DNA-169, used in an assay described in the invention.  
CC  
SQ Sequence 209 BP; 36 A; 60 C; 69 G; 44 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 8; Length 209;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGGGACCCCAACTACTC 20  
DB 170 TTGGGACCCCAACTACTC 151  
RESULT 86  
AD005658/C  
ID AD005658 standard; DNA; 226 BP.  
XX  
AC AD005658;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE HCV template DNA fragment.  
XX  
DE Nucleic acid amplification; mutation detection; cytosstatic;  
XX  
KW antinflammatory; hepatotropic; virocid; cancer; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2004035832-A1.  
XX  
PD 29-APR-2004.  
XX  
PF 17-OCT-2003; 2003WO-KR002179.  
XX  
PR 18-OCT-2002; 2002KR-00063832.  
XX  
PR 02-SEP-2003; 2003KR-00061066.  
XX  
PA (GENE-) GENEMATRIX INC.  
XX  
PI Kim N, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;  
PI Jee M, Hwang S, Hong S;  
XX  
DR WPI; 2004-348478/32.  
XX  
PT Detecting a mutation, useful in diagnosing and treating e.g. cancer or  
PT hepatitis, comprises generating fragments of polynucleotides using  
PT specific primers and measuring molecular weight of cleaved fragments.  
XX  
PS Example 4; SEQ ID NO 19; 58pp; English.  
XX

CC The invention relates to detecting a mutation. The method involves  
CC amplifying a target polynucleotide using a forward primer and a reverse  
CC primer; generating fragments of two or more single-stranded  
CC polynucleotides including one or more mutations sequence having the size  
CC of 2-32 bases by cleaving the amplified target polynucleotide with  
CC restriction enzymes, where the second restriction enzyme does not react  
CC while a first restriction enzyme is reacted with the amplified  
CC polynucleotide; and measuring the molecular weight of the cleaved  
CC fragments. The polynucleotide is cleaved to include one mutation among  
CC two or more different mutations in only one single stranded  
CC polynucleotide fragment and all mutations in the other single stranded  
CC nucleotide fragment. Restrictions enzyme treatment step is performed  
CC using restriction enzymes having different optimum temperatures. The  
CC method is useful in detecting a mutation. The method and primer are  
CC useful in diagnosing, prognosing, treating and preventing a disease, e.g.  
CC cancer or hepatitis B or C virus. The present sequence represents a HCV  
CC template DNA sequence.  
CC  
SQ Sequence 226 BP; 41 A; 64 C; 73 G; 48 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 226;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGGGACCCCAACTACTC 20  
DB 200 TTGGGACCCCAACTACTC 181  
RESULT 87  
AD005662  
ID AD005662 standard; DNA; 230 BP.  
XX  
AC AD005662;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE PCR amplified HCV DNA fragment.  
XX  
XX  
XX Nucleic acid amplification; mutation detection; cytosstatic;  
XX  
KW antinflammatory; hepatotropic; virocid; cancer; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2004035832-A1.  
XX  
PD 29-APR-2004.  
XX  
PF 17-OCT-2003; 2003WO-KR002179.  
XX  
PR 18-OCT-2002; 2002KR-00063832.  
XX  
PR 02-SEP-2003; 2003KR-00061066.  
XX  
PA (GENE-) GENEMATRIX INC.  
XX  
PI Kim N, Kim S, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;  
PI Jee M, Hwang S, Hong S;  
XX  
DR WPI; 2004-348478/32.  
XX  
PT Detecting a mutation, useful in diagnosing and treating e.g. cancer or  
PT hepatitis, comprises generating fragments of polynucleotides using  
PT specific primers and measuring molecular weight of cleaved fragments.  
XX  
PS Example 4; SEQ ID NO 23; 58pp; English.  
XX  
CC The invention relates to detecting a mutation. The method involves  
CC amplifying a target polynucleotide using a forward primer and a reverse  
CC primer; generating fragments of two or more single-stranded  
CC polynucleotides including one or more mutations sequence having the size  
CC of 2-32 bases by cleaving the amplified target polynucleotide with  
CC restriction enzymes, where the second restriction enzyme does not react  
CC while a first restriction enzyme is reacted with the amplified

CC polynucleotide; and measuring the molecular weight of the cleaved  
 CC fragments. The polynucleotide is cleaved to include one mutation among  
 CC two or more different mutations in only one single stranded  
 CC polynucleotide fragment and all mutations in the other single stranded  
 CC nucleotide fragment. Restrictions enzyme treatment step is performed  
 CC using restriction enzymes having different optimum temperatures. The  
 CC method is useful in detecting a mutation. The method and primer are  
 CC useful in diagnosing, prognosing, treating and preventing a disease, e.g.  
 CC cancer or hepatitis B or C virus. The present sequence represents a PCR  
 CC amplified HCV DNA fragment.

SO Sequence 230 BP; 48 A; 76 C; 64 G; 42 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 20; DB 12; Length 230;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
 DB 27 TTGCGAGCCCACTACTC 46

RESULT 88

AD005661/c

ID AD005661 standard; DNA; 230 BP.

AC AD005661;

DT 15-JUL-2004 (first entry)

DE PCR amplified HCV DNA fragment.

XX Nucleic acid amplification; mutation detection; cytostratic;

KW antiinflammatory; hepatotropic; virucide; cancer; ds.

XX Hepatitis C virus.

PN WO2004035832-A1.

PD 29-APR-2004.

PF 17-OCT-2003; 2003WO-KR002179.

PR 18-OCT-2002; 2002KR-00063832.

PR 02-SEP-2003; 2003KR-00061066.

PA (GENE-) GENEMATRIX INC.

PI Kim N, Kim S, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;

PI Jee M, Hwang S, Hong S;

DR WPI; 2004-348478/32.

PT Detecting a mutation, useful in diagnosing and treating e.g. cancer or  
 PT hepatitis, comprises generating fragments of polynucleotides using  
 PT specific primers and measuring molecular weight of cleaved fragments.

PS Example 4; SEQ ID NO 22; 58pp; English.

CC The invention relates to detecting a mutation. The method involves  
 CC amplifying a target polynucleotide using a forward primer and a reverse  
 CC primer; generating fragments of two or more single-stranded  
 CC polynucleotides including one or more mutations sequence having the size  
 CC of 2-32 bases by cleaving the amplified target polynucleotide with  
 CC restriction enzymes, where the second restriction enzyme does not react  
 CC while a first restriction enzyme is reacted with the amplified  
 CC polynucleotide; and measuring the molecular weight of the cleaved  
 CC fragments. The polynucleotide is cleaved to include one mutation among  
 CC two or more different mutations in only one single stranded  
 CC polynucleotide fragment and all mutations in the other single stranded  
 CC nucleotide fragment. Restrictions enzyme treatment step is performed  
 CC using restriction enzymes having different optimum temperatures. The  
 CC method is useful in detecting a mutation. The method and primer are

CC useful in diagnosing, prognosing, treating and preventing a disease, e.g.  
 CC cancer or hepatitis B or C virus. The present sequence represents a PCR  
 CC amplified HCV DNA fragment.

SO Sequence 230 BP; 42 A; 64 C; 76 G; 48 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 20; DB 12; Length 230;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
 DB 204 TTGCGAGCCCACTACTC 185

RESULT 89

AAV70460/c

ID AAV70460 standard; DNA; 232 BP.

AC AAV70460;

DT 08-APR-1999 (first entry)

DE Partial sequence of HCV subtype 1b amplicon #86.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;

KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.

XX Hepatitis C virus.

PN WO9850403-A1.

PD 12-NOV-1998.

PF 05-MAY-1998; 98WO-US003194.

PR 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;

PI Anderson TA, Dahlberg JE;

DR WPI; 1998-610317/51.

PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.

PS Example 5; Page 172-173; 279pp; English.

CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).



CC The methods are powerful in that they allow for analysis of longer  
CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
CC 61 represent partial sequences of different amplicons of hepatitis C  
CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
CC for identifying the HCV subtypes

XX  
SQ Sequence 232 BP; 40 A; 65 C; 76 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
Db 199 TTGGGACCCCAACTACTC 180

RESULT 90  
ABLA6070/C  
ID ABLA6070 standard; DNA; 232 BP.

XX ABLA6070;  
AC  
XX  
DT 26-APR-2002 (first entry)

XX Hepatitis C virus partial sequence #86 SEQ ID NO:37.

XX Nucleic acid accessible hybridisation site; detection; hybridisation;  
KW characterisation; identification; nucleic acid structure; diagnosis;  
XX PCR primer; probe; ss.

OS Hepatitis C virus.  
XX Synthetic.

XX WO200198537-A2.

XX 27-DEC-2001.

XX 15-JUN-2001; 2001WO-US019401.

XX 17-JUN-2000; 2000US-0212308P.

PR 15-JUN-2001; 2001US-00212308.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Lyamichev V, Alawi H, Dong F, Neri BP, Vener IT;

DR WPI; 2002-049698/06.

XX  
XX  
PT Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.

XX Example 5; Page 366; 409pp; English.

XX The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABLA6034 to ABLA6367 represent  
CC sequences used in the exemplification of the present invention

XX Sequence 232 BP; 40 A; 65 C; 76 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
Db 199 TTGGGACCCCAACTACTC 180

RESULT 91  
ADK82260/C  
ID ADK82260 standard; DNA; 232 BP.

XX ADK82260;

XX 03-JUN-2004 (first entry)

XX Hepatitis C virus polynucleotide seqid 37.

XX nucleic acid analysis; hepatitis C virus;  
KW non-contiguous single-stranded region; NCSR; cleavage structure;  
KW clinical; diagnostic; microorganism detection;  
KW microorganism identification; hepatitis C virus; HCV; ds.

XX Hepatitis C virus.

XX US6709815-B1.

XX 23-MAR-2004.

XX 18-JUL-2000; 2000US-00402618.

XX 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Dong F, Lyamichev VI, Prudent JR, Fore L, Neri BP, Brow MAD;

PI Anderson TA, Dahlberg JE;

XX WPI; 2004-256067/24.

XX  
XX  
PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.

XX Example 5; SEQ ID NO 37; 143pp; English.

XX The invention describes a method of analysing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR; a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analysing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC polynucleotide that is sufficient for identification of HCV subtypes  
CC using the analysis methods of the invention.

XX Sequence 232 BP; 40 A; 65 C; 76 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
Db 199 TTGGGACCCCAACTACTC 180

RESULT 92  
AAV70459/C  
ID AAV70459 standard; DNA; 239 BP.

```

XX AC AAV70455;
XX DT 08-APR-1999 (first entry)
XX DE Partial sequence of HCV subtype 1a amplicon #85.
XX KM Nucleic acid detection; nucleic acid characterisation; hybridisation;
XX KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.
XX OS Hepatitis C virus.
XX PN WO9850403-A1.
XX PD 12-NOV-1998.
XX PF 05-MAY-1998; 98WO-US003194.
XX PR 05-MAY-1997; 97US-00851588.
XX PR 19-SEP-1997; 97US-00934097.
XX PR 03-MAR-1998; 98US-00034205.
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
XX PI Anderson TA, Dahlberg JE;
XX DR WPI; 1998-610317/51.
XX PT Detection and characterisation of nucleic acid sequences - by mixing a
XX PT folded target and one or more probes to form a probe/folded target
XX PT complex and detecting and characterising the complexes.
XX PS Example 5; Page 172; 279pp; English.
XX CC The invention relates to methods and compositions of detection and
XX CC characterisation of nucleic acid sequences and sequence changes. One
XX CC method of detection and characterisation comprises: (a) providing: (i) a
XX CC folded target having a DNA sequence comprising at least 1 double stranded
XX CC region and at least 1 single stranded region; and (ii) at least 1 probe
XX CC complementary to at least a portion of the folded target; and (b) mixing
XX CC the target and probes so that the probe hybridises to form a probe
XX CC /folded target complex. Also provided are methods for determination of
XX CC structure formation in nucleic acid targets; for analysing folded nucleic
XX CC acids targets; and for analysis of nucleic acid structures. The methods
XX CC can be used for the detection and characterisation of nucleic acid
XX CC sequences to detect the presence of pathogenic nucleic acid sequences
XX CC indicative of an infection, the presence of variants or alleles of
XX CC mammalian genes associated with disease and cancers, and the
XX CC identification of the source of nucleic acids found in forensic samples,
XX CC as well as in paternity determinations. The methods allow simultaneous
XX CC analysis of both strands (e.g. the sense and antisense strands) and are
XX CC ideal for high-level multiplexing. The products produced are amenable to
XX CC qualitative, quantitative and positional analysis. The methods may be
XX CC performed in solution or in the solid phase (e.g. on a solid support).
XX CC The methods are powerful in that they allow for analysis of longer
XX CC fragments of nucleic acid than current methodologies. Sequences AAV70453-
XX CC 61 represent partial sequences of different amplicons of hepatitis C
XX CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used
XX CC for identifying the HCV subtypes
XX SQ Sequence 239 BP; 45 A; 64 C; 77 G; 53 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCAACTACTC 20
Db 206 TTGCGACCCCAACTACTC 187

```

RESULT 93

```

AAV70455/c
ID AAV70455 standard; DNA; 239 BP.
XX AC AAV70455;
XX DT 08-APR-1999 (first entry)
XX DE Partial sequence of HCV subtype 1a amplicon #72.
XX KM Nucleic acid detection; nucleic acid characterisation; hybridisation;
XX KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.
XX OS Hepatitis C virus.
XX PN WO9850403-A1.
XX PD 12-NOV-1998.
XX PF 05-MAY-1998; 98WO-US003194.
XX PR 05-MAY-1997; 97US-00851588.
XX PR 19-SEP-1997; 97US-00934097.
XX PR 03-MAR-1998; 98US-00034205.
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
XX PI Anderson TA, Dahlberg JE;
XX DR WPI; 1998-610317/51.
XX PT Detection and characterisation of nucleic acid sequences - by mixing a
XX PT folded target and one or more probes to form a probe/folded target
XX PT complex and detecting and characterising the complexes.
XX PS Example 5; Page 171; 279pp; English.
XX CC The invention relates to methods and compositions of detection and
XX CC characterisation of nucleic acid sequences and sequence changes. One
XX CC method of detection and characterisation comprises: (a) providing: (i) a
XX CC folded target having a DNA sequence comprising at least 1 double stranded
XX CC region and at least 1 single stranded region; and (ii) at least 1 probe
XX CC complementary to at least a portion of the folded target; and (b) mixing
XX CC the target and probes so that the probe hybridises to form a probe
XX CC /folded target complex. Also provided are methods for determination of
XX CC structure formation in nucleic acid targets; for analysing folded nucleic
XX CC acids targets; and for analysis of nucleic acid structures. The methods
XX CC can be used for the detection and characterisation of nucleic acid
XX CC sequences to detect the presence of pathogenic nucleic acid sequences
XX CC indicative of an infection, the presence of variants or alleles of
XX CC mammalian genes associated with disease and cancers, and the
XX CC identification of the source of nucleic acids found in forensic samples,
XX CC as well as in paternity determinations. The methods allow simultaneous
XX CC analysis of both strands (e.g. the sense and antisense strands) and are
XX CC ideal for high-level multiplexing. The products produced are amenable to
XX CC qualitative, quantitative and positional analysis. The methods may be
XX CC performed in solution or in the solid phase (e.g. on a solid support).
XX CC The methods are powerful in that they allow for analysis of longer
XX CC fragments of nucleic acid than current methodologies. Sequences AAV70453-
XX CC 61 represent partial sequences of different amplicons of hepatitis C
XX CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used
XX CC for identifying the HCV subtypes
XX SQ Sequence 239 BP; 45 A; 63 C; 78 G; 53 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCAACTACTC 20
Db 206 TTGCGACCCCAACTACTC 187

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RESULT 94
ABL46065/C
ID ABL46065 standard; DNA; 239 BP.
XX
AC ABL46065;
XX
DT 26-APR-2002 (first entry)
XX
DE Hepatitis C virus partial sequence #72 SEQ ID NO:32.
XX
KM Nucleic acid accessible hybridisation site; detection; hybridisation;
KM characterisation; identification; nucleic acid structure; diagnosis;
KM PCR primer; probe; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO200198537-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamchev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
WPI; 2002-049698/06.
XX
DR
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 5; Page 365; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 239 BP; 45 A; 63 C; 78 G; 53 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 6; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGGGACCCCAACTACTC 20
DB 206 TTGGGACCCCAACTACTC 187
XX
RESULT 95
ABL46069/C
ID ABL46069 standard; DNA; 239 BP.
XX
AC ABL46069;
XX
DT 26-APR-2002 (first entry)
XX
DE Hepatitis C virus partial sequence #85 SEQ ID NO:36.
XX
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KM Nucleic acid accessible hybridisation site; detection; hybridisation;
KM characterisation; identification; nucleic acid structure; diagnosis;
KM PCR primer; probe; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO200198537-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamchev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
WPI; 2002-049698/06.
XX
DR
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 5; Page 366; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 239 BP; 45 A; 64 C; 77 G; 53 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 6; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGGGACCCCAACTACTC 20
DB 206 TTGGGACCCCAACTACTC 187
XX
RESULT 96
ADK82255/C
ID ADK82255 standard; DNA; 239 BP.
XX
AC ADK82255;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis C virus polynucleotide seqid 32.
XX
KM Nucleic acid analysis; hepatitis C virus;
KM non-contiguous single-stranded region; NCSR; cleavage structure;
KM clinical; diagnostic; microorganism detection;
KM microorganism identification; hepatitis C virus; HCV; ds.
XX
OS Hepatitis C virus.
XX
PN US6709815-B1.
XX
PD 23-MAR-2004.
XX
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PF 18-JUL-2000; 2000US-00402618.
XX
XX 05-MAY-1997; 97US-00851588.
PR 19-SEP-1997; 97US-00934097.
RR 03-MAR-1998; 98US-00034205.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI Anderson TA, Dahlberg JE;
XX
XX WPI; 2004-256067/24.
XX
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX oligonucleotide and cleavage agent to form cleavage structure.
XX
XX Example 5; SEQ ID NO 32; 143bp; English.
XX
XX The invention describes a method of analyzing nucleic acids comprising
XX providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX having non-contiguous single-stranded regions (NCSR) separated by an
XX intervening region, a bridging oligonucleotide capable of binding to the
XX first and second NCSR, a second oligonucleotide binding to a portion of
XX the first NCSR and a cleavage agent, and mixing the contents to form a
XX cleavage structure. The method is useful for analyzing nucleic acids,
XX e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX purposes and detection and identification of pathogenic microorganisms
XX such as hepatitis C virus. This sequence represents a hepatitis C virus
XX polynucleotide that is sufficient for identification of HCV subtypes
XX using the analysis methods of the invention.
SQ Sequence 239 BP; 45 A; 63 C; 78 G; 53 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 206 TTGGGACCCCAACTACTC 187

RESULT 97
ADK82259/C
ID ADK82259 standard; DNA; 239 BP.
XX
XX ADK82259;
XX
XX 03-JUN-2004 (first entry)
XX
XX Hepatitis C virus polynucleotide seqid 36.
XX
XX nucleic acid analysis; hepatitis C virus;
XX non-contiguous single-stranded region; NCSR; cleavage structure;
XX clinical; diagnostic; microorganism detection;
XX microorganism identification; hepatitis C virus; HCV; ds.
XX
XX Hepatitis C virus.
XX
XX US6709815-B1.
XX
XX 23-MAR-2004.
XX
XX 18-JUL-2000; 2000US-00402618.
XX
XX 05-MAY-1997; 97US-00851588.
PR 19-SEP-1997; 97US-00934097.
PR 03-MAR-1998; 98US-00034205.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI

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PI Anderson TA, Dahlberg JE;
XX
XX WPI; 2004-256067/24.
XX
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX oligonucleotide and cleavage agent to form cleavage structure.
XX
XX Example 5; SEQ ID NO 36; 143bp; English.
XX
XX The invention describes a method of analyzing nucleic acids comprising
XX providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX having non-contiguous single-stranded regions (NCSR) separated by an
XX intervening region, a bridging oligonucleotide capable of binding to the
XX first and second NCSR, a second oligonucleotide binding to a portion of
XX the first NCSR and a cleavage agent, and mixing the contents to form a
XX cleavage structure. The method is useful for analyzing nucleic acids,
XX e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX purposes and detection and identification of pathogenic microorganisms
XX such as hepatitis C virus. This sequence represents a hepatitis C virus
XX polynucleotide that is sufficient for identification of HCV subtypes
XX using the analysis methods of the invention.
SQ Sequence 239 BP; 45 A; 64 C; 77 G; 53 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 206 TTGGGACCCCAACTACTC 187

RESULT 98
AAV70458/C
ID AAV70458 standard; DNA; 240 BP.
XX
XX AAV70458;
XX
XX 08-APR-1999 (first entry)
XX
XX Partial sequence of HCV subtype 3a amplicon #81.
XX
XX Nucleic acid detection; nucleic acid characterisation; hybridisation;
XX infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.
XX
XX Hepatitis C virus.
XX
XX WO9850403-A1.
XX
XX 12-NOV-1998.
XX
XX 05-MAY-1998; 98WO-US0003194.
PR 05-MAY-1997; 97US-00851588.
PR 19-SEP-1997; 97US-00934097.
PR 03-MAR-1998; 98US-00034205.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI Anderson TA, Dahlberg JE;
XX
XX WPI; 1998-610317/51.
XX
XX Detection and characterisation of nucleic acid sequences - by mixing a
XX folded target and one or more probes to form a probe/folded target
XX complex and detecting and characterising the complexes.
XX
XX Example 5; Page 172; 279pp; English.
XX
XX The invention relates to methods and compositions of detection and

```

CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers; and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
 CC 61 represent partial sequences of different amplicons of hepatitis C  
 CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
 CC for identifying the HCV subtypes

SQ Sequence 240 BP; 45 A; 66 C; 79 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCCAACTACTC 20  
 |||||  
 Db 207 TTCCGACCCCAACTACTC 188

RESULT 99  
 AAV70456/C  
 ID AAV70456 standard; DNA; 240 BP.

XX AAV70456;  
 AC  
 DT 08-APR-1999 (first entry)

DE Partial sequence of HCV subtype 1a amplicon #73.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 OS Hepatitis C virus.

XX WO9850403-A1.

XX 12-NOV-1998.

XX 05-MAY-1998; 98WO-US003194.

XX 05-MAY-1997; 97US-00851588.

XX 19-SEP-1997; 97US-00934097.

XX 03-MAR-1998; 98US-00034205.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;

XX WPI; 1998-610317/51.

PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.

PS Example 5; Page 171; 279pp; English.

XX The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers; and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
 CC 61 represent partial sequences of different amplicons of hepatitis C  
 CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
 CC for identifying the HCV subtypes

SQ Sequence 240 BP; 47 A; 63 C; 78 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCCAACTACTC 20  
 |||||  
 Db 207 TTCCGACCCCAACTACTC 188

RESULT 100  
 AAV70461/C  
 ID AAV70461 standard; DNA; 240 BP.

XX AAV70461;  
 AC  
 DT 08-APR-1999 (first entry)

DE Partial sequence of HCV subtype 3a amplicon #91.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 OS Hepatitis C virus.

XX WO9850403-A1.

XX 12-NOV-1998.

XX 05-MAY-1998; 98WO-US003194.

XX 05-MAY-1997; 97US-00851588.

XX 19-SEP-1997; 97US-00934097.

XX 03-MAR-1998; 98US-00034205.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;

XX WPI; 1998-610317/51.

PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.

XX Example 5; Page 173; 279pp; English.

PS The invention relates to methods and compositions of detection and

CC characterisation of nucleic acid sequences and sequence changes. One

CC method of detection and characterisation comprises: (a) providing: (1) a

CC folded target having a DNA sequence comprising at least 1 double stranded

CC region and at least 1 single stranded region; and (11) at least 1 probe

CC complementary to at least a portion of the folded target; and (b) mixing

CC the target and probes so that the probe hybridises to form a probe

CC /folded target complex. Also provided are methods for determination of

CC structure formation in nucleic acid targets; for analysing folded nucleic

CC acids targets; and for analysis of nucleic acid structures. The methods

CC can be used to detect the presence of pathogenic nucleic acid sequences

CC indicative of an infection, the presence of variants or alleles of

CC mammalian genes associated with disease and cancers, and the

CC identification of the source of nucleic acids found in forensic samples,

CC as well as in paternity determinations. The methods allow simultaneous

CC analysis of both strands (e.g. the sense and antisense strands) and are

CC ideal for high-level multiplexing. The products produced are amenable to

CC qualitative, quantitative and positional analysis. The methods may be

CC performed in solution or in the solid phase (e.g. on a solid support).

CC The methods are powerful in that they allow for analysis of longer

CC fragments of nucleic acid than current methodologies. Sequences AAV70453-

CC 61 represent partial sequences of different amplicons of hepatitis C

CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used

CC for identifying the HCV subtypes

XX

SQ Sequence 240 BP; 47 A; 66 C; 77 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCACACTACTC 20

DB 208 TTGCGACCCACACTACTC 189

RESULT 101

ABLA6066/C

ID ABLA6066 standard; DNA; 240 BP.

AC ABLA6066;

XX

XX 26-APR-2002 (first entry)

DE Hepatitis C virus partial sequence #73 SEQ ID NO:33.

XX

KW Nucleic acid accessible hybridisation site; detection; hybridisation;

KW characterisation; identification; nucleic acid structure; diagnosis;

KW PCR primer; probe; ss.

XX

OS Hepatitis C virus.

OS Synthetic.

XX

XX WO200198537-A2.

XX

XX 27-DEC-2001.

XX

XX 15-JUN-2001; 2001WO-US019401.

XX

XX 17-JUN-2000; 2000US-0212308P.

XX

XX 15-JUN-2001; 2001US-00212308.

XX

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

XX

XX WPI; 2002-049698/06.

XX

PT Identifying oligonucleotides hybridizing to nucleic acids containing

PT secondary structure, useful in clinical diagnosis, comprises identifying

PT primers that interact with the target to form an extension product under

PT amplification conditions.

XX

XX Example 5; Page 366; 409pp; English.

PS The present invention describes a method for identifying oligonucleotides

CC with desired hybridisation properties to nucleic acid targets containing

CC secondary structure. The method comprises amplifying a target nucleic

CC acid having at least one accessible and one inaccessible site. Primers

CC that form an extension product are identified as the oligonucleotides

CC from the present invention can be used in novel detection methods for

CC clinical diagnostic purposes, including the detection and identification

CC of pathogenic organisms (e.g. HIV). The method allows the ability to

CC rapidly analyse nucleic acid structures. ABLA6034 to ABLA6367 represent

CC sequences used in the exemplification of the present invention

XX

SQ Sequence 240 BP; 47 A; 63 C; 78 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCACACTACTC 20

DB 207 TTGCGACCCACACTACTC 188

RESULT 102

ABLA6068/C

ID ABLA6068 standard; DNA; 240 BP.

AC ABLA6068;

XX

XX 26-APR-2002 (first entry)

DE Hepatitis C virus partial sequence #81 SEQ ID NO:35.

XX

KW Nucleic acid accessible hybridisation site; detection; hybridisation;

KW characterisation; identification; nucleic acid structure; diagnosis;

KW PCR primer; probe; ss.

XX

OS Hepatitis C virus.

OS Synthetic.

XX

XX WO200198537-A2.

XX

XX 27-DEC-2001.

XX

XX 15-JUN-2001; 2001WO-US019401.

XX

XX 17-JUN-2000; 2000US-0212308P.

XX

XX 15-JUN-2001; 2001US-00212308.

XX

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

XX

XX WPI; 2002-049698/06.

XX

PT Identifying oligonucleotides hybridizing to nucleic acids containing

PT secondary structure, useful in clinical diagnosis, comprises identifying

PT primers that interact with the target to form an extension product under

PT amplification conditions.

XX

XX Example 5; Page 366; 409pp; English.

XX

XX The present invention describes a method for identifying oligonucleotides

CC with desired hybridisation properties to nucleic acid targets containing

CC secondary structure. The method comprises amplifying a target nucleic

CC acid having at least one accessible and one inaccessible site. Primers

CC that form an extension product are identified as the oligonucleotides

CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention  
 CC

XX Sequence 240 BP; 45 A; 66 C; 79 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 DB 207 TTGGGACCCCAACTACTC 188

RESULT 103

ABL46071/C

ID ABL46071 standard; DNA; 240 BP.

XX ABL46071;

DT 26-APR-2002 (first entry)

DE Hepatitis C virus partial sequence #91 SEQ ID NO:38.

KM Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KM characterisation; identification; nucleic acid structure; diagnosis;  
 KM PCR primer; probe; seq.

OS Hepatitis C virus.  
 OS Synthetic.

PN WO200198537-A2.

PD 27-DEC-2001.

PF 15-JUN-2001; 2001WO-US019401.

PR 17-JUN-2000; 2000US-0212308P.

PR 15-JUN-2001; 2001US-00212308.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

DR WPI; 2002-049698/06.

XX Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX

PS Example 5; Page 367; 409pp; English.

XX The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention  
 CC

XX Sequence 240 BP; 47 A; 66 C; 77 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 DB 208 TTGGGACCCCAACTACTC 189

RESULT 104

ADK82261/C

ID ADK82261 standard; DNA; 240 BP.

XX ADK82261;

DT 03-JUN-2004 (first entry)

DE Hepatitis C virus polynucleotide seqid 38.

KM nucleic acid analysis; hepatitis C virus;  
 KM non-contiguous single-stranded region; NCSR; cleavage structure;  
 KM clinical; diagnostic; microorganism detection;  
 KM microorganism identification; hepatitis C virus; HCV; ds.

OS Hepatitis C virus.

XX US6709815-B1.

PD 23-MAR-2004.

PF 18-JUL-2000; 2000US-00402618.

PR 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MMD;

DR WPI; 2004-256067/24.

XX Analyzing nucleic acids, comprises mixing target nucleic acid such as  
 PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
 PT oligonucleotide and cleavage agent to form cleavage structure.  
 XX

PS Example 5; SEQ ID NO 38; 143pp; English.

XX The invention describes a method of analysing nucleic acids comprising  
 CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
 CC having non-contiguous single-stranded regions (NCSR) separated by an  
 CC intervening region, a bridging oligonucleotide capable of binding to the  
 CC first and second NCSR; a second oligonucleotide binding to a portion of  
 CC the first NCSR and a cleavage agent, and mixing the contents to form a  
 CC cleavage structure. The method is useful for analysing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC polynucleotide that is sufficient for identification of HCV subtypes  
 CC using the analysis methods of the invention.  
 CC

XX Sequence 240 BP; 47 A; 66 C; 77 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 DB 208 TTGGGACCCCAACTACTC 189

RESULT 105

ADK82258/C

```

ID      ADK82258 standard; DNA; 240 BP.
XX
XX      ADK82258;
AC
XX      03-JUN-2004 (first entry)
DT
XX      Hepatitis C virus polynucleotide seqid 35.
XX
XX      nucleic acid analysis; hepatitis C virus;
DE      non-contiguous single-stranded region; NCSR; cleavage structure;
XX      clinical; diagnostic; microorganism detection;
XX      microorganism identification; hepatitis C virus; HCV; ds.
OS
XX      Hepatitis C virus.
XX
XX      US6709815-B1.
PN
XX      23-MAR-2004.
PD
XX      18-JUL-2000; 2000US-00402618.
XX
XX      05-MAY-1997; 97US-00851588.
PR      19-SEP-1997; 97US-00934097.
PR      03-MAR-1998; 98US-00034205.
XX
XX      (THIR-) THIRD WAVE TECHNOLOGIES INC.
PA
XX      Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI      Anderson TA, Dahlberg JE;
XX
XX      WPI; 2004-256067/24.
DR
XX      Analyzing nucleic acids, comprises mixing target nucleic acid such as
PT      hepatitis C virus nucleic acid, bridging oligonucleotide, second
PT      oligonucleotide and cleavage agent to form cleavage structure.
XX
XX      Example 5; SEQ ID NO 35; 143bp; English.
PS
XX      The invention describes a method of analysing nucleic acids comprising
XX      providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX      having non-contiguous single-stranded regions (NCSR) separated by an
XX      intervening region, a bridging oligonucleotide capable of binding to the
XX      first and second NCSR; a second oligonucleotide binding to a portion of
XX      the first NCSR and a cleavage agent, and mixing the contents to form a
XX      cleavage structure. The method is useful for analysing nucleic acids,
XX      e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX      purposes and detection and identification of pathogenic microorganisms
XX      such as hepatitis C virus. This sequence represents a hepatitis C virus
XX      polynucleotide that is sufficient for identification of HCV subtypes
XX      using the analysis methods of the invention.
SQ
XX      Sequence 240 BP; 45 A; 66 C; 79 G; 50 T; 0 U; 0 Other;
SQ
Query Match      100.0%; Score 20; DB 12; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTCCGACCCCAACTACTC 20
DB      207 TTCCGACCCCAACTACTC 188

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KW      non-contiguous single-stranded region; NCSR; cleavage structure;
KW      clinical; diagnostic; microorganism detection;
KW      microorganism identification; hepatitis C virus; HCV; ds.
XX
XX      Hepatitis C virus.
XX
XX      US6709815-B1.
XX
XX      23-MAR-2004.
XX
XX      18-JUL-2000; 2000US-00402618.
XX
XX      05-MAY-1997; 97US-00851588.
PR      19-SEP-1997; 97US-00934097.
PR      03-MAR-1998; 98US-00034205.
XX
XX      (THIR-) THIRD WAVE TECHNOLOGIES INC.
PA
XX      Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI      Anderson TA, Dahlberg JE;
XX
XX      WPI; 2004-256067/24.
DR
XX      Analyzing nucleic acids, comprises mixing target nucleic acid such as
PT      hepatitis C virus nucleic acid, bridging oligonucleotide, second
PT      oligonucleotide and cleavage agent to form cleavage structure.
XX
XX      Example 5; SEQ ID NO 33; 143bp; English.
PS
XX      The invention describes a method of analysing nucleic acids comprising
XX      providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX      having non-contiguous single-stranded regions (NCSR) separated by an
XX      intervening region, a bridging oligonucleotide capable of binding to the
XX      first and second NCSR; a second oligonucleotide binding to a portion of
XX      the first NCSR and a cleavage agent, and mixing the contents to form a
XX      cleavage structure. The method is useful for analysing nucleic acids,
XX      e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX      purposes and detection and identification of pathogenic microorganisms
XX      such as hepatitis C virus. This sequence represents a hepatitis C virus
XX      polynucleotide that is sufficient for identification of HCV subtypes
XX      using the analysis methods of the invention.
SQ
XX      Sequence 240 BP; 47 A; 63 C; 78 G; 52 T; 0 U; 0 Other;
SQ
Query Match      100.0%; Score 20; DB 12; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTCCGACCCCAACTACTC 20
DB      207 TTCCGACCCCAACTACTC 188

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RESULT 106
ADK82256/c
ID      ADK82256 standard; DNA; 240 BP.
XX
XX      ADK82256;
AC
XX      03-JUN-2004 (first entry)
DT
XX      Hepatitis C virus polynucleotide seqid 33.
XX      nucleic acid analysis; hepatitis C virus;
KW

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RESULT 107
AAD43290/c
ID      AAD43290 standard; DNA; 241 BP.
XX
XX      AAD43290;
AC
XX      14-NOV-2002 (first entry)
DT
XX      HCV target DNA.
XX
XX      Amplification; target nucleic acid; ds.
XX
XX      Hepatitis C virus.
OS
XX      EPI236805-A1.
XX
XX      04-SEP-2002.
PD
XX      27-FEB-2002; 2002EP-00004483.
XX

```



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PR 02-MAR-2001; 2001EP-00105172.
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Jaeger S;
XX WPI; 2002-610695/66.
DR WPI; 2002-610695/66.
XX
XX Amplification of a target nucleic acid region using a specific control
PT sequence.
XX
XX Example 1; Page 18; 28pp; English.
XX
XX The invention relates to a method for amplification of a target nucleic
CC acid region in a sample using a specific control sequence. The invention
CC is also directed to a method of determination of a target nucleic acid
CC using a special control nucleic acid. Nucleic acids of the invention are
CC used as a control in a reaction for amplifying target nucleic acids and
CC as a control in a hybridisation reaction for determination of target
CC nucleic acids. The present sequence is HCV (Hepatitis C virus) type 1
CC target DNA. This sequence is used to illustrate the methods of the
CC invention.
XX
SQ Sequence 241 BP; 44 A; 67 C; 79 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 108
AAD43742/C
ID AAD43742 standard; DNA; 241 BP.
XX
XX AAD43742;
AC
XX 07-AUG-2003 (revised)
DT 14-NOV-2002 (first entry)
XX
XX HCV amplicon.
DE
XX Amplification; target nucleic acid; control nucleic acid; ds.
KW
XX Hepatitis C virus.
OS
XX
XX EP1236804-A1.
FN
XX
XX 04-SEP-2002.
PD
XX
XX 02-MAR-2001; 2001EP-00105172.
PF
XX
XX 02-MAR-2001; 2001EP-00105172.
PR
XX
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Jaeger S;
PI
XX WPI; 2002-610694/66.
DR
XX
XX Amplification of a target nucleic acid region using control sequences.
PT
XX
XX Example 1; Page 18; 29pp; English.
XX
XX The invention relates to a method for amplification of a target nucleic
CC acid region. The method is useful for amplification of a nucleic acid
CC molecule using control nucleic acid sequences. The control nucleic acid
CC sequences are at least in part parallel-complementary to the sequence of

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CC the target nucleic acid. The present sequence is HCV amplicon used to
CC illustrate the method of the invention. (Updated on 07-AUG-2003 to
CC correct OS field.)
XX
XX
SQ Sequence 241 BP; 44 A; 67 C; 79 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 109
AAV70454/C
ID AAV70454 standard; DNA; 244 BP.
XX
XX AAV70454;
AC
XX 08-APR-1999 (first entry)
DT
XX
XX Partial sequence of HCV subtype 1a amplicon #69.
DE
XX
XX Nucleic acid detection; nucleic acid characterisation; hybridisation;
KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.
KW
XX Hepatitis C virus.
OS
XX
XX WO9850403-A1.
PN
XX
XX 12-NOV-1998.
PD
XX
XX 05-MAY-1998; 98WO-US003194.
XX
XX 05-MAY-1997; 97US-00851588.
PR 19-SEP-1997; 97US-00934097.
PR 03-MAR-1998; 98US-00034205.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
PA
XX Dong F. Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MMD;
PI Anderson TA, Dahlberg JE;
XX
XX WPI; 1998-610317/51.
DR
XX
XX Detection and characterisation of nucleic acid sequences - by mixing a
PT folded target and one or more probes to form a probe/folded target
PT complex and detecting and characterising the complexes.
XX
XX
XX Example 5; Page 170-171; 279pp; English.
XX
XX The invention relates to methods and compositions of detection and
CC characterisation of nucleic acid sequences and sequence changes. One
CC method of detection and characterisation comprises: (a) providing: (i) a
CC folded target having a DNA sequence comprising at least 1 double stranded
CC region and at least 1 single stranded region; and (ii) at least 1 probe
CC complementary to at least a portion of the folded target; and (b) mixing
CC the target and probes so that the probe hybridises to form a probe
CC /folded target complex. Also provided are methods for determination of
CC structure formation in nucleic acid targets; for analysing folded nucleic
CC acids targets; and for analysis of nucleic acid structures. The methods
CC can be used for the detection and characterisation of nucleic acid
CC sequences to detect the presence of pathogenic nucleic acid sequences
CC indicative of an infection, the presence of variants or alleles of
CC mammalian genes associated with disease and cancers, and the
CC identification of the source of nucleic acids found in forensic samples,
CC as well as in paternity determinations. The methods allow simultaneous
CC analysis of both strands (e.g. the sense and antisense strands) and are
CC ideal for high-level multiplexing. The products produced are amenable to
CC qualitative, quantitative and positional analysis. The methods may be
CC performed in solution or in the solid phase (e.g. on a solid support).

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CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
 CC 61 represent partial sequences of different amplicons of hepatitis C  
 CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
 CC for identifying the HCV subtypes  
 CC XX

SO Sequence 244 BP; 49 A; 64 C; 79 G; 52 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 20; DB 2; Length 244;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCGACACTACTC 20  
 Db 208 TTGCGACCCGACACTACTC 189

RESULT 110  
 ID AAV70450 standard; DNA; 244 BP.

XX AAV70450;  
 AC AAV70449;  
 DT 08-APR-1999 (first entry)  
 DE HCV subtype 1b PCR fragment.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 OS Hepatitis C virus.

XX WO9850403-A1.

PN 12-NOV-1998.

PD 05-MAY-1998; 98WO-US003194.

PF 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

(THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;

DR WPI; 1998-610317/51.

XX Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 XX

XX Example 3; Page 169; 279pp; English.

XX The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to

CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70449-  
 CC 52 represent a hepatitis C virus (HCV) subtype sequences produced by PCR.  
 CC These PCR products can be used in hybridisation analysis using multiple  
 CC capture probes for HCV genotyping  
 CC XX

SO Sequence 244 BP; 44 A; 67 C; 81 G; 52 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 20; DB 2; Length 244;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCGACACTACTC 20  
 Db 208 TTGCGACCCGACACTACTC 189

RESULT 111  
 ID AAV70449 standard; DNA; 244 BP.

XX AAV70449;  
 AC AAV70449;  
 DT 08-APR-1999 (first entry)  
 DE HCV subtype 1a PCR fragment.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 OS Hepatitis C virus.

XX WO9850403-A1.

PN 12-NOV-1998.

PD 05-MAY-1998; 98WO-US003194.

PF 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

(THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;

DR WPI; 1998-610317/51.

XX Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 XX

XX Example 3; Page 169; 279pp; English.

XX The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous

CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70449-  
 CC 52 represent a hepatitis C virus (HCV) subtype sequences produced by PCR.  
 CC These PCR products can be used in hybridisation analysis using multiple  
 CC capture probes for HCV genotyping

SO Sequence 244 BP; 46 A; 67 C; 80 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
 DB 208 TTCCGACCCCACTACTC 189

RESULT 112  
 AAV70452/C  
 ID AAV70452 standard; DNA; 244 BP.  
 XX  
 AC AAV70452;  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE HCV subtype 3a PCR fragment.  
 XX  
 KM Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN MO9850403-A1.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US003194.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934087.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 XX  
 DR WPI; 1998-610317/51.  
 XX  
 PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 XX  
 PS Example 3; Page 170; 279pp; English.  
 XX  
 CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the

CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70449-  
 CC 52 represent a hepatitis C virus (HCV) subtype sequences produced by PCR.  
 CC These PCR products can be used in hybridisation analysis using multiple  
 CC capture probes for HCV genotyping

SO Sequence 244 BP; 48 A; 69 C; 79 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
 DB 208 TTCCGACCCCACTACTC 189

RESULT 113  
 ABL46062/C  
 ID ABL46062 standard; DNA; 244 BP.  
 XX  
 AC ABL46062;  
 XX  
 DT 26-APR-2002 (first entry)  
 XX  
 DE Hepatitis C virus subtype 3a target DNA PCR product SEQ ID NO:29.  
 XX  
 KM Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KM characterisation; identification; nucleic acid structure; diagnosis;  
 KM PCR primer; probe; ss.  
 XX  
 OS Hepatitis C virus.  
 OS Synthetic.  
 XX  
 PN MO200198537-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 15-JUN-2001; 2001WO-US019401.  
 XX  
 PR 17-JUN-2000; 2000US-0212308P.  
 PR 15-JUN-2001; 2001US-00212308.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Lyamichiev V, Allawi H, Dong F, Neri BP, Vener IT;  
 PI WPI; 2002-049696/06.  
 XX  
 PT Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX  
 PS Example 3; Page 365; 409pp; English.  
 XX  
 CC The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention

XX Sequence 244 BP; 48 A; 69 C; 79 G; 48 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 20; DB 6; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACACTACTC 20  
DB 208 TTGCGACCCCAACACTACTC 189

RESULT 114  
ABL46059/c  
ID ABL46059 standard; DNA; 244 BP.

AC ABL46059;  
XX  
XX 26-APR-2002 (first entry)

DE Hepatitis C virus subtype 1a target DNA PCR product SEQ ID NO:26.

KM Nucleic acid accessible hybridisation site; detection; hybridisation;  
KM characterisation; identification; nucleic acid structure; diagnosis;  
KM PCR primer; probe; ss.

OS Hepatitis C virus.  
OS Synthetic.

PN MO200198537-A2.

PD 27-DEC-2001.

PF 15-JUN-2001; 2001WO-US019401.

PR 17-JUN-2000; 2000US-0212308P.

PR 15-JUN-2001; 2001US-00212308.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

DR WPI; 2002-049698/06.

XX Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.

XX Example 3; Page 364; 409pp; English.

XX The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention

SQ Sequence 244 BP; 46 A; 67 C; 80 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACACTACTC 20  
DB 208 TTGCGACCCCAACACTACTC 189

RESULT 115  
ABL46060/c  
ID ABL46060 standard; DNA; 244 BP.

AC ABL46060;  
XX  
XX 26-APR-2002 (first entry)

DE Hepatitis C virus subtype 1b target DNA PCR product SEQ ID NO:27.

KM Nucleic acid accessible hybridisation site; detection; hybridisation;  
KM characterisation; identification; nucleic acid structure; diagnosis;  
KM PCR primer; probe; ss.

OS Hepatitis C virus.  
OS Synthetic.

PN MO200198537-A2.

PD 27-DEC-2001.

PF 15-JUN-2001; 2001WO-US019401.

PR 17-JUN-2000; 2000US-0212308P.

PR 15-JUN-2001; 2001US-00212308.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

DR WPI; 2002-049698/06.

XX Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.

XX Example 3; Page 364; 409pp; English.

XX The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention

SQ Sequence 244 BP; 44 A; 67 C; 81 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACACTACTC 20  
DB 208 TTGCGACCCCAACACTACTC 189

RESULT 116

ABL46064/c  
ID ABL46064 standard; DNA; 244 BP.

AC ABL46064;

XX 26-APR-2002 (first entry)

DE Hepatitis C virus partial sequence #69 SEQ ID NO:31.

KW Nucleic acid accessible hybridisation site; detection; hybridisation;  
KM Characterisation; identification; nucleic acid structure; diagnosis;  
XX PCR primer; probe; ss.  
XX Hepatitis C virus.  
OS Synthetic.  
XX WO200198537-A2.  
PN  
XX  
PD 27-DEC-2001.  
XX  
PF 15-JUN-2001; 2001WO-US019401.  
XX  
PR 17-JUN-2000; 2000US-0212308P.  
PR 15-JUN-2001; 2001US-00212308.  
XX  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;  
XX  
DR WPI; 2002-049698/06.  
XX  
PT Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.  
XX  
XX Example 5; Page 365; 409pp; English.  
XX  
CC The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 244 BP; 49 A; 64 C; 79 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 117  
ADK82254/C  
ID ADK82254 standard; DNA; 244 BP.  
XX  
AC ADK82254;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Hepatitis C virus polynucleotide seqid 31.  
XX  
KW nucleic acid analysis; hepatitis C virus;  
KW non-contiguous single-stranded region; NCSR; cleavage structure;  
KW clinical; diagnostic; microorganism detection;  
KW microorganism identification; hepatitis C virus; HCV; ds.  
XX  
OS Hepatitis C virus.  
XX  
XX US6709815-B1.  
XX  
XX 23-MAR-2004.  
XX

PF 18-JUN-2000; 2000US-00402618.  
XX  
XX 05-MAY-1997; 97US-00851588.  
PR 19-SEP-1997; 97US-00934097.  
PR 03-MAR-1998; 98US-00034205.  
XX  
XX  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
PI Anderson TA, Dahlberg JE;  
XX  
XX WPI; 2004-256067/24.  
XX  
DR  
XX  
PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX  
XX Example 5; SEQ ID NO 31; 143pp; English.  
XX  
CC The invention describes a method of analysing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR; a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analysing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC polynucleotide that is sufficient for identification of HCV subtypes  
XX using the analysis methods of the invention.

Query Match 100.0%; Score 20; DB 12; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 118  
ADK82351  
ID ADK82351 standard; RNA; 244 BP.  
XX  
AC ADK82351;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Hepatitis C virus subtype 1a 5'UTR RNA.  
XX  
KW nucleic acid analysis; hepatitis C virus;  
KW non-contiguous single-stranded region; NCSR; cleavage structure;  
KW clinical; diagnostic; microorganism detection;  
KW microorganism identification; hepatitis C virus; HCV; subtype 1a; ds;  
KW 5'UTR; 5' untranslated region.  
XX  
OS Hepatitis C virus.  
XX  
XX US6709815-B1.  
XX  
XX 23-MAR-2004.  
XX  
PF 18-JUN-2000; 2000US-00402618.  
XX  
PR 05-MAY-1997; 97US-00851588.  
PR 19-SEP-1997; 97US-00934097.  
PR 03-MAR-1998; 98US-00034205.  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX

PI Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
PI Anderson TA, Dahlberg JE;  
XX WPI; 2004-256067/24.  
XX  
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX  
PS Example 8; SEQ ID NO 128; 143bp; English.  
XX  
XX The invention describes a method of analyzing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR, a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analyzing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC subtype 1a 5'UTR that can be used in the analysis of folded structures  
CC using the method of the invention.  
SQ Sequence 244 BP; 51 A; 80 C; 67 G; 0 T; 46 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 244;  
Best Local Similarity 80.0%; Pred. No. 0.054; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
DB 37 TTGCGACCCCAACTACTC 56  
RESULT 119  
ADK82250/C  
ID ADK82250 standard; DNA; 244 BP.  
XX  
XX ADK82250;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Hepatitis C virus subtype 1b polynucleotide segid 27.  
XX  
XX nucleic acid analysis; hepatitis C virus;  
XX non-contiguous single-stranded region; NCSR; cleavage structure;  
XX clinical; diagnostic; microorganism detection;  
XX microorganism identification; hepatitis C virus; HCV; subtype 1b; ds.  
OS  
XX Hepatitis C virus.  
XX  
XX US6709815-B1.  
XX  
XX 23-MAR-2004.  
XX  
XX 18-JUL-2000; 2000US-00402618.  
XX  
XX 05-MAY-1997; 97US-00851588.  
XX  
XX 19-SEP-1997; 97US-00934097.  
XX  
XX 03-MAR-1998; 98US-00034205.  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
XX Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
XX Anderson TA, Dahlberg JE;  
XX  
XX WPI; 2004-256067/24.  
XX  
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX

PS Example 3; SEQ ID NO 27; 143bp; English.  
XX  
XX The invention describes a method of analyzing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR, a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analyzing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC subtype 1b polynucleotide identified using the analysis methods of the  
CC invention.  
SQ Sequence 244 BP; 44 A; 67 C; 81 G; 52 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189  
RESULT 120  
ADK82347  
ID ADK82347 standard; DNA; 244 BP.  
XX  
XX ADK82347;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Hepatitis C virus subtype 1a 5'UTR.  
XX  
XX nucleic acid analysis; hepatitis C virus;  
XX non-contiguous single-stranded region; NCSR; cleavage structure;  
XX clinical; diagnostic; microorganism detection;  
XX microorganism identification; hepatitis C virus; HCV; subtype 1a; ds;  
XX 5'UTR; 5' untranslated region.  
XX  
XX Hepatitis C virus.  
OS  
XX US6709815-B1.  
XX  
XX 23-MAR-2004.  
XX  
XX 18-JUL-2000; 2000US-00402618.  
XX  
XX 05-MAY-1997; 97US-00851588.  
XX  
XX 19-SEP-1997; 97US-00934097.  
XX  
XX 03-MAR-1998; 98US-00034205.  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
XX Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
XX Anderson TA, Dahlberg JE;  
XX  
XX WPI; 2004-256067/24.  
XX  
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX  
XX Example 8; SEQ ID NO 124; 143bp; English.  
XX  
XX The invention describes a method of analyzing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR, a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC the first NCSR and a cleavage agent, and mixing the contents to form a

CC cleavage structure. The method is useful for analysing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC subtype 1a 5'UTR that can be used in the analysis of folded structures  
CC using the method of the invention.

XX Sequence 244 BP; 51 A; 80 C; 67 G; 46 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 37 TTGGGACCCCAACTACTC 56

RESULT 121  
ADK82252/C  
ID ADK82252 standard; DNA; 244 BP.

XX AC ADK82252;

XX DT 03-JUN-2004 (first entry)

XX DE Hepatitis C virus subtype 3a polynucleotide seqid 29.

XX KW nucleic acid analysis; hepatitis C virus;  
KW non-contiguous single-stranded region; NCSR; cleavage structure;

XX KW clinical; diagnostic; microorganism detection;

XX KW microorganism identification; hepatitis C virus; HCV; subtype 3a; ds.

XX OS Hepatitis C virus.

XX XX US6709815-B1.

XX PD 23-MAR-2004.

XX PF 18-JUL-2000; 2000US-00402618.

XX PR 05-MAY-1997; 97US-00851588.

XX PR 19-SEP-1997; 97US-00934097.

XX PR 03-MAR-1998; 98US-00034205.

XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;

XX PI Anderson TA, Dahlberg JE;

XX XX WPI; 2004-256067/24.

XX DR WPI; 2004-256067/24.

XX PT Analyzing nucleic acids, comprises mixing target nucleic acid such as

XX PT hepatitis C virus nucleic acid, bridging oligonucleotide, second

XX PT oligonucleotide and cleavage agent to form cleavage structure.

XX PS Example 3; SEQ ID NO 29; 143pp; English.

XX XX The invention describes a method of analysing nucleic acids comprising

XX CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid

XX CC having non-contiguous single-stranded regions (NCSR) separated by an

XX CC intervening region, a bridging oligonucleotide capable of binding to the

XX CC first and second NCSR, a second oligonucleotide binding to a portion of

XX CC the first NCSR and a cleavage agent, and mixing the contents to form a

XX CC cleavage structure. The method is useful for analysing nucleic acids,

XX CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic

XX CC purposes and detection and identification of pathogenic microorganisms

XX CC such as hepatitis C virus. This sequence represents a hepatitis C virus

XX CC subtype 3a polynucleotide identified using the analysis methods of the

XX CC invention.

XX CC Sequence 244 BP; 48 A; 69 C; 79 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 122  
ADK82350  
ID ADK82350 standard; DNA; 244 BP.

XX AC ADK82350;

XX DT 03-JUN-2004 (first entry)

XX DE Hepatitis C virus subtype 3a 5'UTR.

XX KW nucleic acid analysis; hepatitis C virus;  
KW non-contiguous single-stranded region; NCSR; cleavage structure;

XX KW clinical; diagnostic; microorganism detection;

XX KW microorganism identification; hepatitis C virus; HCV; subtype 3a; ds;  
5'UTR; 5' untranslated region.

XX OS Hepatitis C virus.

XX XX US6709815-B1.

XX PD 23-MAR-2004.

XX PF 18-JUL-2000; 2000US-00402618.

XX PR 05-MAY-1997; 97US-00851588.

XX PR 19-SEP-1997; 97US-00934097.

XX PR 03-MAR-1998; 98US-00034205.

XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;

XX PI Anderson TA, Dahlberg JE;

XX XX WPI; 2004-256067/24.

XX PS Example 8; SEQ ID NO 127; 143pp; English.

XX XX The invention describes a method of analysing nucleic acids comprising

XX CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid

XX CC having non-contiguous single-stranded regions (NCSR) separated by an

XX CC intervening region, a bridging oligonucleotide capable of binding to the

XX CC first and second NCSR, a second oligonucleotide binding to a portion of

XX CC the first NCSR and a cleavage agent, and mixing the contents to form a

XX CC cleavage structure. The method is useful for analysing nucleic acids,

XX CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic

XX CC purposes and detection and identification of pathogenic microorganisms

XX CC such as hepatitis C virus. This sequence represents a hepatitis C virus

XX CC subtype 3a 5'UTR that can be used in the analysis of folded structures

XX CC using the method of the invention.

XX CC Sequence 244 BP; 48 A; 79 C; 69 G; 48 T; 0 U; 0 Other;

QY 1 TTGGGACCCCAACTACTC 20

DB 37 TTGGGACCCCAACTACTC 56

DE	Hepatitis C virus subtype 1b 5'UTR.
XX	
KW	nucleic acid analysis; hepatitis C virus;
KW	non-contiguous single-stranded region; NCSR; cleavage structure;
KW	clinical; diagnostic; microorganism detection;
KW	microorganism identification; hepatitis C virus; HCV; subtype 1b; ds;
XX	5'UTR; 5' untranslated region.
OS	Hepatitis C virus.
PN	
PM	US6709815-B1.
PD	
BD	23-MAR-2004.
XX	
PF	18-JUL-2000; 2000US-00402618.
XX	
PR	05-MAY-1997; 97US-00851588.
PR	19-SEP-1997; 97US-00934097.
PR	03-MAR-1998; 98US-00034205.
XX	
PA	(THIR-) THIRD WAVE TECHNOLOGIES INC.
PI	Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI	Anderson TA, Dahlberg JE,
XX	
DR	WPI; 2004-256067/24.
XX	
PT	Analyzing nucleic acids, comprises mixing target nucleic acid such as
PT	hepatitis C virus nucleic acid, bridging oligonucleotide, second
PT	oligonucleotide and cleavage agent to form cleavage structure.
XX	
PS	Example 8; SEQ ID NO 125; 143pp; English.
XX	
CC	The invention describes a method of analyzing nucleic acids comprising
CC	providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
CC	having non-contiguous single-stranded regions (NCSR) separated by an
CC	intervening region, a bridging oligonucleotide capable of binding to the
CC	C first and second NCSR; a second oligonucleotide binding to a portion of
CC	the first NCSR and a cleavage agent, and mixing the contents to form a
CC	cleavage structure. The method is useful for analyzing nucleic acids,
CC	e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
CC	purposes and detection and identification of pathogenic microorganisms
CC	such as hepatitis C virus. This sequence represents a hepatitis C virus
CC	subtype 1b 5'UTR that can be used in the analysis of folded structures
CC	using the method of the invention.
XX	
SQ	Sequence 244 BP; 52 A; 81 C; 67 G; 44 T; 0 U; 0 Other;
Query Match	100.0%; Score 20; DB 12; Length 244;
Best Local Similarity	100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTGGGACCCCAACTACTC 20
DB	37 TTGGGACCCCAACTACTC 56
RESULT 125	
AD005655/C	
ID	ADO05655 standard; DNA; 244 BP.
XX	
AC	ADO05655;
XX	
DT	15-JUL-2004 (first entry)
XX	
DE	HCV 5' NCR (non coding region) template DNA.
XX	
KW	Nucleic acid amplification; mutation detection; cytostatic;
KW	antiinflammatory; hepatotropic; virucide; cancer; ds.
XX	
OS	Hepatitis C virus.
XX	



```

XX 29-APR-2004.
PD
XX
PF 17-OCT-2003; 2003WO-KR002179.
XX
XX 18-OCT-2002; 2002KR-00063832.
PR
XX 02-SEP-2003; 2003KR-00061066.
PR
XX (GENE-) GENEMATRIX INC.
PA
XX
XX Kim N, Kim S, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H,
PI Jee M, Hwang S, Hong S;
XX
XX WPI; 2004-348478/32.
DR
XX
XX Detecting a mutation, useful in diagnosing and creating e.g. cancer or
PT hepatitis, comprises generating fragments of polynucleotides using
PT specific primers and measuring molecular weight of cleaved fragments.
XX
XX Example 4; SEQ ID NO 16; 58bp; English.
PS
XX
XX The invention relates to detecting a mutation. The method involves
CC amplifying a target polynucleotide using a forward primer and a reverse
CC primer; generating fragments of two or more single-stranded
CC polynucleotides including one or more mutations sequence having the size
CC of 2-33 bases by cleaving the amplified target polynucleotide with
CC restriction enzymes, where the second restriction enzyme does not react
CC while a first restriction enzyme is reacted with the amplified
CC polynucleotide; and measuring the molecular weight of the cleaved
CC fragments. The polynucleotide is cleaved to include one mutation among
CC two or more different mutations in only one single stranded
CC polynucleotide fragment and all mutations in the other single stranded
CC nucleotide fragment. Restrictions enzyme treatment step is performed
CC using restriction enzymes having different optimum temperatures. The
CC method is useful in detecting a mutation. The method and primer are
CC useful in diagnosing, prognosis, creating and preventing a disease, e.g.
CC cancer or hepatitis B or C virus. The present sequence represents a HCV
CC 5' NCR (non coding region) template DNA sequence.
XX
XX Sequence 244 BP; 46 A; 67 C; 80 G; 51 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 12; Length 244;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCGGACCCCAACTACTC 20
DB 208 TTCGGACCCCAACTACTC 189

```

```

XX (CHTR ) CHIRON CORP.
PA
XX
XX Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX
XX WPI; 1992-398869/48.
DR
XX
XX Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
PT related to HCV-1, useful for treating and detecting HCV-1 infections and
PT as a vaccine.
XX
XX Claim 8; Page 85; 186pp; English.
PS
XX
XX This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
CC within the 5' untranslated region of HCV-1 of genotype GI1. This sequence
CC (from isolate us4) is identical to that of isolates nac5, arg2, spl, ghl
CC and 115; it differs by one nucleotide from isolate jhl (AAQ31072). The
CC sequence is a preferred example of an oligonucleotide for use as a probe
CC in hybridisation assays, as a primer for synthesis of HCV genotype-
CC specific nucleic acid, as a binding partner for separating HCV nucleic
CC acid or as an antisense oligonucleotide to prevent expression of HCV
CC genes. Polypeptides encoded by oligonucleotides of the invention (no
CC sequences given in the specification) are useful in vaccines against HCV
CC and to produce antibodies to detect the virus. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 252 BP; 43 A; 72 C; 84 G; 53 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 2; Length 252;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCGGACCCCAACTACTC 20
DB 186 TTCGGACCCCAACTACTC 167

```

CC This is a non-HCV-1 sequence which corresponds to a nucleotide sequence  
 CC within the 5' untranslated region of HCV-1 of genotype GI. The sequence is  
 CC a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

XX  
 SQ Sequence 252 BP; 45 A; 72 C; 83 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGAGCCCAACACTACTC 20  
 DB 186 TTGCGAGCCCAACACTACTC 167

RESULT 128

AAQ31070/c  
 ID AAQ31070 standard; DNA; 252 BP.

XX AAQ31070;

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

DE HCV-1 genotype GI 5'UT region sequence 121.

KW Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;  
 ss.

OS Synthetic.

PN WO9219743-A2.

XX 12-NOV-1992.

PF 08-MAY-1992; 92WO-US004036.

PR 08-MAY-1991; 91US-00697326.

XX (CHIR) CHIRON CORP.

PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;

XX WPI; 1992-398869/48.

PT Compn. comprising a non-hepatitis C virus-1 nucleotide sequence -  
 PT related to HCV-1, useful for treating and detecting HCV-1 infections and  
 PT as a vaccine.

PS Claim 8; Page 84; 186pp; English.

XX This is a non-HCV-1 sequence which corresponds to a nucleotide sequence  
 CC within the 5' untranslated region of HCV-1 of genotype GI. The sequence is  
 CC a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

SQ Sequence 252 BP; 45 A; 71 C; 83 G; 53 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGAGCCCAACACTACTC 20  
 DB 186 TTGCGAGCCCAACACTACTC 167

RESULT 129

AAQ31068/c  
 ID AAQ31068 standard; DNA; 252 BP.

XX AAQ31068;

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

DE HCV-1 genotype GI 5'UT region sequence sp2.

KW Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;  
 ss.

OS Synthetic.

PN WO9219743-A2.

XX 12-NOV-1992.

PF 08-MAY-1992; 92WO-US004036.

PR 08-MAY-1991; 91US-00697326.

XX (CHIR) CHIRON CORP.

PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;

XX WPI; 1992-398869/48.

PT Compn. comprising a non-hepatitis C virus-1 nucleotide sequence -  
 PT related to HCV-1, useful for treating and detecting HCV-1 infections and  
 PT as a vaccine.

PS Claim 8; Page 82-83; 186pp; English.

XX This is a non-HCV-1 sequence which corresponds to a nucleotide sequence  
 CC within the 5' untranslated region of HCV-1 of genotype GI. The sequence is  
 CC a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

SQ Sequence 252 BP; 44 A; 71 C; 84 G; 53 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGAGCCCAACACTACTC 20  
 DB 186 TTGCGAGCCCAACACTACTC 167

RESULT 130

AAQ31081/c  
 ID AAQ31081 standard; DNA; 252 BP.

XX AAQ31081;

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

```

XX DE HCV-1 genotype GIV 5'UT region sequence gj61329.
XX XX Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;
XX KM ss.
XX OS Synthetic.
XX PN WO9219743-A2.
XX PD 12-NOV-1992.
XX PF 08-MAY-1992; 92MO-US004036.
XX PR 08-MAY-1991; 91US-00697326.
XX PA (CHIR ) CHIRON CORP.
XX PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX DR WPI, 1992-398869/48.
XX PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX PT related to HCV-1, useful for treating and detecting HCV-1 infections and
XX PT as a vaccine.
XX PS Claim 8; Page 93; 186pp; English.
XX CC This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
XX CC within the 5'untranslated region of HCV-1 of genotype GIV. The sequence
XX CC is a preferred example of an oligonucleotide for use as a probe in
XX CC hybridisation assays, as a primer for synthesis of HCV genotype-specific
XX CC nucleic acid, as a binding partner for separating HCV nucleic acid or as
XX CC an antisense oligonucleotide to prevent expression of HCV genes.
XX CC Polypeptides encoded by oligonucleotides of the invention (no sequences
XX CC given in the specification) are useful in vaccines against HCV and to
XX CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX SQ Sequence 252 BP; 46 A; 71 C; 83 G; 52 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 252;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 186 TTCCGACCCCAACTACTC 167

RESULT 131
AAQ31080/c
ID AAQ31080 standard; DNA; 252 BP.
XX
XX AC AAQ31080;
XX DT 25-MAR-2003 (revised)
XX DT 24-MAR-1993 (first entry)
XX
XX DE HCV-1 genotype GIV 5'UT region sequence s21.
XX KM Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;
XX KM ss.
XX OS Synthetic.
XX PN WO9219743-A2.
XX PD 12-NOV-1992.
XX PF 08-MAY-1992; 92MO-US004036.
XX PR 08-MAY-1991; 91US-00697326.
XX PA (CHIR ) CHIRON CORP.
XX PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX DR WPI, 1992-398869/48.
XX PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX PT related to HCV-1, useful for treating and detecting HCV-1 infections and
XX PT as a vaccine.
XX PS Claim 8; Page 93; 186pp; English.
XX CC This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
XX CC within the 5'untranslated region of HCV-1 of genotype GIV. The sequence
XX CC is a preferred example of an oligonucleotide for use as a probe in
XX CC hybridisation assays, as a primer for synthesis of HCV genotype-specific
XX CC nucleic acid, as a binding partner for separating HCV nucleic acid or as
XX CC an antisense oligonucleotide to prevent expression of HCV genes.
XX CC Polypeptides encoded by oligonucleotides of the invention (no sequences
XX CC given in the specification) are useful in vaccines against HCV and to
XX CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX SQ Sequence 252 BP; 46 A; 71 C; 83 G; 52 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 252;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 186 TTCCGACCCCAACTACTC 167

```

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XX PA (CHIR ) CHIRON CORP.
XX PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX DR WPI, 1992-398869/48.
XX PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX PT related to HCV-1, useful for treating and detecting HCV-1 infections and
XX PT as a vaccine.
XX PS Claim 8; Page 92; 186pp; English.
XX CC This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
XX CC within the 5'untranslated region of HCV-1 of genotype GIV. The sequence
XX CC is a preferred example of an oligonucleotide for use as a probe in
XX CC hybridisation assays, as a primer for synthesis of HCV genotype-specific
XX CC nucleic acid, as a binding partner for separating HCV nucleic acid or as
XX CC an antisense oligonucleotide to prevent expression of HCV genes.
XX CC Polypeptides encoded by oligonucleotides of the invention (no sequences
XX CC given in the specification) are useful in vaccines against HCV and to
XX CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX SQ Sequence 252 BP; 46 A; 71 C; 83 G; 52 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 252;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 186 TTCCGACCCCAACTACTC 167

RESULT 132
AAQ31067/c
ID AAQ31067 standard; DNA; 252 BP.
XX
XX AC AAQ31067;
XX DT 25-MAR-2003 (revised)
XX DT 24-MAR-1993 (first entry)
XX
XX DE HCV-1 genotype GI 5'UT region sequence aus.
XX KM Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;
XX KM ss.
XX OS Synthetic.
XX PN WO9219743-A2.
XX PD 12-NOV-1992.
XX PF 08-MAY-1992; 92MO-US004036.
XX PR 08-MAY-1991; 91US-00697326.
XX PA (CHIR ) CHIRON CORP.
XX PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX DR WPI, 1992-398869/48.
XX PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX PT related to HCV-1, useful for treating and detecting HCV-1 infections and
XX PT as a vaccine.
XX PS Claim 8; Page 82; 186pp; English.
XX CC This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
XX CC within the 5'untranslated region of HCV-1 of genotype GI. The sequence is

```

CC a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX

SO Sequence 252 BP; 46 A; 73 C; 81 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
 DB 186 TTGCGACCCACACTACTC 167

RESULT 133

ID AAQ31066 standard; DNA; 252 BP.

AC AAQ31066;

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

DE HCV-1 genotype GI 5'UT region sequence us5.

KW Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;  
 ss.

OS Synthetic.

PN WO9219743-A2.

PD 12-NOV-1992.

PF 08-MAY-1992; 92WO-US004036.

PR 08-MAY-1991; 91US-00697326.

PA (CHIR) CHIRON CORP.

PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;

DR WPI; 1992-398869/48.

PT Composn. comprising a non-hepatitis C virus-1 nucleotide sequence -  
 PT related to HCV-1, useful for treating and detecting HCV-1 infections and  
 PT as a vaccine.

PS Claim 8; Page 81; 186pp; English.

XX This is a non-HCV-1 sequence which corresponds to a nucleotide sequence  
 XX within the 5'untranslated region of HCV-1 of genotype GI. The sequence is  
 CC a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX

SO Sequence 252 BP; 44 A; 72 C; 83 G; 53 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
 DB 186 TTGCGACCCACACTACTC 167

RESULT 134

ID AAQ31072 standard; DNA; 252 BP.

AC AAQ31072;

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

DE HCV-1 genotype GI 5'UT region sequence jhl.

KW Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;  
 ss.

OS Synthetic.

PN WO9219743-A2.

PD 12-NOV-1992.

PF 08-MAY-1992; 92WO-US004036.

PR 08-MAY-1991; 91US-00697326.

PA (CHIR) CHIRON CORP.

PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;

DR WPI; 1992-398869/48.

PT Composn. comprising a non-hepatitis C virus-1 nucleotide sequence -  
 PT related to HCV-1, useful for treating and detecting HCV-1 infections and  
 PT as a vaccine.

PS Claim 8; Page 86; 186pp; English.

XX This is a non-HCV-1 sequence which corresponds to a nucleotide sequence  
 XX within the 5'untranslated region of HCV-1 of genotype GI. The sequence  
 CC is a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX

SO Sequence 252 BP; 43 A; 71 C; 84 G; 54 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
 DB 186 TTGCGACCCACACTACTC 167

RESULT 135

ID AAQ32981 standard; DNA; 256 BP.

AC AAQ32981;

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)  
 DT 14-MAY-1993 (first entry)

```

DE HCV EI 5' non-coding region.
XX
XX PCR; amplification; prototype; HCV pt; ss.
KM Hepatitis C virus; HCVel.
OS
XX WO9221759-A1.
PN
XX 10-DEC-1992.
PD
XX
XX 04-JUN-1992; 92WO-FR000501.
PF
XX 06-JUN-1991; 91FR-00006882.
PR
XX (INSP ) INST PASTEUR.
PA
XX Brechot C, Kremendorf D, Porchon C;
XX
XX WPI; 1992-433657/52.
DR
XX
XX New nucleotide and peptide sequences - specific for French isolate of
PT hepatitis C virus and useful in diagnosing and treating related
PT infections.
PS
XX Disclosure; Fig 2; 50pp; French.
XX
XX RNA was extracted from the serum of an HCV-positive blood donor, subjected
CC to reverse transcription and the cDNA formed amplified by PCR.
CC Amplification prods. were cloned, screened with a probe derived from the
CC HCV prototype and inserts sequenced. The results showed marked
CC conservation in the non-coding region, significant variability in the
CC structural region (encoding envelope proteins) and reduced variability in
CC the non-structural region. The non-coding region corresponds to positions
CC -259 to -4 of HCV prototype (HCV pt) (WO-A-90/14436). (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 256 BP; 44 A; 73 C; 85 G; 54 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCCGACCCCAACTACTC 20
DB 193 TTCCGACCCCAACTACTC 174

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XX Porchon C, Brechot C, Kremendorf D;
XX
XX WPI; 1999-394595/33.
DR
XX
XX Nucleotides and peptides from hepatitis C virus isolate for detecting EI-
PT specific antigens.
XX
XX Disclosure; Col 9-10; 45pp; English.
PS
XX This sequence is the hepatitis C virus (HCV) EI 5' non-coding region. The
CC invention relates to human or murine monoclonal antibodies directed
CC against a HCV EI protein sequence. The monoclonal antibodies and their
CC fragments are useful for the in vitro diagnosis of HCV EI-specific
CC antigens. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 256 BP; 44 A; 73 C; 85 G; 54 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCCGACCCCAACTACTC 20
DB 193 TTCCGACCCCAACTACTC 174

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OY 1 TTGGGACCCCACTACTC 20  
 DB 193 TTGGGACCCCACTACTC 174

RESULT 138  
 ADF08496/c  
 ID ADF08496 standard; DNA, 263 BP.

AC ADF08496;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus (HCV) genomic DNA 5'UTR region.

KM Hepatitis C virus; HCV; inducible promoter; HCV infection; ds; 5'UTR.

OS Hepatitis C virus.

PN US2003148267-A1.

PD 07-AUG-2003.

PF 08-NOV-2002; 2002US-00292129.

PR 09-NOV-2001; 2001US-0345405P.

PA (SCHM/) SCHMIDT E V.

PI (CHUN/) CHUNG R T.

DR Schmidt EV, Chung RT;

WPI; 2003-897533/82.

Identifying a compound that increases the mutation rate of hepatitis C virus (HCV) comprises detecting an increase in HCV quasispecies produced by the cell in the presence of the candidate compound.

Example 13; SEQ ID NO 13; 35pp; English.

The invention relates to a method for identifying a compound that increases the mutation rate of hepatitis C virus (HCV), comprising detecting an increase in HCV quasispecies produced by the cell in the presence of the candidate compound by e.g. sequencing HCV nucleic acid molecules isolated from the test cell. The method involves providing a test cell containing a nucleic acid molecule comprising a first nucleotide sequence consisting of an infectious hepatitis C viral genome or its DNA copy, a second nucleotide consisting of a ribozyme or its DNA copy and an inducible promoter operably linked to the first and second nucleotide sequences, where the ribozyme is configured to remove a 3' sequence unnecessary for replication of the hepatitis C viral genome from a transcript initiated by the promoter, inducing the inducible promoter, contacting the test cell with a candidate compound and detecting an increase in HCV quasispecies produced by the cell in the presence of the candidate compound compared to that in the absence of the compound, where an increase in the HCV quasispecies indicates that the compound increases the mutation rate of HCV. The method is useful in identifying compounds that may be used for treating HCV infection. This sequence represents an HCV genomic DNA 5'UTR region used in the method of the invention.

Sequence 263 BP; 51 A; 72 C; 86 G; 54 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 263;

Best Local Similarity 100.0%; Pred. No. 0.054; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
 DB 217 TTGGGACCCCACTACTC 198

RESULT 139  
 ABN79973/c

ID ABN79973 standard; DNA; 278 BP.

AC ABN79973;

DT 15-JUL-2002 (first entry)

DE Hepatitis C virus 5' untranslated region genotype 3a.

KM Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus; tissue typing; untranslated region; UTR; ds; HCV.

OS Hepatitis C virus.

PN WO200220837-A2.

PD 14-MAR-2002.

PF 10-SEP-2001; 2001WO-GB004042.

PR 08-SEP-2000; 2000GB-00022069.

PA (PYRO-) PYROSEQUENCING AB.

PI (STRD) UNIV LEIAND STANFORD JUNIOR.

DR Ronaghi M, Ekstroem B, Pourmand N;

WPI; 2002-393849/42.

Typing nucleic acid for obtaining information about several variable sites involves simultaneously or sequentially performing two or more primer extension reactions, and determining the pattern of nucleotide incorporation.

Example 1; Fig 2; 86pp; English.

The invention relates to a novel method for obtaining typing information about several variable sites within target nucleic acid, or typing one or more nucleic acid molecules. The methods of the invention are useful for typing one or more nucleic acid molecules containing two or more variable sites, preferably nucleic acid molecules containing three or more variable sites are typed, where three or more primer extension reactions are performed. The method is also useful for diagnosis of pathological conditions characterized by the presence of specific nucleic acid molecule(s). The methods are particularly suited for identifying microbial species or their subtypes, and in typing procedures e.g. typing of polymorphisms, tissue typing or in clinical applications. The sequence represents the 5' untranslated region (UTR) of a hepatitis C virus (HCV) genotype, amplified in the invention to type HCV-positive sera

Sequence 278 BP; 51 A; 81 C; 89 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 278;

Best Local Similarity 100.0%; Pred. No. 0.053; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
 DB 233 TTGGGACCCCACTACTC 214

RESULT 140

AAT29118/c  
 ID AAT29118 standard; DNA, 281 BP.

AC AAT29118;

DT 02-DEC-1996 (first entry)

DE Hepatitis C virus genome fragment (Clone HCV3.1).

KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus; Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;

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KW Staphylococcus; identification; detection; ds.
XX
OS Hepatitis C virus.
XX
PN W09615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US014673.
XX
PR 09-NOV-1994; 94US-00337164.
PR 09-MAR-1995; 95US-00402601.
PR 07-JUN-1995; 95US-00484956.
PR 30-AUG-1995; 95US-00520946.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Dahlberg JE, Lyamichev VI, Brow MAD, Oldenburg MC, Heisler LM;
PI Fors L, Olive DM;
XX
DR WPI: 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection esp.
PT in human p53 gene, to identify strains of microorganisms and viruses.
XX
PS Example 32; Page 301; 43pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease selected
CC from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus
CC DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli
CC ExoIII and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic
CC acid substrate is preferably an oligonucleotide containing a human p53
CC gene sequence or alternatively, microbial gene sequences. Cleavage
CC products are compared to the cleavage products of reference gene
CC sequences. The method is used for detecting mutation in the human p53
CC gene; for identifying strains of microorganisms, especially bacteria
CC selected from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The
CC method may also be used for the identification of viruses, especially
CC hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Four
CC primers (AAT29110-113) were used to generate six DNA HCV fragments by RT-
CC PCR. The sequence described in AAT29110 is an external antisense primer.
CC The sequence described in AAT29111 is a sense primer used after
CC termination of the reverse transcription reaction. The remaining two
CC primers (AAT29112, AAT29113) were used in a second round of amplification
CC reactions which produced a 281 bp product which corresponds to a
CC conserved 5' noncoding region of HCV between positions -284 and -4 of the
CC HCV genome. The amplified sequences are described in AAT29116-121
XX
SQ Sequence 281 BP; 48 A; 80 C; 92 G; 61 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGCGACCCCAACTACTC 20
Db 218 TTGCGACCCCAACTACTC 199

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XX
OS Hepatitis C virus.
XX
PN W09615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US014673.
XX
PR 09-NOV-1994; 94US-00337164.
PR 09-MAR-1995; 95US-00402601.
PR 07-JUN-1995; 95US-00484956.
PR 30-AUG-1995; 95US-00520946.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Dahlberg JE, Lyamichev VI, Brow MAD, Oldenburg MC, Heisler LM;
PI Fors L, Olive DM;
XX
DR WPI: 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection esp.
PT in human p53 gene, to identify strains of microorganisms and viruses.
XX
PS Example 32; Page 302; 43pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease selected
CC from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus
CC DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli
CC ExoIII and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic
CC acid substrate is preferably an oligonucleotide containing a human p53
CC gene sequence or alternatively, microbial gene sequences. Cleavage
CC products are compared to the cleavage products of reference gene
CC sequences. The method is used for detecting mutation in the human p53
CC gene; for identifying strains of microorganisms, especially bacteria
CC selected from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The
CC method may also be used for the identification of viruses, especially
CC hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Four
CC primers (AAT29110-113) were used to generate six DNA HCV fragments by RT-
CC PCR. The sequence described in AAT29110 is an external antisense primer.
CC The sequence described in AAT29111 is a sense primer used after
CC termination of the reverse transcription reaction. The remaining two
CC primers (AAT29112, AAT29113) were used in a second round of amplification
CC reactions which produced a 281 bp product which corresponds to a
CC conserved 5' noncoding region of HCV between positions -284 and -4 of the
CC HCV genome. The amplified sequences are described in AAT29116-121
XX
SQ Sequence 281 BP; 51 A; 82 C; 91 G; 57 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGCGACCCCAACTACTC 20
Db 218 TTGCGACCCCAACTACTC 199

```

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OS Hepatitis C virus.
XX
XX MO9615267-A1.
XX
XX 23-MAY-1996.
XX
XX
XX 09-NOV-1995; 95WO-US014673.
XX
XX PR 09-NOV-1994; 94US-00337164.
XX PR 09-MAR-1995; 95US-00402601.
XX PR 07-JUN-1995; 95US-00484956.
XX PR 30-AUG-1995; 95US-00520946.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Dahlberg JE, Lyamichiev VI, Brow MAD, Oldenburg MC, Heisler IM;
XX Forts L, Olive DM;
XX WPI; 1996-259862/26.
XX
XX
XX Cleavage of nucleic acids to detect mutation(s) - allows detection esp.
XX in human p53 gene, to identify strains of microorganisms and viruses.
XX
XX Example 32; Page 300; 433pp; English.
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease selected
XX from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus
XX DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli
XX EcoRI and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic
XX acid substrate is preferably an oligonucleotide containing a human p53
XX gene sequence or alternatively, microbial gene sequences. Cleavage
XX products are compared to the cleavage products of reference gene
XX sequences. The method is used for detecting mutation in the human p53
XX gene; for identifying strains of microorganisms, especially bacteria
XX selected from the group of members of the genera Campylobacter,
XX Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The
XX method may also be used for the identification of viruses, especially
XX hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Four
XX primers (AAT29110-115) were used to generate six DNA HCV fragments by RT-
XX PCR. The sequence described in AAT29110 is an external antisense primer.
XX The sequence described in AAT29111 is a sense primer used after
XX termination of the reverse transcription reaction. The remaining two
XX primers (AAT29112, AAT29113) were used in a second round of amplification
XX reactions which produced a 281 bp product which corresponds to a
XX conserved 5' noncoding region of HCV between positions -284 and -4 of the
XX HCV genome. The amplified sequences are described in AAT29116-121.
XX
XX Sequence 281 BP; 50 A; 80 C; 92 G; 59 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTCCGACCCCAACTACTC 20
XX 218 TTCCGACCCCAACTACTC 199
XX
XX RESULT 143
XX ADB16264/c
XX ID ADB16264 standard; DNA; 281 BP.
XX
XX ADB16264;
XX
XX 20-NOV-2003 (first entry)
XX
XX Cleavase BN DNA substrate #41.
XX
XX de; DNA polymerase; microorganism strain identification; bacteria;
XX Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX Mycobacterium tuberculosis.
XX

```

```

OS Hepatitis C virus.
XX
XX US2003054338-A1.
XX
XX
XX 20-MAR-2003.
XX
XX
XX 28-AUG-2001; 2001US-00940925.
XX
XX PR 07-DEC-1992; 92US-00986330.
XX PR 04-JUN-1993; 93US-00073384.
XX PR 06-JUN-1994; 94US-00254359.
XX PR 09-NOV-1994; 94US-00337164.
XX PR 09-MAR-1995; 95US-00402601.
XX PR 07-JUN-1995; 95US-00484956.
XX PR 30-AUG-1995; 95US-00520946.
XX PR 06-FEB-1997; 97US-00789079.
XX PR 19-FEB-1997; 97US-00802233.
XX PR 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
XX (BROW/) BROW M A D.
XX (LYAM/) LYAMICHEV V I.
XX
XX Dahlberg JE, Brow MAD, Lyamichiev VI;
XX WPI; 2003-615811/58.
XX
XX
XX Identification of strains of microorganisms, by treating nucleic acid
XX cleavage structure(s) derived from microorganisms with nuclease to form
XX cleavage products(s) and detecting the product(s).
XX
XX Example 34; Fig 82; 303pp; English.
XX
XX The invention relates to a method of detecting and identifying strains of
XX microorganisms by providing a nuclease and a nucleic acid substrate
XX containing sequences derived from microorganism(s), treating the nucleic
XX acid substrate to form cleavage structure(s) and reacting the nucleic
XX with the cleavage structures so that cleavage product(s) are produced.
XX The method is used for the identification of strains of microorganisms.
XX The microorganism comprises bacteria including Campylobacter,
XX Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a
XX virus comprising hepatitis C virus or simian immunodeficiency virus.
XX Mycobacterium comprises strains of multi-drug resistant Mycobacterium
XX tuberculosis. The method is less sensitive to size so that entire genes,
XX rather than gene fragments, may be analysed. It facilitates the use of
XX internal standards for subsequent analysis and data comparison, and
XX increases the productivity of personnel and equipment. The present
XX sequence represents a Cleavase BN substrate DNA.
XX
XX Sequence 281 BP; 48 A; 80 C; 92 G; 61 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 9; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTCCGACCCCAACTACTC 20
XX 218 TTCCGACCCCAACTACTC 199
XX
XX RESULT 144
XX ADB16262/c
XX ID ADB16262 standard; DNA; 281 BP.
XX
XX ADB16262;
XX
XX 20-NOV-2003 (first entry)
XX
XX Cleavase BN DNA substrate #39.
XX
XX de; DNA polymerase; microorganism strain identification; bacteria;
XX Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX

```



KW Mycobacterium tuberculosis.  
 XX Hepatitis C virus.  
 OS  
 XX US2003054338-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 28-AUG-2001; 2001US-00940925.  
 XX  
 PR 07-DEC-1992; 92US-00986330.  
 PR 04-JUN-1993; 93US-00073384.  
 PR 06-JUN-1994; 94US-00254359.  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00464956.  
 PR 30-AUG-1995; 95US-00520946.  
 PR 06-FEB-1997; 97US-00789079.  
 PR 19-FEB-1997; 97US-00802233.  
 PR 05-SEP-2000; 2000US-00655378.  
 XX  
 PA (DAHL/) DAHLBERG J E.  
 PA (BROW/) BROW M A D.  
 PA (LYAM/) LYAMICHEV V I.  
 XX  
 PI Dahlberg JE, Brow MAD, Lyamichev VI;  
 DR WPI; 2003-615811/58.  
 XX  
 PT Identification of strains of microorganisms, by treating nucleic acid  
 PT cleavage structure(s) derived from microorganisms with nuclease to form  
 PT cleavage products(s) and detecting the product(s).  
 XX  
 PS Example 34; Fig 82; 303jp; English.  
 XX  
 CC The invention relates to a method of detecting and identifying strains of  
 CC microorganisms by providing a nuclease and a nucleic acid substrate  
 CC containing sequences derived from microorganism(s), treating the nucleic  
 CC acid substrate to form cleavage structure(s) and reacting the nuclease  
 CC with the cleavage structures so that cleavage product(s) are produced.  
 CC The method is used for the identification of strains of microorganisms.  
 CC The microorganism comprises bacteria including Campylobacter,  
 CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
 CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
 CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
 CC tuberculosis. The method is less sensitive to size so that entire genes,  
 CC rather than gene fragments, may be analysed. It facilitates the use of  
 CC internal standards for subsequent analysis and data comparison, and  
 CC increases the productivity of personnel and equipment. The present  
 CC sequence represents a cleavage BN substrate DNA.  
 XX  
 SQ Sequence 281 BP; 50 A; 80 C; 92 G; 59 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 9; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 218 TTGCGACCCCAACTACTC 199  
 RESULT 145  
 ADB16267/c  
 ID ADB16267 standard; DNA; 281 BP.  
 XX  
 AC ADB16267;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Cleavage BN DNA substrate #44.  
 XX  
 KW db; DNA polymerase; microorganism strain identification; bacteria;

KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;  
 KW Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;  
 KW Mycobacterium tuberculosis.  
 XX Hepatitis C virus.  
 OS  
 XX US2003054338-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 28-AUG-2001; 2001US-00940925.  
 XX  
 PR 07-DEC-1992; 92US-00986330.  
 PR 04-JUN-1993; 93US-00073384.  
 PR 06-JUN-1994; 94US-00254359.  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00464956.  
 PR 30-AUG-1995; 95US-00520946.  
 PR 06-FEB-1997; 97US-00789079.  
 PR 19-FEB-1997; 97US-00802233.  
 PR 05-SEP-2000; 2000US-00655378.  
 XX  
 PA (DAHL/) DAHLBERG J E.  
 PA (BROW/) BROW M A D.  
 PA (LYAM/) LYAMICHEV V I.  
 XX  
 PI Dahlberg JE, Brow MAD, Lyamichev VI;  
 DR WPI; 2003-615811/58.  
 XX  
 PT Identification of strains of microorganisms, by treating nucleic acid  
 PT cleavage structure(s) derived from microorganisms with nuclease to form  
 PT cleavage products(s) and detecting the product(s).  
 XX  
 PS Example 34; Fig 82; 303jp; English.  
 XX  
 CC The invention relates to a method of detecting and identifying strains of  
 CC microorganisms by providing a nuclease and a nucleic acid substrate  
 CC containing sequences derived from microorganism(s), treating the nucleic  
 CC acid substrate to form cleavage structure(s) and reacting the nuclease  
 CC with the cleavage structures so that cleavage product(s) are produced.  
 CC The method is used for the identification of strains of microorganisms.  
 CC The microorganism comprises bacteria including Campylobacter,  
 CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
 CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
 CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
 CC tuberculosis. The method is less sensitive to size so that entire genes,  
 CC rather than gene fragments, may be analysed. It facilitates the use of  
 CC internal standards for subsequent analysis and data comparison, and  
 CC increases the productivity of personnel and equipment. The present  
 CC sequence represents a cleavage BN substrate DNA.  
 XX  
 SQ Sequence 281 BP; 51 A; 82 C; 91 G; 57 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 9; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 218 TTGCGACCCCAACTACTC 199  
 RESULT 146  
 ADB16268  
 ID ADB16268 standard; DNA; 281 BP.  
 XX  
 AC ADB16268;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Cleavage BN DNA substrate #45.

XX de; DNA polymerase; microorganism strain identification; bacteria;  
 KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;  
 KW Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;  
 KW Mycobacterium tuberculosis.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2003054338-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 28-AUG-2001; 2001US-00940925.  
 XX  
 PR 07-DEC-1992; 92US-00986330.  
 PR 04-JUN-1993; 93US-00073384.  
 PR 06-JUN-1994; 94US-00254359.  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00484956.  
 PR 30-AUG-1995; 95US-00520946.  
 PR 06-FEB-1997; 97US-00789079.  
 PR 19-FEB-1997; 97US-00802233.  
 PR 05-SEP-2000; 2000US-00655378.  
 XX  
 PA (DAHL/) DAHLBERG J E.  
 PA (BROW/) BROW M A D.  
 PA (LYAM/) LYAMICHEV V I.  
 XX  
 PI Dahlberg JE, Brow MAD, Lyamichev VI;  
 XX  
 DR WPI; 2003-615811/58.  
 XX  
 PT Identification of strains of microorganisms, by treating nucleic acid  
 PT cleavage structure(s) derived from microorganisms with nuclease to form  
 PT cleavage products(s) and detecting the product(s).  
 XX  
 PS Example 34; Page 163; 303pp; English.  
 XX  
 CC The invention relates to a method of detecting and identifying strains of  
 CC microorganisms by providing a nuclease and a nucleic acid substrate  
 CC containing sequences derived from microorganism(s), treating the nucleic  
 CC acid substrate to form cleavage structure(s) and reacting the nuclease  
 CC with the cleavage structures so that cleavage product(s) are produced.  
 CC The method is used for the identification of strains of microorganisms.  
 CC The microorganism comprises bacteria including Campylobacter,  
 CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
 CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
 CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
 CC tuberculosis. The method is less sensitive to size so that entire genes,  
 CC rather than gene fragments, may be analysed. It facilitates the use of  
 CC internal standards for subsequent analysis and data comparison, and  
 CC increases the productivity of personnel and equipment. The present  
 CC sequence represents a Cleavage BN substrate DNA.  
 XX  
 SQ Sequence 281 BP; 59 A; 92 C; 80 G; 50 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 9; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 TTGCGACCCCAACTACTC 20  
 DB 64 TTGCGACCCCAACTACTC 83

RESULT 147  
 ID ADB16273 standard; DNA; 281 BP.  
 AC ADB16273;  
 XX  
 DT 20-NOV-2003 (first entry)

XX  
 DE Cleavage BN DNA substrate #50.  
 XX  
 KW de; DNA polymerase; microorganism strain identification; bacteria;  
 KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;  
 KW Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;  
 KW Mycobacterium tuberculosis.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2003054338-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 28-AUG-2001; 2001US-00940925.  
 XX  
 PR 07-DEC-1992; 92US-00986330.  
 PR 04-JUN-1993; 93US-00073384.  
 PR 06-JUN-1994; 94US-00254359.  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00484956.  
 PR 30-AUG-1995; 95US-00520946.  
 PR 06-FEB-1997; 97US-00789079.  
 PR 19-FEB-1997; 97US-00802233.  
 PR 05-SEP-2000; 2000US-00655378.  
 XX  
 PA (DAHL/) DAHLBERG J E.  
 PA (BROW/) BROW M A D.  
 PA (LYAM/) LYAMICHEV V I.  
 XX  
 PI Dahlberg JE, Brow MAD, Lyamichev VI;  
 XX  
 DR WPI; 2003-615811/58.  
 XX  
 PT Identification of strains of microorganisms, by treating nucleic acid  
 PT cleavage structure(s) derived from microorganisms with nuclease to form  
 PT cleavage products(s) and detecting the product(s).  
 XX  
 PS Example 34; Page 164; 303pp; English.  
 XX  
 CC The invention relates to a method of detecting and identifying strains of  
 CC microorganisms by providing a nuclease and a nucleic acid substrate  
 CC containing sequences derived from microorganism(s), treating the nucleic  
 CC acid substrate to form cleavage structure(s) and reacting the nuclease  
 CC with the cleavage structures so that cleavage product(s) are produced.  
 CC The method is used for the identification of strains of microorganisms.  
 CC The microorganism comprises bacteria including Campylobacter,  
 CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
 CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
 CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
 CC tuberculosis. The method is less sensitive to size so that entire genes,  
 CC rather than gene fragments, may be analysed. It facilitates the use of  
 CC internal standards for subsequent analysis and data comparison, and  
 CC increases the productivity of personnel and equipment. The present  
 CC sequence represents a Cleavage BN substrate DNA.  
 XX  
 SQ Sequence 281 BP; 57 A; 91 C; 82 G; 51 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 9; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 TTGCGACCCCAACTACTC 20  
 DB 64 TTGCGACCCCAACTACTC 83

RESULT 148  
 ID ADB16269 standard; DNA; 281 BP.  
 AC ADB16269;  
 XX  
 DT 20-NOV-2003 (first entry)

```

XX XX 20-NOV-2003 (first entry)
XX XX
XX XX Cleavase BN DNA substrate #46.
XX XX
XX XX ds; DNA polymerase; microorganism strain identification; bacteria;
XX XX Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX XX Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX XX Mycobacterium tuberculosis.
XX XX
XX XX Hepatitis C virus.
XX XX
XX XX US2003054338-A1.
XX XX
XX XX 20-MAR-2003.
XX XX
XX XX 28-AUG-2001; 2001US-00940925.
XX XX
XX XX 07-DEC-1992; 92US-00986330.
XX XX 04-JUN-1993; 93US-00073388.
XX XX 06-JUN-1994; 94US-00254359.
XX XX 09-NOV-1994; 94US-00337164.
XX XX 09-MAR-1995; 95US-00402601.
XX XX 07-JUN-1995; 95US-00484956.
XX XX 30-AUG-1995; 95US-00520946.
XX XX 06-FEB-1997; 97US-00789079.
XX XX 19-FEB-1997; 97US-00802233.
XX XX 05-SEP-2000; 2000US-00655378.
XX XX
XX XX (DAHL/) DAHLBERG J E.
XX XX (BROW/) BROW M A D.
XX XX (LYAM/) LYAMICHEV V I.
XX XX
XX XX Dahlberg JE, Brow MAD, Lyamichev VI;
XX XX
XX XX WPI: 2003-615811/58.
XX XX
XX XX Identification of strains of microorganisms, by treating nucleic acid
XX XX cleavage structure(s) derived from microorganisms with nuclease to form
XX XX cleavage products(s) and detecting the product(s).
XX XX
XX XX Example 34; Page 163; 303pp; English.
XX XX
XX XX The invention relates to a method of detecting and identifying strains of
XX XX microorganisms by providing a nuclease and a nucleic acid substrate
XX XX containing sequences derived from microorganism(s), treating the nucleic
XX XX acid substrate to form cleavage structure(s) and reacting the nuclease
XX XX with the cleavage structures so that cleavage product(s) are produced.
XX XX The method is used for the identification of strains of microorganisms.
XX XX The microorganism comprises bacteria including Campylobacter,
XX XX Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a
XX XX virus comprising hepatitis C virus or simian immunodeficiency virus. The
XX XX mycobacterium comprises strains of multi-drug resistant Mycobacterium
XX XX tuberculosis. The method is less sensitive to size so that entire genes,
XX XX rather than gene fragments, may be analysed. It facilitates the use of
XX XX internal standards for subsequent analysis and data comparison, and
XX XX increases the productivity of personnel and equipment. The present
XX XX sequence represents a Cleavase BN substrate DNA.
XX XX
XX XX Sequence 281 BP; 60 A; 91 C; 80 G; 50 T; 0 U; 0 Other;
XX XX
XX XX Query Match 100.0%; Score 20; DB 9; Length 281;
XX XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX XX
XX XX 1 TTCGGACCCCAACTACTC 20
XX XX |||||||
XX XX 64 TTCGGACCCCAACTACTC 83

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AC ADB16270;  
ADT 20-NOV-2003 (first entry)  
DE Cleavase BN DNA substrate #47.  
KM ds; DNA polymerase; microorganism strain identification; bacteria;  
KM Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;  
KM Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;  
XX Mycobacterium tuberculosis.  
OS Hepatitis C virus.  
PN US2003054338-A1.  
PD 20-MAR-2003.  
PF 28-AUG-2001; 2001US-00940925.  
PR 07-DEC-1992; 92US-00986330.  
PR 04-JUN-1993; 93US-00073384.  
PR 06-JUN-1994; 94US-00254359.  
PR 09-NOV-1994; 94US-00337164.  
PR 09-MAR-1995; 95US-00402601.  
PR 07-JUN-1995; 95US-00484956.  
PR 30-AUG-1995; 95US-00520946.  
PR 06-FEB-1997; 97US-0078079.  
PR 19-FEB-1997; 97US-00802233.  
PR 05-SEP-2000; 2000US-00655378.  
XX (DAHL/) DAHLBERG J E.  
PA (BROW/) BROW M A D.  
PA (LYAM/) LYAMICHEV V I.  
XX Dahlberg JE, Brow MAD, Lyamichev VI;  
PI WPI; 2003-615811/58.  
DR Identification of strains of microorganisms, by treating nucleic acid  
PT cleavage structure(s) derived from microorganisms with nuclease to form  
PT cleavage products(s) and detecting the product(s).  
XX  
XX  
XX Example 34; Page 163; 303pp; English.  
PS  
XX The invention relates to a method of detecting and identifying strains of  
XX microorganisms by providing a nuclease and a nucleic acid substrate  
CC containing sequences derived from microorganism(s), treating the nucleic  
CC acid substrate to form cleavage structure(s) and reacting the nuclease  
CC with the cleavage structures so that cleavage product(s) are produced.  
CC The method is used for the identification of strains of microorganisms.  
CC The microorganism comprises bacteria including Campylobacter,  
CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
CC tuberculosis. The method is less sensitive to size so that entire genes,  
CC rather than gene fragments, may be analysed. It facilitates the use of  
CC internal standards for subsequent analysis and data comparison, and  
CC increases the productivity of personnel and equipment. The present  
CC sequence represents a Cleavase BN substrate DNA.  
XX  
SQ Sequence 281 BP; 61 A; 92 C; 80 G; 48 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 9; Length 281;  
Best Local Similarity 100.0%; P-adj. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGGACCCGACACTACTC 20  
Db ||||||||||||||||||||  
64 TTGCGGACCCGACACTACTC 83

```

AD02537/c
ID  ADC02537 standard; DNA; 281 BP.
XX
AC  ADC02537;
XX
DT  18-DEC-2003 (first entry)
XX
DE  HCV clone 3.1.
XX
KM  ds; nucleic acid treatment system; nucleic acid sequence detection;
KW  nucleic acid sequence characterisation; microbial gene sequence change;
XX  bacterial pathogen; viral pathogen.
XX
OS  Hepatitis C virus.
XX
PN  US2003108873-A1.
XX
PD  12-JUN-2003.
XX
PF  28-AUG-2001; 2001US-00941193.
XX
PR  07-DEC-1992; 92US-00986330.
PR  04-JUN-1993; 93US-00073384.
PR  06-JUN-1994; 94US-00254359.
PR  09-NOV-1994; 94US-00337164.
PR  09-MAR-1995; 95US-00402601.
PR  07-JUN-1995; 95US-00484956.
PR  30-AUG-1995; 95US-00520946.
PR  06-FEB-1997; 97US-00789079.
PR  19-FEB-1997; 97US-00802233.
PR  05-SEP-2000; 2000US-00655378.
XX
PA  (DAHL/) DAHLBERG J E.
PA  (BROW/) BROW M A D.
PA  (LYAM/) LYAMICHEV V I.
XX
PI  Dahlberg JE, Brow MAD, Lyamichev VI;
XX
DR  WPI; 2003-708773/67.
XX
PT  Treatment system for detection and characterization of nucleic acid
PT  sequences and sequence changes, comprises target nucleic acid, and three
XX  oligonucleotides.
XX
PS  Disclosure; SEQ ID NO 123; 165bp; English.
XX
CC  The invention relates to a nucleic acid treatment system which consists
CC  of a target nucleic acid having first and second regions; a first
CC  oligonucleotide having a 3' portion complementary to the first region,
CC  and a 5' portion; a second oligonucleotide having a portion complementary
CC  to the second region; and a third oligonucleotide having a portion
CC  complementary to 5' portion of first oligonucleotide. The system is
CC  useful for detection and characterization of nucleic acid sequences and
CC  sequence changes in microbial gene sequences. The inventive system is
CC  robust. The system allows detection of and identification of bacterial
CC  and viral pathogens in a sample. The present sequence represents a HCV
CC  clone.
XX
SQ  Sequence 281 BP; 48 A; 80 C; 93 G; 60 T; 0 U; 0 Other;
XX
Query Match      100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1 TTGCGACCCCAACTACTC 20
    |||||
DB  218 TTGCGACCCCAACTACTC 199

```

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AC  AD02535;
XX
DT  18-DEC-2003 (first entry)
XX
DE  HCV clone 1.1.
XX
KM  ds; nucleic acid treatment system; nucleic acid sequence detection;
KW  nucleic acid sequence characterisation; microbial gene sequence change;
XX  bacterial pathogen; viral pathogen.
XX
OS  Hepatitis C virus.
XX
PN  US2003108873-A1.
XX
PD  12-JUN-2003.
XX
PF  28-AUG-2001; 2001US-00941193.
XX
PR  07-DEC-1992; 92US-00986330.
PR  04-JUN-1993; 93US-00073384.
PR  06-JUN-1994; 94US-00254359.
PR  09-NOV-1994; 94US-00337164.
PR  09-MAR-1995; 95US-00402601.
PR  07-JUN-1995; 95US-00484956.
PR  30-AUG-1995; 95US-00520946.
PR  06-FEB-1997; 97US-00789079.
PR  19-FEB-1997; 97US-00802233.
PR  05-SEP-2000; 2000US-00655378.
XX
PA  (DAHL/) DAHLBERG J E.
PA  (BROW/) BROW M A D.
PA  (LYAM/) LYAMICHEV V I.
XX
PI  Dahlberg JE, Brow MAD, Lyamichev VI;
XX
DR  WPI; 2003-708773/67.
XX
PT  Treatment system for detection and characterization of nucleic acid
PT  sequences and sequence changes, comprises target nucleic acid, and three
XX  oligonucleotides.
XX
PS  Disclosure; SEQ ID NO 121; 165bp; English.
XX
CC  The invention relates to a nucleic acid treatment system which consists
CC  of a target nucleic acid having first and second regions; a first
CC  oligonucleotide having a 3' portion complementary to the first region,
CC  and a 5' portion; a second oligonucleotide having a portion complementary
CC  to the second region; and a third oligonucleotide having a portion
CC  complementary to 5' portion of first oligonucleotide. The system is
CC  useful for detection and characterization of nucleic acid sequences and
CC  sequence changes in microbial gene sequences. The inventive system is
CC  robust. The system allows detection of and identification of bacterial
CC  and viral pathogens in a sample. The present sequence represents a HCV
CC  clone.
XX
SQ  Sequence 281 BP; 50 A; 80 C; 92 G; 59 T; 0 U; 0 Other;
XX
Query Match      100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1 TTGCGACCCCAACTACTC 20
    |||||
DB  218 TTGCGACCCCAACTACTC 199

```

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RESULT 151
AD02535/c
ID  ADC02535 standard; DNA; 281 BP.
XX
DT  18-DEC-2003 (first entry)

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```

RESULT 152
AD02536/c
ID  ADC02536 standard; DNA; 261 BP.
XX
AC  AD02536;
XX
DT  18-DEC-2003 (first entry)

```

```
XX HCv clone 2.1.
DE
XX ds; nucleic acid treatment system; nucleic acid sequence detection;
KW nucleic acid sequence characterisation; microbial gene sequence change;
KW bacterial pathogen; viral pathogen.
XX
XX Hepatitis C virus.
OS
XX US2003108873-A1.
PN
XX 12-JUN-2003.
PD
XX 28-AUG-2001; 2001US-00941193.
PF
XX 07-DEC-1992; 92US-00986330.
PR
XX 04-JUN-1993; 93US-00073384.
PR 06-JUN-1994; 94US-00254359.
PR 09-NOV-1994; 94US-00337164.
PR 09-MAR-1995; 95US-00402601.
PR 07-JUN-1995; 95US-00484956.
PR 30-AUG-1995; 95US-00520946.
PR 06-FEB-1997; 97US-00789079.
PR 19-FEB-1997; 97US-00802233.
PR 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
PA (BROW/) BROW M A D.
PA (LYAM/) LYAMICHEV V I.
XX
XX Dahlberg JE, Brow MAD, Lyamichev VI;
PI WPI; 2003-708773/67.
XX
XX Treatment system for detection and characterization of nucleic acid
PT sequences and sequence changes, comprises target nucleic acid, and three
PT oligonucleotides.
XX
XX Disclosure; SEQ ID NO 122; 165bp; English.
PS
XX The invention relates to a nucleic acid treatment system which consists
CC of a target nucleic acid having first and second regions; a first
CC oligonucleotide having a 3' portion complementary to the first region,
CC and a 5' portion; a second oligonucleotide having a portion complementary
CC to the second region; and a third oligonucleotide having a portion
CC complementary to 5' portion of first oligonucleotide. The system is
CC useful for detection and characterisation of nucleic acid sequences and
CC sequence changes in microbial gene sequences. The inventive system is
CC robust. The system allows detection of and identification of bacterial
CC and viral pathogens in a sample. The present sequence represents a HCV
CC clone.
XX
XX Sequence 281 BP; 50 A; 80 C; 91 G; 60 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 218 TTCCGACCCCAACTACTC 199
XX
XX RESULT 153
AD C02540/C
ID ADC02540 standard; DNA; 281 BP.
XX
XX AC ADC02540;
XX
XX 18-DEC-2003 (first entry)
XX
XX HCV clone 7.1.
XX
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KW ds; nucleic acid treatment system; nucleic acid sequence detection;
KW nucleic acid sequence characterisation; microbial gene sequence change;
KW bacterial pathogen; viral pathogen.
XX
XX Hepatitis C virus.
OS
XX US2003108873-A1.
PN
XX 12-JUN-2003.
PD
XX 28-AUG-2001; 2001US-00941193.
PF
XX 07-DEC-1992; 92US-00986330.
PR 04-JUN-1993; 93US-00073384.
PR 06-JUN-1994; 94US-00254359.
PR 09-NOV-1994; 94US-00337164.
PR 09-MAR-1995; 95US-00402601.
PR 07-JUN-1995; 95US-00484956.
PR 30-AUG-1995; 95US-00520946.
PR 06-FEB-1997; 97US-00789079.
PR 19-FEB-1997; 97US-00802233.
PR 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
PA (BROW/) BROW M A D.
PA (LYAM/) LYAMICHEV V I.
XX
XX Dahlberg JE, Brow MAD, Lyamichev VI;
PI WPI; 2003-708773/67.
XX
XX Treatment system for detection and characterization of nucleic acid
PT sequences and sequence changes, comprises target nucleic acid, and three
PT oligonucleotides.
XX
XX Disclosure; SEQ ID NO 126; 165bp; English.
PS
XX The invention relates to a nucleic acid treatment system which consists
CC of a target nucleic acid having first and second regions; a first
CC oligonucleotide having a 3' portion complementary to the first region,
CC and a 5' portion; a second oligonucleotide having a portion complementary
CC to the second region; and a third oligonucleotide having a portion
CC complementary to 5' portion of first oligonucleotide. The system is
CC useful for detection and characterisation of nucleic acid sequences and
CC sequence changes in microbial gene sequences. The inventive system is
CC robust. The system allows detection of and identification of bacterial
CC and viral pathogens in a sample. The present sequence represents a HCV
CC clone.
XX
XX Sequence 281 BP; 51 A; 82 C; 91 G; 57 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 218 TTCCGACCCCAACTACTC 199
XX
XX RESULT 154
AAT29119/C
ID AAT29119 standard; DNA; 282 BP.
XX
XX AC AAT29119;
XX
XX 02-DEC-1996 (first entry)
XX
XX Hepatitis C virus genome fragment (Clone HCV4.2).
XX
XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
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XX OS Hepatitis C virus.
XX PN W09615267-A1.
XX PD 23-MAY-1996.
XX PF 09-NOV-1995; 95WO-US014673.
XX PR 09-NOV-1994; 94US-00337164.
XX PR 09-MAR-1995; 95US-00402601.
XX PR 07-JUN-1994; 95US-00484956.
XX PR 30-AUG-1995; 95US-00520946.
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX PI Dahlberg JE, Lyamichiev VI, Brow MAD, Oldenburg MC, Heisler LM,
XX PI Fors L, Olive DM;
XX DR WPI; 1996-259862/26.
XX PT Cleavage of nucleic acids to detect mutation(s) - allows detection esp.
XX PT in human p53 gene, to identify strains of microorganisms and viruses.
XX PS Example 32; Page 301; 433pp; English.
XX CC Cleavage of nucleic acids using an enzyme, especially a nuclease selected
XX CC from the group consisting of cleavage (RTM) BN enzyme, Thermus aquaticus
XX CC DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli
XX CC ExoIII and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic
XX CC acid substrate is preferably an oligonucleotide containing a human p53
XX CC gene sequence or alternatively, microbial gene sequences. Cleavage
XX CC products are compared to the cleavage products of reference gene
XX CC sequences. The method is used for detecting mutation in the human p53
XX CC gene, for identifying strains of microorganisms, especially bacteria
XX CC selected from the group of members of the genera Campylobacter,
XX CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The
XX CC method may also be used for the identification of viruses, especially
XX CC hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Four
XX CC primers (AAT29110-113) were used to generate six DNA HCV fragments by RT-
XX CC PCR. The sequence described in AAT29110 is an external antisense primer.
XX CC The sequence described in AAT29111 is a sense primer used after
XX CC termination of the reverse transcription reaction. The remaining two
XX CC primers (AAT29112, AAT29113) were used in a second round of amplification
XX CC reactions which produced a 281 bp product which corresponds to -4 of the
XX CC conserved 5' noncoding region of HCV between positions -284 and -4 of the
XX CC HCV genome. The amplified sequences are described in AAT29116-121
XX SQ Sequence 282 BP; 50 A; 79 C; 93 G; 60 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGAGCCCAACTACTC 20
DB 219 TTGCGAGCCCAACTACTC 200

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XX OS Hepatitis C virus.
XX PN US2003054338-A1.
XX PD 20-MAR-2003.
XX PF 28-AUG-2001; 2001US-00940925.
XX PR 07-DEC-1992; 92US-00986330.
XX PR 04-JUN-1993; 93US-00073384.
XX PR 06-JUN-1994; 94US-00254359.
XX PR 09-NOV-1994; 94US-00337164.
XX PR 09-MAR-1995; 95US-00402601.
XX PR 07-JUN-1995; 95US-00484956.
XX PR 30-AUG-1995; 95US-00520946.
XX PR 06-FEB-1997; 97US-00789079.
XX PR 19-FEB-1997; 97US-00802233.
XX PR 05-SEP-2000; 2000US-00655378.
XX PA (DAHL/) DAHLBERG J E.
XX PA (BROW/) BROW M A D.
XX PA (LYAM/) LYAMICHEV V I.
XX PI Dahlberg JE, Brow MAD, Lyamichiev VI;
XX DR WPI; 2003-615811/58.
XX PT Identification of strains of microorganisms, by treating nucleic acid
XX PT cleavage structure(s) derived from microorganisms with nuclease to form
XX PT cleavage products(s) and detecting the product(s).
XX PS Example 34; Fig 82; 303pp; English.
XX CC The invention relates to a method of detecting and identifying strains of
XX CC microorganisms by providing a nuclease and a nucleic acid substrate
XX CC containing sequences derived from microorganism(s), treating the nucleic
XX CC acid substrate to form cleavage structure(s) and reacting the nuclease
XX CC with the cleavage structures so that cleavage product(s) are produced.
XX CC The method is used for the identification of strains of microorganisms.
XX CC The microorganism comprises bacteria including Campylobacter,
XX CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus.
XX CC The virus comprising hepatitis C virus or simian immunodeficiency virus.
XX CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium
XX CC tuberculosis. The method is less sensitive to size so that entire genes,
XX CC rather than gene fragments, may be analysed. It facilitates the use of
XX CC internal standards for subsequent analysis and data comparison, and
XX CC increases the productivity of personnel and equipment. The present
XX CC sequence represents a cleavage BN substrate DNA.
XX SQ Sequence 282 BP; 50 A; 79 C; 93 G; 60 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGAGCCCAACTACTC 20
DB 219 TTGCGAGCCCAACTACTC 200

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RESULT 155
ADBI6265/c
ID ADBI6265 standard; DNA; 282 BP.
XX AC ADBI6265;
XX DT 20-NOV-2003 (first entry)
XX DE Cleavage BN DNA substrate #42.
XX KW ds; DNA polymerase; microorganism strain identification; bacteria;
XX KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX KW Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX KW Mycobacterium tuberculosis.

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RESULT 156
ADBI6271
ID ADBI6271 standard; DNA; 282 BP.
XX AC ADBI6271;
XX DT 20-NOV-2003 (first entry)
XX DE Cleavage BN DNA substrate #48.
XX KW ds; DNA polymerase; microorganism strain identification; bacteria;
XX KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;

```

KW Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;  
 KW Mycobacterium tuberculosis.  
 OS Hepatitis C virus.  
 XX US2003054338-A1.  
 XX  
 XX 20-MAR-2003.  
 PD  
 XX 28-AUG-2001; 2001US-00940925.  
 PF  
 XX 07-DEC-1992; 92US-00986330.  
 PR 04-JUN-1993; 93US-00073384.  
 PR 06-JUN-1994; 94US-00254359.  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00484956.  
 PR 30-AUG-1995; 95US-00520946.  
 PR 06-FEB-1997; 97US-00789079.  
 PR 19-FEB-1997; 97US-00802233.  
 PR 05-SEP-2000; 2000US-00655378.  
 XX  
 XX (DAHL/) DAHLBERG J E.  
 PA (BROW/) BROW M A D.  
 PA (LYAM/) LYAMICHEV V I.  
 XX  
 PI Dahlberg JE, Brow MAD, Lyamichev VI;  
 DR WPI; 2003-615811/58.  
 XX  
 XX Identification of strains of microorganisms, by treating nucleic acid  
 PT cleavage structure(s) derived from microorganisms with nuclease to form  
 PT cleavage products(s) and detecting the product(s).  
 XX  
 XX Example 34; Page 164; 303pp; English.  
 PS  
 XX The invention relates to a method of detecting and identifying strains of  
 CC microorganisms by providing a nuclease and a nucleic acid substrate  
 CC containing sequences derived from microorganism(s), treating the nucleic  
 CC acid substrate to form cleavage structure(s) and reacting the nuclease  
 CC with the cleavage structures so that cleavage product(s) are produced.  
 CC The method is used for the identification of strains of microorganisms.  
 CC The microorganism comprises bacteria including Campylobacter.  
 CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
 CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
 CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
 CC tuberculosis. The method is less sensitive to size so that entire genes,  
 CC rather than gene fragments, may be analysed. It facilitates the use of  
 CC internal standards for subsequent analysis and data comparison, and  
 CC increases the productivity of personnel and equipment. The present  
 CC sequence represents a cleavage BN substrate DNA.  
 CC  
 XX  
 SQ Sequence 282 BP; 60 A; 93 C; 79 G; 50 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 9; Length 282;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGAGCCCAACTACTC 20  
 Db 64 TTGCGAGCCCAACTACTC 83  
 RESULT 157  
 AAV70444/c  
 ID AAV70444 standard; DNA; 286 BP.  
 XX  
 XX AAV70444;  
 AC  
 XX 08-APR-1999 (first entry)  
 DT  
 XX HCV subtype 1b target sequence.  
 DE  
 XX

KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 XX Hepatitis C virus.  
 XX WO9850403-A1.  
 XX  
 XX 12-NOV-1998.  
 PD  
 XX 05-MAY-1998; 98WO-US003194.  
 PF  
 XX 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PA  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 XX WPI; 1998-610317/51.  
 DR  
 XX  
 XX Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 XX  
 XX Example 3; Fig 6; 279pp; English.  
 PS  
 XX The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. The present  
 CC sequence represents a hepatitis C virus (HCV) subtype 1b sequence that  
 CC can be used as a target in the hybridisation analysis using multiple  
 CC capture probes for HCV genotyping  
 CC  
 XX  
 SQ Sequence 286 BP; 50 A; 80 C; 93 G; 63 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGAGCCCAACTACTC 20  
 Db 222 TTGCGAGCCCAACTACTC 203  
 RESULT 158  
 ABL46054/c  
 ID ABL46054 standard; DNA; 286 BP.  
 XX  
 XX ABL46054;  
 AC  
 XX 26-APR-2002 (first entry)  
 DT  
 XX

DE Hepatitis C virus subtype 1b target DNA sequence SEQ ID NO:21.  
 XX  
 XX Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KM characterisation; identification; nucleic acid structure; diagnosis;  
 KM PCR primer; probe; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200198537-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 15-JUN-2001; 2001WO-US019401.  
 XX  
 PR 17-JUN-2000; 2000US-0212308P.  
 XX  
 PR 15-JUN-2001; 2001US-00212308.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;  
 DR WPI; 2002-049698/06.  
 XX  
 PT Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX  
 PS Example 3; Fig 6; 409pp; English.  
 XX  
 CC The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABI46034 to ABI46367 represent  
 CC sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 286 BP; 50 A; 80 C; 93 G; 63 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TTGCGACCCCAACTACTC 20  
 Db 222 TTGCGACCCCAACTACTC 203  
 RESULT 159  
 ADK82244/c  
 ID ADK82244 standard; DNA; 286 BP.  
 XX  
 AC ADK82244;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Hepatitis C virus subtype 1b polynucleotide seqid 21.  
 XX  
 KM nucleic acid analysis; hepatitis C virus;  
 KM non-contiguous single-stranded region; NCSR; cleavage structure;  
 KM clinical; diagnostic; microorganism detection;  
 KM microorganism identification; hepatitis C virus; HCV; subtype 1b; ds.  
 OS Hepatitis C virus.  
 XX  
 PN US6709815-B1.  
 XX  
 PD 23-MAR-2004.

XX  
 PF 18-JUL-2000; 2000US-00402618.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 XX  
 PR 19-SEP-1997; 97US-00934097.  
 XX  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 DR WPI; 2004-25667/24.  
 XX  
 PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
 PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
 PT oligonucleotide and cleavage agent to form cleavage structure.  
 XX  
 PS Example 3; SEQ ID NO 21; 143pp; English.  
 XX  
 CC The invention describes a method of analysing nucleic acids comprising  
 CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
 CC having non-contiguous single-stranded regions (NCSR) separated by an  
 CC intervening region, a bridging oligonucleotide capable of binding to the  
 CC first and second NCSR, a second oligonucleotide binding to a portion of  
 CC the first NCSR and a cleavage agent, and mixing the contents to form a  
 CC cleavage structure. The method is useful for analysing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC subtype 1b polynucleotide identified using the analysis methods of the  
 CC invention.  
 XX  
 SQ Sequence 286 BP; 50 A; 80 C; 93 G; 63 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 12; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TTGCGACCCCAACTACTC 20  
 Db 222 TTGCGACCCCAACTACTC 203  
 RESULT 160  
 AAV70443/c  
 ID AAV70443 standard; DNA; 289 BP.  
 XX  
 AC AAV70443;  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE HCV consensus sequence.  
 XX  
 KM Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 OS Hepatitis C virus.  
 XX  
 PN WO9850403-A1.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US003194.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 XX  
 PR 19-SEP-1997; 97US-00934097.  
 XX  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;



XX DR WPI; 1998-610317/51.  
XX PT Detection and characterisation of nucleic acid sequences - by mixing a  
PT folded target and one or more probes to form a probe/folded target  
PT complex and detecting and characterising the complexes.  
XX PS Example 3; Fig 6; 279pp; English.  
XX CC The invention relates to methods and compositions of detection and  
CC characterisation of nucleic acid sequences and sequence changes. One  
CC method of detection and characterisation comprises: (a) providing: (i) a  
CC folded target having a DNA sequence comprising at least 1 double stranded  
CC region and at least 1 single stranded region; and (ii) at least 1 probe  
CC complementary to at least a portion of the folded target; and (b) mixing  
CC the target and probes so that the probe hybridises to form a probe  
CC /folded target complex. Also provided are methods for determination of  
CC structure formation in nucleic acid targets; for analysing folded nucleic  
CC acids targets; and for analysis of nucleic acid structures. The methods  
CC can be used for the detection and characterisation of nucleic acid  
CC sequences to detect the presence of pathogenic nucleic acid sequences  
CC indicative of an infection, the presence of variants or alleles of  
CC mammalian genes associated with disease and cancers, and the  
CC identification of the source of nucleic acids found in forensic samples,  
CC as well as in paternity determinations. The methods allow simultaneous  
CC analysis of both strands (e.g. the sense and antisense strands) and are  
CC ideal for high-level multiplexing. The products produced are amenable to  
CC qualitative, quantitative and positional analysis. The methods may be  
CC performed in solution or in the solid phase (e.g. on a solid support).  
CC The methods are powerful in that they allow for analysis of longer  
CC fragments of nucleic acid than current methodologies. The present  
CC sequence represents a hepatitis C virus (HCV) consensus sequence. The HCV  
CC subtype 1a sequence is identical to this consensus sequence  
XX SQ Sequence 289 BP; 53 A; 81 C; 92 G; 63 T; 0 U; 0 Other;  
XX Query Match 100.0%; Score 20; DB 2; Length 289;  
XX Best Local Similarity 100.0%; Pred. No. 0.053;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGGACCCCACTACTC 20  
DB 222 TTGCGGACCCCACTACTC 203  
XX RESULT 161  
XX AAV70446/c  
XX ID AAV70446 standard; DNA; 289 BP.  
XX AC AAV70446;  
XX DT 08-APR-1999 (first entry)  
XX DE HCV subtype 3a target sequence.  
XX KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
XX infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
XX OS Hepatitis C virus.  
XX PN WO9850403-A1.  
XX PD 12-NOV-1998.  
XX PF 05-MAY-1998; 98WO-US003194.  
XX PR 05-MAY-1997; 97US-00851588.  
XX PR 19-SEP-1997; 97US-00934097.  
XX PR 03-MAR-1998; 98US-00034205.  
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;

PI Anderson TA, Dahlberg JE;  
XX DR WPI; 1998-610317/51.  
XX PT Detection and characterisation of nucleic acid sequences - by mixing a  
PT folded target and one or more probes to form a probe/folded target  
PT complex and detecting and characterising the complexes.  
XX PS Example 3; Fig 6; 279pp; English.  
XX CC The invention relates to methods and compositions of detection and  
CC characterisation of nucleic acid sequences and sequence changes. One  
CC method of detection and characterisation comprises: (a) providing: (i) a  
CC folded target having a DNA sequence comprising at least 1 double stranded  
CC region and at least 1 single stranded region; and (ii) at least 1 probe  
CC complementary to at least a portion of the folded target; and (b) mixing  
CC the target and probes so that the probe hybridises to form a probe  
CC /folded target complex. Also provided are methods for determination of  
CC structure formation in nucleic acid targets; for analysing folded nucleic  
CC acids targets; and for analysis of nucleic acid structures. The methods  
CC can be used for the detection and characterisation of nucleic acid  
CC sequences to detect the presence of pathogenic nucleic acid sequences  
CC indicative of an infection, the presence of variants or alleles of  
CC mammalian genes associated with disease and cancers, and the  
CC identification of the source of nucleic acids found in forensic samples,  
CC as well as in paternity determinations. The methods allow simultaneous  
CC analysis of both strands (e.g. the sense and antisense strands) and are  
CC ideal for high-level multiplexing. The products produced are amenable to  
CC qualitative, quantitative and positional analysis. The methods may be  
CC performed in solution or in the solid phase (e.g. on a solid support).  
CC The methods are powerful in that they allow for analysis of longer  
CC fragments of nucleic acid than current methodologies. The present  
CC sequence represents a hepatitis C virus (HCV) subtype 3a sequence that  
CC can be used as a target in the hybridisation analysis using multiple  
CC capture probes for HCV genotyping  
XX SQ Sequence 289 BP; 55 A; 83 C; 91 G; 60 T; 0 U; 0 Other;  
XX Query Match 100.0%; Score 20; DB 2; Length 289;  
XX Best Local Similarity 100.0%; Pred. No. 0.053;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGGACCCCACTACTC 20  
DB 222 TTGCGGACCCCACTACTC 203  
XX RESULT 162  
XX ABL46053/c  
XX ID ABL46053 standard; DNA; 289 BP.  
XX AC ABL46053;  
XX DT 26-APR-2002 (first entry)  
XX DE Hepatitis C virus subtype 1a target DNA sequence SEQ ID NO:21.  
XX KW Nucleic acid accessible hybridisation site; detection; hybridisation;  
XX characterisation; identification; nucleic acid structure; diagnosis;  
XX PCR primer; probe; ss.  
XX OS Hepatitis C virus.  
XX PN WO200198537-A2.  
XX PD 27-DEC-2001.  
XX PF 15-JUN-2001; 2001WO-US019401.  
XX PR 17-JUN-2000; 2000US-0212308P.  
XX PR 15-JUN-2001; 2001US-00212308.  
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX PI

```

XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 3; Fig 6; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 289 BP; 53 A; 81 C; 92 G; 63 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 6; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGGGACCCCACTACTC 20
Db 222 TTGGGACCCCACTACTC 203
XX
RESULT 163
ABL46056/C
ID ABL46056 standard; DNA; 289 BP.
XX
AC ABL46056;
XX
DT 26-APR-2002 (first entry)
XX
DE Hepatitis C virus subtype 3a target DNA sequence SEQ ID NO:23.
XX
KM Nucleic acid accessible hybridisation site; detection; hybridisation;
KM characterisation; identification; nucleic acid structure; diagnosis;
KM PCR primer; probe; ss.
XX
OS Hepatitis C virus.
XX
PN WO200198537-A2.
XX
XX
XX 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 3; Fig 6; 409pp; English.
XX

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```

CC
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 289 BP; 55 A; 83 C; 91 G; 60 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 6; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGGGACCCCACTACTC 20
Db 222 TTGGGACCCCACTACTC 203
XX
RESULT 164
ADK82246/C
ID ADK82246 standard; DNA; 289 BP.
XX
AC ADK82246;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis C virus subtype 3a polynucleotide segid 23.
XX
KM Nucleic acid analysis; hepatitis C virus;
KM non-contiguous single-stranded region; NCSR; cleavage structure;
KM clinical; diagnostic; microorganism detection;
KM microorganism identification; hepatitis C virus; HCV; subtype 3a; ds.
XX
OS Hepatitis C virus.
XX
PN US6709815-B1.
XX
PD 23-MAR-2004.
XX
PF 18-JUL-2000; 2000US-00402618.
XX
PR 05-MAY-1997; 97US-00851588.
PR 19-SEP-1997; 97US-00934097.
PR 03-MAR-1998; 98US-00034205.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI Anderson TA, Dahlberg JE;
XX
DR WPI; 2004-256067/24.
XX
XX
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX oligonucleotide and cleavage agent to form cleavage structure.
XX
PS Example 3; SEQ ID NO 23; 143pp; English.
XX
CC The invention describes a method of analyzing nucleic acids comprising
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
CC having non-contiguous single-stranded regions (NCSR) separated by an
CC intervening region, a bridging oligonucleotide capable of binding to the
CC first and second NCSR; a second oligonucleotide binding to a portion of
CC the first NCSR and a cleavage agent, and mixing the contents to form a
CC cleavage structure. The method is useful for analysing nucleic acids,
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
CC purposes and detection and identification of pathogenic microorganisms
CC such as hepatitis C virus. This sequence represents a hepatitis C virus

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CC subtype 3a polynucleotide identified using the analysis methods of the  
CC invention.  
XX  
SQ Sequence 289 BP; 55 A; 83 C; 91 G; 60 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
DB 222 TTGCGACCCCAACTACTC 203  
RESULT 165  
ADK82243/c  
ID ADK82243 standard; DNA; 289 BP.  
XX  
AC ADK82243;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Hepatitis C virus subtype 1a polynucleotide seqid 20.  
XX  
KW nucleic acid analysis; hepatitis C virus;  
KW non-contiguous single-stranded region; NCSR; cleavage structure;  
KW clinical; diagnostic; microorganism detection;  
KW microorganism identification; hepatitis C virus; HCV; subtype 1a; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN US6709815-B1.  
XX  
PD 23-MAR-2004.  
XX  
PF 18-JUL-2000; 2000US-00402618.  
XX  
PR 05-MAY-1997; 97US-00851568.  
PR 19-SEP-1997; 97US-00934087.  
PR 03-MAR-1998; 98US-00034205.  
XX  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MMD;  
PI Anderson TA, Dahlberg JE;  
XX  
DR WPI; 2004-256067/24.  
XX  
PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX  
PS Example 3; SEQ ID NO 20; 143bp; English.  
XX  
CC The invention describes a method of analysing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR; a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analysing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC subtype 1a polynucleotide identified using the analysis methods of the  
CC invention.  
XX  
SQ Sequence 289 BP; 53 A; 81 C; 92 G; 63 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 222 TTGCGACCCCAACTACTC 203  
RESULT 166  
AAH75861/c  
ID AAH75861 standard; DNA; 297 BP.  
XX  
AC AAH75861;  
XX  
DT 26-OCT-2001 (first entry)  
XX  
DE Mycobacterium tuberculosis gene fragment #2.  
XX  
KW Mycobacterium tuberculosis detection; ds.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN RU2163638-C1.  
XX  
PD 27-FEB-2001.  
XX  
PF 06-DEC-1999; 99RU-00125164.  
XX  
PR 06-DEC-1999; 99RU-00125164.  
XX  
PA (ASIB=) AS SIBE BIOCHEM RES INST.  
XX  
PI Beklemishev AB, Khorocheva EM, Nomokonova N Yu;  
XX  
DR WPI; 2001-280317/29.  
XX  
PT Detection of DNA from tuberculosis mycobacterium complex comprising a  
PT polymerase chain reaction method.  
XX  
PS Claim 9; Col 19-20; 13pp; Russian.  
XX  
CC The present invention relates to a PCR-based method for the detection of  
CC Mycobacterium tuberculosis. The present sequence was used to illustrate  
CC the method of the present invention  
XX  
SQ Sequence 297 BP; 50 A; 87 C; 97 G; 63 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 4; Length 297;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
DB 233 TTGCGACCCCAACTACTC 214  
RESULT 167  
AAD55565/c  
ID AAD55565 standard; DNA; 299 BP.  
XX  
AC AAD55565;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE IG57272 Hepatitis C virus (HCV) isolate 5' non-coding region (NCR).  
XX  
KW Hepatitis C virus; HCV; HCV typing; infection; gene therapy; vaccine;  
KW virucide; hepatotropic; antiinflammatory; non-coding region; NCR; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003020970-A2.  
XX  
PD 13-MAR-2003.  
XX  
PF 30-AUG-2002; 2002WO-EP009731.

XX 31-AUG-2001; 2001EP-00120969.  
 PR 08-JAN-2002; 2002US-0345642P.  
 XX (INNO-) INNOGENETICS NV.  
 XX  
 XX Sablon E, Van Doorn L, Quint W;  
 DR WPI; 2003-230206/28.  
 XX  
 PT Novel isolated hepatitis C virus polypeptide of a genotype different from  
 PT clade 6 genotypes 6-9 and 11, and polynucleotides encoding the  
 PT polypeptides, useful for preventing and treating HCV infection.  
 XX  
 PS Claim 1; Fig 1A; 78bp; English.  
 XX  
 CC The invention relates to genomic sequences and amino acid sequences  
 CC corresponding to the non-coding and coding region of a new type of  
 CC Hepatitis C virus (HCV). HCV protein is useful for detecting antibodies  
 CC to HCV and for HCV typing. HCV DNA is useful for detecting the presence  
 CC of HCV virus and for determining the genotype of a HCV virus. Antibody is  
 CC useful for detecting HCV antigens. The invention is useful for preventing  
 CC or treating a HCV infection and is also used in gene therapy. Vaccine is  
 CC useful for immunizing a mammal against HCV infection. The present  
 CC sequence is 16572/2 HCV isolate 5' non-coding region (NCR).  
 SQ Sequence 299 BP; 53 A; 85 C; 95 G; 66 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 233 TTGCGACCCCAACTACTC 214  
 RESULT 168  
 ACD27586/C  
 ID ACD27586 standard; DNA; 301 BP.  
 AC ACD27586;  
 AC ACD27586;  
 DT 16-SEP-2003 (first entry)  
 DE Hepatitis B and C detection method associated cDNA #2.  
 DE Gene chip reagent kit; hepatitis B; hepatitis C; ss.  
 KM  
 XX Unidentified.  
 OS  
 XX CN1366067-A.  
 PN  
 XX 28-AUG-2002.  
 PD  
 XX 15-JAN-2001; 2001CN-00105214.  
 PF  
 XX 15-JAN-2001; 2001CN-00105214.  
 PR  
 XX (BOHU-) BOHUA GENE CHIP TECHNOLOGY CO LTD SHANGH.  
 PA  
 PI Mao Y, Xie Y, Wu H;  
 PI WPI; 2003-230559/23.  
 DR  
 XX  
 PT Gene chip reagent kit for detecting hepatitis B and C and its preparing  
 PT process and application.  
 PT  
 XX Claim 6; Page 33 (Disclosure); 48bp; Chinese.  
 PS  
 XX The invention describes a gene chip reagent kit for detecting hepatitis B  
 CC and C, its components and preparing process. The method for detecting and  
 CC the result analysis, and the usage of the reagent kit are disclosed. This

CC sequence represents a cDNA associated with the method of detecting  
 CC hepatitis B and C  
 XX  
 SQ Sequence 301 BP; 66 A; 83 C; 91 G; 61 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 301;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 114 TTGCGACCCCAACTACTC 95  
 RESULT 169  
 AAT87088/C  
 ID AAT87088 standard; DNA; 305 BP.  
 AC AAT87088;  
 AC AAT87088;  
 DT 25-MAR-2003 (revised)  
 DT 07-JAN-1998 (first entry)  
 DE HCV amplification product.  
 XX  
 KM RNA; plasma; HCV; polymerase chain reaction; PCR; ss.  
 XX Hepatitis C virus.  
 OS  
 XX US5654179-A.  
 PN  
 XX 05-ANG-1997.  
 PD  
 XX 03-OCT-1994; 94US-00317220.  
 PF  
 XX 14-NOV-1990; 90US-00614921.  
 PR 19-JUN-1992; 92US-00901545.  
 PR 08-APR-1993; 93US-00044649.  
 XX  
 PA (HYDS ) HRI RES INC.  
 XX  
 PI Lin L;  
 PI WPI; 1997-401849/37.  
 DR  
 XX Preparation of RNA samples from plasma - by alcohol precipitation after  
 PT lysis with guanidinium thiocyanate.  
 PT  
 XX Disclosure; Fig 22; 60pp; English.  
 PS  
 XX This DNA sequence comprises an RT-PCR amplification product of hepatitis  
 CC C virus RNA recovered from plasma. A claimed method for preparing RNA  
 CC samples comprises: (a) mixing plasma with an aqueous buffer solution  
 CC containing guanidinium thiocyanate and beta-mercaptoethanol; (b) heating  
 CC the mixture; (c) adding an equal volume of an alcohol to precipitate RNA;  
 CC and (d) recovering the RNA. The method can be used to prepare RNA samples  
 CC for subsequent amplification, especially for detecting pathogens, e.g.  
 CC HCV or HIV. Compared with the known "Isoquick" and "RNAzol" methods,  
 CC the method uses fewer tubes (just one), requires fewer steps, takes less  
 CC time and produces no toxic waste. (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX  
 SQ Sequence 305 BP; 59 A; 91 C; 92 G; 63 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 275 TTGCGACCCCAACTACTC 256

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RESULT 170
ABN79969/C
ID   ABN79969 standard; DNA; 305 BP.
XX
XX   ABN79969;
AC
XX   15-JUL-2002 (first entry)
DT
XX   Hepatitis C virus 5' untranslated region genotype 1a.
DE
XX   Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus;
KM   tissue typing; untranslated region; UTR; de; HCV.
XX
OS   Hepatitis C virus.
XX
XX   WO200220837-A2.
XX
XX   14-MAR-2002.
XX
XX   10-SEP-2001; 2001WO-GB004042.
XX
XX   08-SEP-2000; 2000GB-00022069.
XX
XX   (PYRO-) PYROSEQUENCING AB.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (GARD/) GARDNER R.
XX
XX   Ronaghi M, Ekstroem B, Pourmand N;
PI
XX   WPI; 2002-393849/42.
XX
XX   Typing nucleic acid for obtaining information about several variable
PT   sites involves simultaneously or sequentially performing two or more
PT   primer extension reactions, and determining the pattern of nucleotide
PT   incorporation.
XX
XX   Example 1; Fig 2; 86pp; English.
XX
XX   The invention relates to a novel method for obtaining typing information
CC   about several variable sites within target nucleic acid, or typing one or
CC   more nucleic acid molecules. The methods of the invention are useful for
CC   typing one or more nucleic acid molecules containing two or more variable
CC   sites, preferably nucleic acid molecules containing three or more
CC   variable sites are typed, where three or more primer extension reactions
CC   are performed. The method is also useful for diagnosis of pathological
CC   conditions characterized by the presence of specific nucleic acid
CC   molecule(s). The methods are particularly suited for identifying
CC   microbial species or their subtypes, and in typing procedures e.g. typing
CC   of polymorphisms, tissue typing or in clinical applications. The sequence
CC   represents the 5' untranslated region (UTR) of a hepatitis C virus (HCV)
CC   genotype, amplified in the invention to type HCV-positive sera
XX
XX   Sequence 305 BP; 57 A; 88 C; 96 G; 64 T; 0 U; 0 Other;
SQ
Query Match          100.0%; Score 20; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY   1   TTCCGACCCCACTACTC 20
      |||||
DB   233 TTCCGACCCCACTACTC 214

RESULT 171
ABN79970/C
ID   ABN79970 standard; DNA; 305 BP.
XX
XX   ABN79970;
AC
XX   15-JUL-2002 (first entry)
DT
XX   Hepatitis C virus 5' untranslated region genotype 1b.
DE
XX
XX

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```

KM   Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus;
KM   tissue typing; untranslated region; UTR; de; HCV.
XX
XX   Hepatitis C virus.
OS
XX   WO200220837-A2.
XX
XX   14-MAR-2002.
XX
XX   10-SEP-2001; 2001WO-GB004042.
XX
XX   08-SEP-2000; 2000GB-00022069.
XX
XX   (PYRO-) PYROSEQUENCING AB.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (GARD/) GARDNER R.
XX
XX   Ronaghi M, Ekstroem B, Pourmand N;
PI
XX   WPI; 2002-393849/42.
XX
XX   Typing nucleic acid for obtaining information about several variable
PT   sites involves simultaneously or sequentially performing two or more
PT   primer extension reactions, and determining the pattern of nucleotide
PT   incorporation.
XX
XX   Example 1; Fig 2; 86pp; English.
XX
XX   The invention relates to a novel method for obtaining typing information
CC   about several variable sites within target nucleic acid, or typing one or
CC   more nucleic acid molecules. The methods of the invention are useful for
CC   typing one or more nucleic acid molecules containing two or more variable
CC   sites, preferably nucleic acid molecules containing three or more
CC   variable sites are typed, where three or more primer extension reactions
CC   are performed. The method is also useful for diagnosis of pathological
CC   conditions characterized by the presence of specific nucleic acid
CC   molecule(s). The methods are particularly suited for identifying
CC   microbial species or their subtypes, and in typing procedures e.g. typing
CC   of polymorphisms, tissue typing or in clinical applications. The sequence
CC   represents the 5' untranslated region (UTR) of a hepatitis C virus (HCV)
CC   genotype, amplified in the invention to type HCV-positive sera
XX
XX   Sequence 305 BP; 56 A; 87 C; 98 G; 64 T; 0 U; 0 Other;
SQ
Query Match          100.0%; Score 20; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY   1   TTCCGACCCCACTACTC 20
      |||||
DB   233 TTCCGACCCCACTACTC 214

RESULT 172
ABN79974/C
ID   ABN79974 standard; DNA; 305 BP.
XX
XX   ABN79974;
AC
XX   15-JUL-2002 (first entry)
DT
XX   Hepatitis C virus 5' untranslated region genotype 3b.
DE
XX   Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus;
KM   tissue typing; untranslated region; UTR; de; HCV.
XX
XX   Hepatitis C virus.
OS
XX   WO200220837-A2.
XX
XX   14-MAR-2002.
XX
XX   10-SEP-2001; 2001WO-GB004042.
XX

```

XX 08-SEP-2000; 2000GB-00022069.  
 PR  
 XX

PA (PYRO-) PYROSEQUENCING AB.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PA (GARD/) GARDNER R.  
 XX

PI Ronaghi M, Ekstroem B, Pourmand N;  
 DR WPI; 2002-393849/42.  
 XX

PT Typing nucleic acid for obtaining information about several variable  
 PT sites involves simultaneously or sequentially performing two or more  
 PT primer extension reactions, and determining the pattern of nucleotide  
 PT incorporation.

PS Example 1; Fig 2; 86pp; English.

XX The invention relates to a novel method for obtaining typing information  
 CC about several variable sites within target nucleic acid, or typing one or  
 CC more nucleic acid molecules. The methods of the invention are useful for  
 CC typing one or more nucleic acid molecules containing two or more variable  
 CC sites, preferably nucleic acid molecules containing three or more variable  
 CC sites are performed. The method is also useful for diagnosis of pathological  
 CC conditions characterized by the presence of specific nucleic acid  
 CC molecule(s). The methods are particularly suited for identifying  
 CC microbial species or their subtypes, and in typing procedures e.g. typing  
 CC of polymorphisms, tissue typing or in clinical applications. The sequence  
 CC represents the 5' untranslated region (UTR) of a hepatitis C virus (HCV)  
 CC genotype, amplified in the invention to type HCV-positive sera  
 SO Sequence 305 BP; 56 A; 88 C; 98 G; 63 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 20; DB 6; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 TTGGGACCCCAACTACTC 20  
 233 TTGGGACCCCAACTACTC 214

RESULT 173  
 AA067079/c

ID AA067079 standard; DNA; 306 BP.

XX AA067079;

DT 14-MAR-1995 (first entry)

DE Hepatitis C virus DNA fragment comprising KpnI restriction site.

KM Hepatitis C virus; restriction endonuclease; KpnI; marker; cleavage site;

KW HCV; ss.

OS Hepatitis C virus.

PN JP06181764-A.

PD 05-JUL-1994.

PF 20-JAN-1993; 93JP-00007721.

PR 22-SEP-1992; 92JP-00252793.

PA (SAKA) OTSUKA PHARM CO LTD.

DR WPI; 1994-251687/31.

PT DNA contg. KpnI recognition site as marker for hepatitis C virus - useful  
 PT in diagnosis of HC.  
 XX

PS Claim 1; Page 7; 9pp; Japanese.

CC This sequence, which is obtained from hepatitis C virus (HCV) comprises a  
 CC KpnI restriction endonuclease recognition site. The restriction site is  
 CC found in the wild type sequence and can therefore be used as a diagnostic  
 CC marker  
 XX

SO Sequence 306 BP; 55 A; 89 C; 96 G; 66 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 20; DB 2; Length 306;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 TTGGGACCCCAACTACTC 20  
 238 TTGGGACCCCAACTACTC 219

RESULT 174  
 ABS53053/c

ID ABS53053 standard; DNA; 306 BP.

XX ABS53053;

DT 15-NOV-2002 (first entry)

DE Hepatitis C virus target polynucleotide.

KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

KW non-B hepatitis; acute hepatitis; chronic hepatitis;

KW hepatocellular carcinoma; virocid; cytostatic; antisense therapy;

KW gene therapy; ss.

OS Hepatitis C virus.

PN US2002081577-A1.

PD 27-JUN-2002.

PF 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

PR 02-JUL-1996; 96US-0021104P.

PA (KILK/) KILKUSKIE R L.

PA (FRAN/) FRANK B L.

PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.

PA (ROBE/) ROBERTS N A.

PA (WALT/) WALTHER D M.

PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,

PI Hamlin HA, Roberts NA, Walther DM;

DR WPI; 2002-537132/57.

PT Synthetic oligonucleotides complementary to a portion of the 5'

PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and

PT treating HCV infections and hepatocellular carcinoma.  
 XX

PS Disclosure; Fig 1; 74pp; English.

XX The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for

CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a hepatitis C virus polynucleotide used as the target for  
CC inhibition of HCV replication and gene expression using the synthetic  
CC oligonucleotides of the invention  
XX  
SQ Sequence 306 BP; 63 A; 87 C; 95 G; 61 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 306;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCCGACCCCAACTACTC 20  
Db 212 TTCCGACCCCAACTACTC 193  
RESULT 175  
AAAT5294/C  
ID AAAT5294 standard; cDNA, 308 BP.  
XX  
AC AAAT5294;  
XX  
DT 15-JAN-2001 (first entry)  
XX  
DE Novel hepatitis C virus cDNA clone 189.  
XX  
KM Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;  
KM viral infectivity; viral replication; ds.  
XX  
OS Hepatitis C virus.  
XX  
EN EPI034785-A2.  
XX  
PD 13-SEP-2000.  
XX  
PF 16-MAR-1990; 2000EP-00109602.  
XX  
PR 17-MAR-1989; 89US-00325338.  
PR 20-APR-1989; 89US-00341334.  
PR 18-MAY-1989; 89US-00355002.  
PR 16-MAR-1990; 90EP-00302866.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Houghton M, Choo Q, Kuo G;  
XX  
DR WPI; 2000-566891/53.  
XX  
PT Novel composition comprising a hepatitis C virus antisense polynucleotide  
PT which is complementary to or corresponds to a sense strand of the virus  
PT genome, and selectively hybridizes to it.  
XX  
PS Example; Fig 14; 75pp; English.  
XX  
CC The specification describes a pharmaceutical composition which comprises  
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is  
CC characterized by a positive stranded RNA genome which has 40% homology at  
CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide  
CC binds to cellular polynucleotides which enhance and/or are required for  
CC viral infectivity, replicative ability or chronicity. The antisense  
CC polynucleotides may also be designed to bind with high specificity, to be  
CC of increased stability, to be stable and to have low toxicity. The  
CC composition also comprises an agent which causes viral RNA to be  
CC inactive. The composition is used for preventing HCV replication in a  
CC system. The present sequence represents a novel HCV cDNA sequence, which  
CC is used in the course of the invention  
XX  
SQ Sequence 308 BP; 59 A; 89 C; 94 G; 66 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 308;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
Db 251 TTCCGACCCCAACTACTC 232  
RESULT 176  
ADN35973/C  
ID ADN35973 standard; cDNA, 308 BP.  
XX  
AC ADN35973;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE HCV cDNA clone 189.  
XX  
KM Antiviral; Vaccine; hepatitis C virus infection; HCV infection; ss.  
XX  
OS Hepatitis C virus.  
XX  
EN EPI394255-A2.  
XX  
PD 03-MAR-2004.  
XX  
PF 16-MAR-1990; 2003EP-00016585.  
XX  
PR 17-MAR-1989; 89US-00325338.  
PR 20-APR-1989; 89US-00341334.  
PR 18-MAY-1989; 89US-00355002.  
PR 16-MAR-1990; 90EP-00302866.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Houghton M, Choo Q, Kuo G;  
XX  
DR WPI; 2004-193149/19.  
DR P-PSDB; ADN35972.  
XX  
PT Novel purified hepatitis C virus polypeptide comprising epitope encoded  
PT by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C  
PT virus.  
XX  
PS Example 1; Fig 14; 79pp; English.  
XX  
CC The present invention relates to hepatitis C virus (HCV) proteins and  
CC cDNA sequences. The sequences are useful in immunoassays for detecting  
CC antibodies directed against HCV antigen; preparing host cells transformed  
CC with a recombinant polynucleotide; screening antiviral agents and  
CC determining the effect of antiviral agent in inhibiting viral replication  
CC in cell culture system; and developing vaccine for treating HCV  
CC infection.  
XX  
SQ Sequence 308 BP; 59 A; 89 C; 94 G; 66 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 308;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCCGACCCCAACTACTC 20  
Db 251 TTCCGACCCCAACTACTC 232  
RESULT 177  
ABK70877/C  
ID ABK70877 standard; DNA, 310 BP.  
XX  
AC ABK70877;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #11 from HCV infected patient BU.

KW Hepatitis C virus infection; HCV; central nervous system; CNS;  
 KW microglial cell precursor; alpha-interferon; monocytic;  
 KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
 OS Hepatitis C virus.  
 XX  
 FN WO200220054-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 31-AUG-2001; 2001WO-GB003901.  
 XX  
 PR 06-SEP-2000; 2000GB-00021859.  
 XX  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
 DR WPI; 2002-383036/41.  
 XX  
 PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
 PT inhibiting infection by HCV of and/or replication of HCV in cells of  
 PT central nervous system.  
 XX  
 PS Example 1; Fig 14; 145pp; English.  
 XX  
 CC The present invention relates to a method of treating a patient with or  
 CC at risk of hepatitis C virus (HCV) infection. The method comprises  
 CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
 CC central nervous system (CNS) of the patient. The method is performed by  
 CC administering to the central nervous system (CNS) a compound capable of  
 CC inhibiting HCV infection and/or replication in the CNS of the patient  
 CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
 CC treating a patient with or at risk of HCV infection by inhibiting HCV  
 CC infection of and/or replication in cells and non-CNS cells. Preferably,  
 CC HCV infection of and/or replication in microglial cells or circulating  
 CC microglial cell precursors is inhibited. The method is carried out in a  
 CC patient who is, has been or will be administered alpha-interferon. Use of  
 CC a pharmacological agent that blocks binding of the brain-specific  
 CC envelope protein to the putative receptor prevents uptake of the virus to  
 CC the CNS, and improves long-term response rates. Reinfection of the liver  
 CC by the virus released by the CNS may be prevented by the above mentioned  
 CC method. The development of resistant strains is reduced or prevented. By  
 CC before, together with or after antiviral therapy. ABK70867-ABK70886  
 CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
 CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
 CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
 CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
 CC All sequences in Fig 14 have been typed in according to their correct  
 CC nucleotide positioning  
 XX  
 SQ Sequence 310 BP; 57 A; 91 C; 96 G; 66 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 247 TTGCGACCCCAACTACTC 228  
 RESULT 178  
 ID AA236198/c  
 XX AA236198 standard; DNA; 312 BP.  
 AC  
 XX AA236198;  
 DT 11-FEB-2000 (first entry)  
 XX  
 DE Adapted HCV 5' non translated region from 5'HCV/R1.orig.  
 XX

KW Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;  
 KW 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;  
 KW bovine viral diarrhoea virus; NADL; vaccine; ss.  
 XX  
 OS Synthetic.  
 OS Hepatitis C virus.  
 XX  
 PN WO955366-A1.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 23-APR-1999; 99WO-US008850.  
 XX  
 PR 24-APR-1998; 98US-0082964P.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Rice CM, Frolow I, McBride MS, Loe Y, Agapov EV, Myers TM;  
 DR WPI; 2000-013359/01.  
 XX  
 PT Chimeric viral RNA, used in vaccine against BVDV.  
 PT  
 XX  
 PS Disclosure; Fig 14; 108pp; English.  
 XX  
 CC The present sequence represents an adapted Hepatitis C virus (HCV) 5' non  
 CC translated region (NTR) from a virus of the invention. Only the sequence  
 CC from the 5' base to the ATG initiating the polypeptide is shown. The  
 CC specification describes chimeric viral RNA comprising a 5' nontranslated  
 CC region (5'NTR); an open reading frame (ORF) region; and a 3' NTR; where  
 CC at least one of the regions is chimeric and comprises a nucleotide  
 CC sequence from a pestivirus in operable linkage with a heterologous  
 CC nucleotide sequence, preferably from HCV. The chimeric viral RNA is  
 CC replication-competent. The chimeric viral RNA can be used in a method for  
 CC identifying compounds having antiviral activity against HCV. When the  
 CC pestivirus viral nucleotide sequence is from bovine viral diarrhoea virus  
 CC (BVDV), the chimeric viral RNA can be used in a vaccine against BVDV  
 XX  
 SQ Sequence 312 BP; 60 A; 88 C; 97 G; 67 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 3; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 243 TTGCGACCCCAACTACTC 224  
 RESULT 179  
 ID AA236197/c  
 XX AA236197 standard; DNA; 314 BP.  
 AC  
 XX AA236197;  
 DT 11-FEB-2000 (first entry)  
 XX  
 DE Adapted HCV 5' non translated region from 5'HCV/R1.cons.  
 XX  
 KW Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;  
 KW 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;  
 KW bovine viral diarrhoea virus; NADL; vaccine; ss.  
 XX  
 OS Synthetic.  
 OS Hepatitis C virus.  
 XX  
 PN WO995366-A1.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 23-APR-1999; 99WO-US008850.  
 XX  
 PR 24-APR-1998; 98US-0082964P.  
 XX



XX (UNIM) UNIV WASHINGTON.  
PA  
XX  
PI Rice CM, Frolov I, McBride MS, Lee Y, Agapov EV, Meers TM;  
XX  
DR WPI; 2000-013359/01.  
XX  
PT Chimeric viral RNA, used in vaccine against BVDV.  
PS  
XX Disclosure; Fig 13; 108pp; English.  
XX  
CC The present sequence represents an adapted Hepatitis C virus (HCV) 5' non  
CC translated region (NTR) from a virus of the invention. Only the sequence  
CC from the 5' base to the ATG initiating the polypeptide is shown. The  
CC specification describes chimeric viral RNA comprising a 5' nontranslated  
CC region (5'NTR); an open reading frame (ORF) region; and a 3' NTR; where  
CC at least one of the regions is chimeric and comprises a nucleotide  
CC sequence from a pestivirus in operable linkage with a heterologous  
CC nucleotide sequence, preferably from HCV. The chimeric viral RNA is  
CC replication-competent. The chimeric viral RNA can be used in a method for  
CC identifying compounds having antiviral activity against HCV. When the  
CC pestivirus viral nucleotide sequence is from bovine viral diarrhoea virus  
CC (BVDV), the chimeric viral RNA can be used in a vaccine against BVDV  
XX  
SQ Sequence 314 BP; 61 A; 88 C; 97 G; 68 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 314;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGCGAGCCGACACTACTC 20  
DB 245 TTGCGAGCCGACACTACTC 226  
RESULT 180  
ABK70883/c  
ID ABK70883 standard; DNA; 323 BP.  
XX  
AC ABK70883;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #17 from HCV infected patient BU.  
XX  
KM Hepatitis C virus infection; HCV; central nervous system; CNS;  
KM microglial cell precursor; alpha-interferon; monocyte;  
XX brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001WO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
XX  
DR WPI; 2002-383036/41.  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises

CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinflection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
SQ Sequence 323 BP; 63 A; 95 C; 98 G; 67 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 323;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGCGAGCCGACACTACTC 20  
DB 260 TTGCGAGCCGACACTACTC 241  
RESULT 181  
ABK70882/c  
ID ABK70882 standard; DNA; 323 BP.  
XX  
AC ABK70882;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #16 from HCV infected patient BU.  
XX  
KM Hepatitis C virus infection; HCV; central nervous system; CNS;  
KM microglial cell precursor; alpha-interferon; monocyte;  
XX brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001WO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
XX  
DR WPI; 2002-383036/41.  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises

CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
CC XX

SO Sequence 323 BP; 63 A; 96 C; 97 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 323;

Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGGACCCCAACTACTC 20

Db 260 TTTCGGACCCCAACTACTC 241

RESULT 182

ABK70880/c

ID ABK70880 standard; DNA; 326 BP.

XX ABK70880;

XX 30-JUL-2002 (first entry)

DE HCV genome 5'UTR sequence #14 from HCV infected patient BU.

XX Hepatitis C virus infection; HCV; central nervous system; CNS;

KW microglial cell precursor; alpha-interferon; monocyte;

KW brain-specific envelope protein; antiviral therapy; virucide; ds.

XX Hepatitis C virus.

OS

PN WO200220054-A2.

XX 14-MAR-2002.

PF 31-AUG-2001; 2001WO-GB003901.

PR 06-SEP-2000; 2000GB-00021859.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PA Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;

PI WPI; 2002-383036/41.

XX Treating patient with or at risk of hepatitis C virus (HCV) infection by

PT inhibiting infection by HCV of and/or replication of HCV in cells of

PT central nervous system.

XX Example 1; Fig 14; 145pp. English.

PS The present invention relates to a method of treating a patient with or

CC at risk of hepatitis C virus (HCV) infection. The method comprises

CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
CC XX

SO Sequence 326 BP; 62 A; 94 C; 101 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 326;

Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGGACCCCAACTACTC 20

Db 263 TTTCGGACCCCAACTACTC 244

RESULT 183

ADP20410/c

ID ADP20410 standard; DNA; 326 BP.

XX ADP20410;

XX 09-SEP-2004 (first entry)

DE Hepatitis C virus internal ribosome entry site, IRES, sequence, SEQ ID 1.

XX Virucide; Cytostatic; p110 subunit;

KW eukaryotic translation initiation factor eIF3; region II;

KW internal ribosome entry site; IRES; aminoglycoside;

KW hepatitis C infection; swine fever; bovine diarrhoea; viral infection;

XX cancer; ds.

OS Hepatitis C virus.

PN FR2848572-A1.

XX 18-JUN-2004.

PF 12-DEC-2002; 2002FR-00015718.

PR 12-DEC-2002; 2002FR-00015718.

XX (UYFO-) UNIV FOURIER JOSEPH.

PA Balakireva L;

PI WPI; 2004-452919/43.

XX In vitro screening for antiviral agents, from ability to inhibit complex

PT formation between the p110 subunit of translation initiation factor eIF3

PT and region II of the viral internal ribosome binding site.

PS Example 1; SEQ ID NO 1; 45pp; French.

CC The present invention relates to an in vitro method of screening for  
CC compounds (A) that inhibit the formation of a complex between the p10  
CC subunit (ADP20412) of the eukaryotic translation initiation factor eIF3  
CC and region II of the internal ribosome entry site (IRES; ADP20411) of  
CC hepatitis C virus (HCV). Preferably the p10 recognition motif (ADP20414)  
CC and the region II consensus sequence (ADP20412), or fragment of it  
CC containing at least 8 consecutive nucleotides, are used. (A) is  
CC especially an aminoglycoside, specifically tobramycin or an  
CC oligonucleotide antisense to consensus sequence ADP20412, or parts of it.  
CC (A) are used for treating infection by hepatitis C, swine fever and  
CC bovine diarrhoea viruses, also for treating viral or non-viral diseases  
CC which involve proteins synthesis of which is initiated from an IRES, e.g.  
CC cancer. The present sequence is the full-length HCV IRES sequence.  
XX  
SQ Sequence 326 BP; 69 A; 90 C; 98 G; 69 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 326;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCAACTACTC 20  
DB 236 TTGCGAGCCCAACTACTC 217  
RESULT 184  
AA236199/C  
ID AA236199 standard; DNA; 327 BP.  
XX  
AC AA236199;  
XX  
DT 11-FEB-2000 (first entry)  
DE  
DE Adapted HCV 5' non translated region from 5'HCV/R2.cons.  
XX  
XX Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;  
KM 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;  
KM bovine viral diarrhoea virus; NADL; vaccine; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
PN WO955366-A1.  
XX  
PD 04-NOV-1999.  
XX  
PF 23-APR-1999; 99WO-US008850.  
XX  
PR 24-APR-1998; 98US-0082964P.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Rice CM, Frolov I, McBride MS, Lee Y, Agapov EV, Myers TM;  
XX WPI; 2000-013359/01.  
DR  
PT Chimeric viral RNA, used in vaccine against BVDV.  
XX  
PS Disclosure; Fig 15; 108pp; English.  
XX  
XX The present sequence represents an adapted Hepatitis C virus (HCV) 5' non  
CC translated region (NTR) from a virus of the invention. Only the sequence  
CC from the 5' base to the ATG initiating the polyprotein is shown. The  
CC specification describes chimeric viral RNA comprising a 5' nontranslated  
CC region (5'NTR); an open reading frame (ORF) region; and a 3' NTR; where  
CC at least one of the regions is chimeric and comprises a nucleotide  
CC sequence from a pestivirus in operable linkage with a heterologous  
CC nucleotide sequence, preferably from HCV. The chimeric viral RNA is  
CC replication-competent. The chimeric viral RNA can be used in a method for  
CC identifying compounds having antiviral activity against HCV. When the  
CC pestivirus viral nucleotide sequence is from bovine viral diarrhoea virus  
CC (BVDV), the chimeric viral RNA can be used in a vaccine against BVDV  
XX

SQ Sequence 327 BP; 65 A; 94 C; 98 G; 70 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 327;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCAACTACTC 20  
DB 258 TTGCGAGCCCAACTACTC 239  
RESULT 185  
ABK70884/C  
ID ABK70884 standard; DNA; 327 BP.  
XX  
AC ABK70884;  
XX  
DT 30-JUL-2002 (first entry)  
DE  
DE HCV genome 5'UTR sequence #18 from HCV infected patient BU.  
XX  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
KM microglial cell precursor; alpha-interferon; monocyte;  
KM brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
OS  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001MO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forston DM;  
XX WPI; 2002-383036/41.  
DR  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
XX inhibiting infection by HCV of and/or replication of HCV in cells of  
XX central nervous system.  
PT  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Re-infection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
XX nucleotide positioning  
XX

SQ Sequence 327 BP; 62 A; 95 C; 101 G; 69 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGACCCCAACTACTC 20  
 Db 264 TTCCGACCCCAACTACTC 245  
 RESULT 186  
 AAT77074/c  
 ID AAT77074 standard; DNA; 328 BP.  
 AC AAT77074;  
 XX  
 DT 11-DEC-1997 (first entry)  
 XX  
 DE Hepatitis C virus 5' non-translating region 1b HCV-J encoding DNA.  
 XX  
 KW HCV; PCR; polymerase chain reaction; restriction enzyme; cleavage;  
 XX recognition; ss.  
 OS Hepatitis C virus.  
 FH Key Location/Qualifiers  
 FT primer\_bind 1..20  
 FT /tag= a  
 FT /label= P1  
 FT primer\_bind 13..37  
 FT /tag= b  
 FT /label= P2  
 FT primer\_bind complement(298..322)  
 FT /tag= c  
 FT /label= P3  
 FT primer\_bind complement(304..328)  
 FT /tag= d  
 FT /label= P4  
 FT  
 FT  
 XX JP09075100-A.  
 XX  
 XX 25-MAR-1997.  
 XX  
 PF 18-SEP-1995; 95JP-00238254.  
 XX  
 PR 18-SEP-1995; 95JP-00238254.  
 XX  
 PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.  
 XX  
 DR WPI; 1997-239280/22.  
 XX  
 PT Determination of the type of hepatitis C virus present in a sample - by  
 PT restriction enzyme analysis.  
 XX  
 PS Example 1; Page 8; 9pp; Japanese.  
 XX  
 CC A method has been developed to determine the type of hepatitis C virus  
 CC (HCV) present in a sample. The method involves: (a) amplifying the 5' non  
 CC translated region of HCV by PCR; and (ii) cleaving the PCR product with  
 CC three restriction enzymes having different cleavage- recognition sites,  
 CC where the restriction enzymes recognise and cleave the base sequences;  
 CC (i) CCGGG; (ii) CGCG; and (iii) CCGGG; and (c) determining the type of  
 CC HCV based on the cleavage pattern after electrophoresis. The present  
 CC sequence represents the 5' non-coding region of HCV  
 XX  
 SQ Sequence 328 BP; 65 A; 92 C; 101 G; 70 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGACCCCAACTACTC 20  
 Db 264 TTCCGACCCCAACTACTC 245

Db 252 TTCCGACCCCAACTACTC 233  
 RESULT 187  
 ABL46275/c  
 ID ABL46275 standard; RNA; 328 BP.  
 AC ABL46275;  
 XX  
 DT 26-APR-2002 (first entry)  
 XX  
 DE Hepatitis C virus subtype 1a mRNA sequence SEQ ID NO:242.  
 XX  
 KW Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KW characterisation; identification; nucleic acid structure; diagnosis;  
 XX gene; ss.  
 OS Hepatitis C virus.  
 XX  
 PN WO200196537-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 15-JUN-2001; 2001WO-US019401.  
 XX  
 PR 17-JUN-2000; 2000US-0212308P.  
 PR 15-JUN-2001; 2001US-00212308.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Lyanchuk V, Allaui H, Dong F, Neri BP, Vener IT;  
 XX  
 DR WPI; 2002-049698/06.  
 XX  
 PT Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX  
 PS Claim 48; Fig 74; 409pp; English.  
 XX  
 CC The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 328 BP; 63 A; 95 C; 102 G; 0 T; 68 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGACCCCAACTACTC 20  
 Db 257 TTCCGACCCCAACTACTC 238  
 RESULT 188  
 ABL46278/c  
 ID ABL46278 standard; RNA; 328 BP.  
 AC ABL46278;  
 XX  
 DT 26-APR-2002 (first entry)  
 XX

DE Hepatitis C virus subtype 3a mRNA sequence SEQ ID NO:245.  
 XX  
 XX Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KM characterisation; identification; nucleic acid structure; diagnosis;  
 KM gene; ss.  
 XX  
 XX Hepatitis C virus.  
 OS  
 XX  
 PN WO200198537-A2.  
 XX  
 XX 27-DEC-2001.  
 PD  
 XX 15-JUN-2001; 2001WO-US019401.  
 PE  
 XX 17-JUN-2000; 2000US-0212308P.  
 PR  
 XX 15-JUN-2001; 2001US-00212308.  
 PR  
 XX  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PA  
 XX  
 PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;  
 FI  
 DR WPI; 2002-049698/06.  
 DR  
 XX  
 XX Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX  
 XX Example 20; Fig 76; 4099p; English.  
 PS  
 XX  
 CC The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention  
 CC  
 XX  
 SQ Sequence 328 BP; 62 A; 98 C; 102 G; 0 T; 66 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 TTGCGAGCCCAACTACTC 20  
 Db 257 TTGCGAGCCCAACTACTC 238  
 RESULT 189  
 ABL46273/C  
 ID ABL46273 standard; RNA; 328 BP.  
 AC  
 XX ABL46273;  
 AC  
 XX  
 DT 26-APR-2002 (first entry)  
 DT  
 XX  
 DE Hepatitis C virus subtype 1a mRNA sequence SEQ ID NO:240.  
 DE  
 XX Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KM characterisation; identification; nucleic acid structure; diagnosis;  
 KM gene; ss.  
 XX  
 XX Hepatitis C virus.  
 OS  
 XX  
 PN WO200198537-A2.  
 PN  
 XX 27-DEC-2001.  
 PD  
 XX

PE 15-JUN-2001; 2001WO-US019401.  
 XX  
 XX 17-JUN-2000; 2000US-0212308P.  
 PR  
 XX 15-JUN-2001; 2001US-00212308.  
 PR  
 XX  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PA  
 XX  
 PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;  
 FI  
 DR WPI; 2002-049698/06.  
 DR  
 XX  
 XX Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX  
 XX Example 20; Fig 73; 4099p; English.  
 PS  
 XX  
 CC The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention  
 CC  
 XX  
 SQ Sequence 328 BP; 65 A; 94 C; 101 G; 0 T; 68 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 TTGCGAGCCCAACTACTC 20  
 Db 257 TTGCGAGCCCAACTACTC 238  
 RESULT 190  
 AAL53724/C  
 ID AAL53724 standard; RNA; 328 BP.  
 AC  
 XX AAL53724;  
 AC  
 XX  
 DT 27-OCT-2003 (revised)  
 DT  
 XX 07-FEB-2003 (first entry)  
 DT  
 XX  
 DE Hepatitis C virus target region SEQ ID NO 18.  
 DE  
 XX Target RNA; target RNA:support-attached test compound; flow cytometry;  
 KM mass spectrometry; high-throughput screening; RNA motif; ss.  
 KM  
 XX Hepatitis C virus; Virus.  
 OS  
 XX  
 PN WO200283837-A1.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 11-APR-2002; 2002WO-US011758.  
 PE  
 XX 11-APR-2001; 2001US-0282966P.  
 PR  
 XX (PTCT-) PTC THERAPEUTICS INC.  
 PA  
 XX  
 PI Altmstead NG;  
 FI  
 DR WPI; 2003-075534/07.  
 DR  
 XX  
 XX Identifying a test compound that binds to a target RNA molecule by  
 PT separating the detectably labeled target RNA:support-attached test

PT compound complex from uncomplexed target RNA molecules and test compounds  
PT by flow cytometry.  
XX  
PS Example; Page 60; 131pp; English.  
XX  
CC The invention relates to a novel method for identifying a test compound  
CC that binds to a target RNA molecule comprising separating the detectably  
CC labeled target RNA: support-attached test compound complex from  
CC uncomplexed target RNA molecules and test compounds. The separating  
CC process is carried out by flow cytometry and determining a structure of  
CC the type of test compound of the RNA: support-attached test compound  
CC complex by mass spectrometry. The method is useful for high-throughput  
CC screening of libraries of compounds to identify pharmaceutical leads.  
CC This polynucleotide sequence represents one of the target RNA motifs/  
CC regions of the invention. (Updated on 27-Oct-2003 to standardise OS  
CC field)  
XX  
SQ Sequence 328 BP; 61 A; 93 C; 103 G; 0 T; 71 U; 0 Other;  
Query Match 100.0%; Score 20; DB 8; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCAACACTACTC 20  
Db 263 TTGCGAGCCCAACACTACTC 244  
RESULT 191  
AAD9656/C  
ID AAD9656 standard; RNA; 328 BP.  
XX  
AC AAD9656;  
XX  
DT 24-MAR-2003 (first entry)  
XX  
DE Human internal ribosome entry site (IRES) RNA #2.  
XX  
KW Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;  
KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;  
KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;  
KW neurodegenerative disorder; Parkinson's disease; gene therapy; virocidic;  
KW haemostatic; antibacterial; mototropic; neuroprotective; cytostatic;  
KW fungicide; human; internal ribosome entry site; IRES; ss.  
XX  
OS Homo sapiens.  
XX  
EN WO200283953-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 11-APR-2002; 2002WO-US011757.  
XX  
PR 11-APR-2001; 2001US-0282965P.  
XX  
PA (PTCT-) PTC THERAPEUTICS INC.  
XX  
PI Rando R, Welch E;  
XX  
PT WPI; 2003-075561/07.  
XX  
DR  
XX  
PT Identifying a test compound that binds to a target RNA molecule for  
PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,  
PT diabetes, by contacting a detectably labeled target RNA molecule with a  
PT library of test compounds.  
XX  
PS Example; Page 68; 152pp; English.  
XX  
CC The invention relates to a method for identifying a test compound that  
CC binds to a target RNA molecule, which comprises contacting a detectably  
CC labeled target RNA molecule with a library of test compounds under  
CC conditions that permit direct binding of the labelled target RNA to a  
CC member of the library of test compounds so that a detectably labeled

CC target RNA: test compound complex is formed. The method is useful for  
CC screening libraries of compounds for those that are selectively bind to a  
CC pre-selected target RNA. The compounds are useful for inhibiting the  
CC formation of a specific bound RNA: host cell factor complexes in vivo.  
CC They are also useful for treating or preventing diseases associated with  
CC overproduction or decreased protein function, such as amyloidosis,  
CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,  
CC inflammation, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,  
CC dwarfism, cystic fibrosis, diabetes, obesity, neurodegenerative  
CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).  
CC The invention is also used in gene therapy. The present sequence is human  
CC internal ribosome entry site (IRES) RNA. This sequence is used to  
CC illustrate the method of the invention  
XX  
SQ Sequence 328 BP; 61 A; 93 C; 103 G; 0 T; 71 U; 0 Other;  
Query Match 100.0%; Score 20; DB 8; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCAACACTACTC 20  
Db 263 TTGCGAGCCCAACACTACTC 244  
RESULT 192  
ABK70871/C  
ID ABK70871 standard; DNA; 329 BP.  
XX  
AC ABK70871;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #5 from HCV infected patient BU.  
XX  
KW Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virocidic; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001WO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
XX  
PT WPI; 2002-383036/41.  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of

CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
SQ Sequence 329 BP; 60 A; 98 C; 100 G; 71 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 6; Length 329;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTCCGACCCCAACTACTC 20  
DB 266 TTCCGACCCCAACTACTC 247  
  
RESULT 193  
ABK70881/C  
ID ABK70881 standard; DNA; 333 BP.  
XX  
AC ABK70881;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #15 from HCV infected patient BU.  
XX  
KW Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001WO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
XX  
DR WPI; 2002-383036/41.  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of

CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
SQ Sequence 333 BP; 60 A; 100 C; 101 G; 72 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 6; Length 333;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTCCGACCCCAACTACTC 20  
DB 270 TTCCGACCCCAACTACTC 251  
  
RESULT 194  
ABK70867/C  
ID ABK70867 standard; DNA; 333 BP.  
XX  
AC ABK70867;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #1 from HCV infected patient BU.  
XX  
KW Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001WO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
XX  
DR WPI; 2002-383036/41.  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of

CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX

SQ Sequence 333 BP; 60 A; 100 C; 101 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 333;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 270 TTGCGACCCCAACTACTC 251

RESULT 195  
ABK70879/C  
ID ABK70879 standard; DNA; 333 BP.  
AC ABK70879;  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX HCV genome 5'UTR sequence #13 from HCV infected patient BU.  
DE  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
XX brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
XX Hepatitis C virus.  
OS  
XX WO200220054-A2.  
PN  
XX 14-MAR-2002.  
PD  
XX 31-AUG-2001; 2001WO-GB003901.  
PF  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
PI WPI; 2002-383036/41.  
XX  
XX WPI; 2002-383036/41.  
DR  
XX  
XX Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
XX Example 1; Fig 14; 145pp; English.  
PS  
XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of

CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX

SQ Sequence 333 BP; 63 A; 97 C; 102 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 333;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 270 TTGCGACCCCAACTACTC 251

RESULT 196  
ABK70876/C  
ID ABK70876 standard; DNA; 333 BP.  
XX  
XX ABK70876;  
AC  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX HCV genome 5'UTR sequence #10 from HCV infected patient BU.  
DE  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
XX brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
XX Hepatitis C virus.  
OS  
XX WO200220054-A2.  
PN  
XX 14-MAR-2002.  
PD  
XX 31-AUG-2001; 2001WO-GB003901.  
PF  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
PI WPI; 2002-383036/41.  
XX  
XX WPI; 2002-383036/41.  
DR  
XX  
XX Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
XX Example 1; Fig 14; 145pp; English.  
PS  
XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of



a pharmacological agent that blocks binding of the brain-specific envelope protein to the putative receptor prevents uptake of the virus to the CNS, and improves long-term response rates. Reinfection of the liver by the virus released by the CNS may be prevented by the above mentioned method. The development of resistant strains is reduced or prevented, by the therapeutic use of a vaccine against brain-specific envelope protein, before, together with or after antiviral therapy. ABK70867-ABK70886 represent HCV genome 5'UTR sequences derived from HCV infected patient BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in the Fig, and should be page 4 of 6 as the nucleotide numbering of the sequences on this page follow correctly from page 3 of 6 (page 16/19). All sequences in Fig 14 have been typed in according to their correct nucleotide positioning

Sequence 333 BP; 60 A; 100 C; 101 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 333;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTGCGAGCCCAACTACTC 20

Db 270 TTGCGAGCCCAACTACTC 251

RESULT 197  
AAQ98272/c  
ID AAQ98272 standard; DNA; 334 BP.  
XX  
AC AAQ98272;  
XX  
DT 19-MAR-1996 (first entry)  
XX  
DE Hepatitis C virus 5' non-translated region for detection primer design.  
XX  
KM Primer; hepatitis C virus; PCR; amplification; reverse transcription;  
KM detection; non-translated region; ss.  
XX  
OS Synthetic.  
XX  
PN JP07184695-A.  
XX  
PD 25-JUL-1995.  
XX  
PF 27-DEC-1993; 93JP-00332662.  
XX  
PR 27-DEC-1993; 93JP-00332662.  
XX  
PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.  
XX  
DR WPI; 1995-287992/38.  
XX  
PT Simple detection of Hepatitis C virus in a single reaction tube - useful  
PT for high sensitivity and ease of reproduction.  
XX  
PS Example 3; Page 11; 14pp; Japanese.  
XX  
CC The primers AAQ98270-94 are used in a novel simple method for the  
CC detection of hepatitis C virus. The novel method involves the steps of  
CC extracting the virus from a sample, synthesizing cDNA from the viral RNA  
CC by reverse transcription, amplifying the cDNA by a first PCR and  
CC reamplifying the amplified product in a second PCR, all of which occur in  
CC a single reaction tube. The primers are designed based on a 334 bp  
CC sequence (AAQ98272) derived from a 5' non-translated region of the viral  
CC genome  
XX  
SQ Sequence 334 BP; 68 A; 98 C; 101 G; 67 T; 0 U; 0 Other;

Db 258 TTGCGAGCCCAACTACTC 239

RESULT 198  
ABK70869/c  
ID ABK70869 standard; DNA; 334 BP.  
XX  
AC ABK70869;  
XX  
DT 30-JUN-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #3 from HCV infected patient BU.  
XX  
KM Hepatitis C virus infection; HCV; central nervous system; CNS;  
KM microglial cell precursor; alpha-interferon; monocyte;  
KM brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
XX  
FN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PE 31-AUG-2001; 2001WO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayannis P, Forton DM;  
XX  
DR WPI; 2002-383036/41.  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
SQ Sequence 334 BP; 60 A; 101 C; 101 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 334;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTGCGAGCCCAACTACTC 20

Db 271 TTGGGACCCAACTACTC 252

RESULT 199  
ABK70868/c  
ID ABK70868 standard; DNA; 335 BP.  
XX  
XX ABK70868;  
AC  
XX  
XX 30-JUL-2002 (first entry)  
DT  
XX  
XX HCV genome 5'UTR sequence #2 from HCV infected patient BU.  
DE  
XX  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
XX microglial cell precursor; alpha-interferon; monocyte;  
XX brain-specific envelope protein; antiviral therapy; virucide; de.  
XX  
XX Hepatitis C virus.  
OS  
XX  
XX WO200220054-A2.  
PN  
XX  
XX 14-MAR-2002.  
PD  
XX  
XX 31-AUG-2001; 2001WO-GB003901.  
PF  
XX  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
XX  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX  
XX Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
PI WPI; 2002-383036/41.  
PT  
XX  
XX Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
XX  
XX Example 1; Fig 14; 145pp; English.  
PS  
XX  
XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
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CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
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CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the virus to  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
XX  
SO Sequence 335 BP; 61 A; 101 C; 101 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCAACTACTC 20

Db 271 TTGGGACCCAACTACTC 252

RESULT 200  
ABK70885/c  
ID ABK70885 standard; DNA; 335 BP.  
XX  
XX ABK70885;  
AC  
XX  
XX 30-JUL-2002 (first entry)  
DT  
XX  
XX HCV genome 5'UTR sequence #19 from HCV infected patient BU.  
DE  
XX  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
XX microglial cell precursor; alpha-interferon; monocyte;  
XX brain-specific envelope protein; antiviral therapy; virucide; de.  
XX  
XX Hepatitis C virus.  
OS  
XX  
XX WO200220054-A2.  
PN  
XX  
XX 14-MAR-2002.  
PD  
XX  
XX 31-AUG-2001; 2001WO-GB003901.  
PF  
XX  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
XX  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX  
XX Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
PI WPI; 2002-383036/41.  
PT  
XX  
XX Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
XX  
XX Example 1; Fig 14; 145pp; English.  
PS  
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CC at risk of hepatitis C virus (HCV) infection. The method comprises  
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CC central nervous system (CNS) of the patient. The method is performed by  
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CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
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CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the virus to  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
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CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
XX  
SO Sequence 335 BP; 64 A; 100 C; 99 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCAACTACTC 20

Tue Apr 26 09:53:17 2005

us-08-887-505b-28.011.rng

Page 101

Db 272 TTGGGACCAACTACTC 253

Search completed: April 25, 2005, 13:45:10  
Job time : 259.947 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:42 ; Search time 865.789 Seconds

(without alignments)  
1119.330 Million cell updates/sec

Title: US-08-887-505B-28

Perfect score: 20

Sequence: 1 TTCCGACCCCACTACTC 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hg:\*  
3: gb\_in:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_ses:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX803655 Sequence
2	20	100.0	24	6	AX803712 Sequence
3	20	100.0	25	6	AR411549 Sequence
4	20	100.0	25	6	BD000275 Sequence
5	20	100.0	27	6	AR106359 Sequence
6	20	100.0	27	6	AR400923 Sequence
7	20	100.0	27	6	AR411548 Sequence
8	20	100.0	27	6	AX286630 Sequence
9	20	100.0	27	6	BD000257 Sequence
10	20	100.0	27	6	BD000274 Sequence
11	20	100.0	28	6	AX803705 Sequence
12	20	100.0	28	6	AX803711 Sequence
13	20	100.0	29	6	BD183048 Nucleic a
14	20	100.0	33	6	AR004396 Sequence
15	20	100.0	33	6	AR064935 Sequence
16	20	100.0	33	6	AR097188 Sequence
17	20	100.0	33	6	AR130686 Sequence
18	20	100.0	33	6	AR172035 Sequence
19	20	100.0	33	6	BD189152 HCV Genom

20	20	100.0	33	6	BD189299	BD189299 HCV Genom
21	20	100.0	33	6	BD189446	BD189446 HCV Genom
22	20	100.0	33	6	182871	182871 Sequence 50
23	20	100.0	40	6	AR153179	AR153179 Sequence
24	20	100.0	40	6	AR163348	AR163348 Sequence
25	20	100.0	40	6	BD242950	BD242950 Method fo
26	20	100.0	40	6	AR53156	AR53156 Sequence
27	20	100.0	46	6	144581	144581 Sequence 10
28	20	100.0	46	6	170986	170986 Sequence 10
29	20	100.0	50	6	AX397948	AX397948 Sequence
30	20	100.0	50	6	AX397960	AX397960 Sequence
31	20	100.0	57	6	BD183034	BD183034 Nucleic a
32	20	100.0	60	6	AX616614	AX616614 Sequence
33	20	100.0	108	6	AR338416	AR338416 Sequence
34	20	100.0	108	6	AR33611	AR33611 Sequence
35	20	100.0	108	6	BD069495	BD069495 Nucleic a
36	20	100.0	108	6	BD083667	BD083667 Nucleic a
37	20	100.0	126	6	BD183033	BD183033 Nucleic a
38	20	100.0	139	14	AF282631	AF282631 Hepatitis
39	20	100.0	139	14	AF282632	AF282632 Hepatitis
40	20	100.0	139	14	AF282633	AF282633 Hepatitis
41	20	100.0	139	14	AF282634	AF282634 Hepatitis
42	20	100.0	139	14	AF282635	AF282635 Hepatitis
43	20	100.0	139	14	AF282637	AF282637 Hepatitis
44	20	100.0	139	14	AF282638	AF282638 Hepatitis
45	20	100.0	139	14	AF282639	AF282639 Hepatitis
46	20	100.0	139	14	AF282640	AF282640 Hepatitis
47	20	100.0	139	14	AF282641	AF282641 Hepatitis
48	20	100.0	139	14	AF282642	AF282642 Hepatitis
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52	20	100.0	139	14	AF282646	AF282646 Hepatitis
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55	20	100.0	139	14	AY003923	AY003923 Hepatitis
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57	20	100.0	139	14	AY003925	AY003925 Hepatitis
58	20	100.0	139	14	AY003928	AY003928 Hepatitis
59	20	100.0	139	14	AY003929	AY003929 Hepatitis
60	20	100.0	139	14	AY003930	AY003930 Hepatitis
61	20	100.0	139	14	AY003932	AY003932 Hepatitis
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65	20	100.0	139	14	AY003936	AY003936 Hepatitis
66	20	100.0	139	14	AY003937	AY003937 Hepatitis
67	20	100.0	139	14	AY003938	AY003938 Hepatitis
68	20	100.0	139	14	AY003939	AY003939 Hepatitis
69	20	100.0	139	14	AY003940	AY003940 Hepatitis
70	20	100.0	139	14	AY003941	AY003941 Hepatitis
71	20	100.0	139	14	AY003942	AY003942 Hepatitis
72	20	100.0	139	14	AY003943	AY003943 Hepatitis
73	20	100.0	139	14	AY003944	AY003944 Hepatitis
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75	20	100.0	139	14	AY003980	AY003980 Hepatitis
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81	20	100.0	139	14	AY003986	AY003986 Hepatitis
82	20	100.0	139	14	AY003987	AY003987 Hepatitis
83	20	100.0	139	14	AY003989	AY003989 Hepatitis
84	20	100.0	139	14	AY003990	AY003990 Hepatitis
85	20	100.0	139	14	AY003992	AY003992 Hepatitis
86	20	100.0	139	14	AY003993	AY003993 Hepatitis
87	20	100.0	139	14	AY003995	AY003995 Hepatitis
88	20	100.0	139	14	AY003996	AY003996 Hepatitis
89	20	100.0	139	14	AY003997	AY003997 Hepatitis
90	20	100.0	139	14	AY003998	AY003998 Hepatitis
91	20	100.0	139	14	AY004000	AY004000 Hepatitis
92	20	100.0	139	14	AY004001	AY004001 Hepatitis

C 93	20	100.0	139	14	AY004007	AY004007	Hepatitis	C 166	20	100.0	178	14	AF463463	AF463463	Hepatitis
C 94	20	100.0	139	14	AY004008	AY004008	Hepatitis	C 167	20	100.0	178	14	AF463464	AF463464	Hepatitis
C 95	20	100.0	139	14	AY004009	AY004009	Hepatitis	C 168	20	100.0	178	14	AF463465	AF463465	Hepatitis
C 96	20	100.0	139	14	AY004010	AY004010	Hepatitis	C 169	20	100.0	178	14	AF463467	AF463467	Hepatitis
C 97	20	100.0	139	14	AY004011	AY004011	Hepatitis	C 170	20	100.0	178	14	AF463468	AF463468	Hepatitis
C 98	20	100.0	139	14	AY004012	AY004012	Hepatitis	C 171	20	100.0	178	14	AF463469	AF463469	Hepatitis
C 99	20	100.0	139	14	AY004013	AY004013	Hepatitis	C 172	20	100.0	178	14	AF463470	AF463470	Hepatitis
C 100	20	100.0	157	14	AF506651	AF506651	Hepatitis	C 173	20	100.0	178	14	AF463471	AF463471	Hepatitis
C 101	20	100.0	163	6	AX172758	AX172758	Sequence	C 174	20	100.0	178	14	AF463472	AF463472	Hepatitis
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LOCUS AX803665
DEFINITION Sequence 28 from Patent EP1331267.
ACCESSION AX803665
VERSION AX803665.1 GI:38502207
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Frank,B.L., Goodchild,J., Hamlin,H.A., Kulikuskie,R.E.,
TITLE Roberts,P.C., Roberts,N.A., Walther,D.M. and Wolfe,J.L.
JOURNAL Oligonucleotides specific for Hepatitis C Virus
PATENT: EP 1331267-A 28 30-JUL-2003;
HYBRIDON, INC. (US)
FEATURES
SOURCE location/Qualifiers
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/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCACTACTC 20
Db 1 TTGCGACCCCACTACTC 20
RESULT 2
AX803712 24 bp DNA linear PAT 24-NOV-2003
LOCUS AX803712
DEFINITION Sequence 75 from Patent EP1331267.

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ACCESSION AX803712
VERSION AX803712.1 GI:38502254
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Frank,B.L., Goodchild,J., Hamlin,H.A., Kulikuskie,R.E.,
TITLE Roberts,P.C., Roberts,N.A., Walther,D.M. and Wolfe,J.L.
JOURNAL Oligonucleotides specific for Hepatitis C Virus
PATENT: EP 1331267-A 75 30-JUL-2003;
HYBRIDON, INC. (US)
FEATURES
SOURCE location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCACTACTC 20
Db 3 TTGCGACCCCACTACTC 22

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RESULT 3
AR411549 25 bp DNA linear PAT 18-DEC-2003
LOCUS AR411549
DEFINITION Sequence 13 from patent US 6638714.
ACCESSION AR411549
VERSION AR411549.1 GI:40163893
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Linmen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
JOURNAL Oligonucleotides and methods of use thereof
PATENT: US 6638714-A 13 28-OCT-2003;
LOCATION/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCACTACTC 20
Db 2 TTGCGACCCCACTACTC 21
RESULT 4
BD000275 25 bp DNA linear PAT 31-JAN-2002
LOCUS BD000275
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof.
ACCESSION BD000275
VERSION BD000275.1 GI:18623354
KEYWORDS JP 2000279200-A/13.
SOURCE synthetic construct
ORGANISM
REFERENCE 1
AUTHORS Lynen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof

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JOURNAL	Patent: JP 2000279200-A 13 10-OCT-2000; ORTHO CLINICAL DIAGNOSTICS INC
COMMENT	OS Artificial Sequence PN JP 2000279200-A/13 PD 10-OCT-2000 PF 03-FEB-2000 JP 2000032656 PR 03-FEB-1999 US 60/118497 PI JEFFREY M LYNNEN KEVIN M GORMAN PC C12Q1/68,C12N15/09/(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,C12R1:92)
FEATURES	source Location/Qualifiers FT 1..25 /organism='Artificial Sequence'. Location/Qualifiers 1..25 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
ORIGIN	
Query Match	100.0%; Score 20; DB 6; Length 25; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 TTCCGACCCCAACTACTC 20       2 TTCCGACCCCAACTACTC 21
Db	
RESULT 5	
LOCUS	AR106359 27 bp DNA linear PAT 14-FEB-2001
DEFINITION	Sequence 21 from patent US 6107028.
ACCESSION	AR106359
VERSION	AR106359.1 GI:12820889
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 27) Kay,M.A. and Lieber,A. Ribozymes for treating hepatitis C Patent: US 6107028-A 21 22-AUG-2000; Location/Qualifiers 1..27 /organism="unknown" /mol_type="unassigned DNA"
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ORIGIN	
Query Match	100.0%; Score 20; DB 6; Length 27; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 TTCCGACCCCAACTACTC 20       24 TTCCGACCCCAACTACTC 5
Db	
RESULT 6	
LOCUS	AR400923 27 bp DNA linear PAT 18-DEC-2001
DEFINITION	Sequence 12 from patent US 6623919.
ACCESSION	AR400923
VERSION	AR400923.1 GI:40148215
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 27) Gorman,K.M., Patterson,D.R., Linnen,J.M. and Song,K. Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and

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JOURNAL      Method of use thereof
FEATURES     Patent: US 6623919-A 12-23-SEP-2003;
SOURCE       Location/Qualifiers
            1..27
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            /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TTCCGGACCCCAACTACTC 20
|||||
4 TTCCGGACCCCAACTACTC 23

RESULT 7
LOCUS      AR411548                27 bp    DNA            linear    PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6638714.
ACCESSION  AR411548
VERSION     AR411548.1  GI:4016392
KEYWORDS
SOURCE      unknown.
ORGANISM    unknown.
REFERENCE   1 (bases 1 to 27)
AUTHORS    Linnen,J.M. and Gorman,K.M.
TITLE      Oligonucleotide primers for efficient detection of hepatitis C
           virus (HCV) and methods of use thereof
JOURNAL    Patent: US 6638714-A 12-28-OCT-2003;
FEATURES
SOURCE      1..27
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TTCCGGACCCCAACTACTC 20
|||||
4 TTCCGGACCCCAACTACTC 23

Db
4 TTCCGGACCCCAACTACTC 23

RESULT 8
LOCUS      AX286630                27 bp    RNA            linear    PAT 21-NOV-2001
DEFINITION Sequence 1 from Patent WO0181627.
ACCESSION  AX286630
VERSION     AX286630.1  GI:17048706
KEYWORDS
SOURCE      Hepatitis C virus
ORGANISM    Hepatitis C virus
REFERENCE   1
AUTHORS     Klinck,R., Walker,S., Afshar,M., Collier,A., Aboul-Ela,F. and
            Westhof,E.
TITLE      In-silico-screening for docking on sub-domain IId of hec-v-ires
JOURNAL    Patent: WO 0181627-A 1 01-NOV-2001;
FEATURES
SOURCE      Ribotargets Limited (GB)
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            Location/Qualifiers
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            /mol_type="unassigned RNA"
            /db_xref="taxon:11103"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TTCCGGACCCCAACTACTC 20
|||||
4 TTCCGGACCCCAACTACTC 23

Db
4 TTCCGGACCCCAACTACTC 23

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCGACCCCAACTACTC 20  
 Db 23 TTGGCGACCCCAACTACTC 4

RESULT 9  
 BD000257  
 LOCUS 27 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof.

ACCESSION BD000257.1 GI:18623336  
 VERSION JP 2000279198-A/12.  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 27)  
 AUTHORS Gorman,K.M., Paterson,D.R., Lynen,J.M. and Son,K.  
 TITLE Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV), and methods of use thereof  
 PATENT: JP 2000279198-A 12 10-OCT-2000;  
 ORTHO CLINICAL DIAGNOSTICS INC

COMMENT  
 JOURNAL  
 OS Artificial Sequence  
 PN JP 2000279198-A/12  
 PD 10-OCT-2000  
 PE 02-FEB-2000 JP 2000030237  
 PR 03-FEB-1999 US 60/118498  
 PT KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNN, KEVIN SON PC  
 C1201/68, C12N15/09/(C12N15/09, C12R1.92), C12N15/00, (C12N15/00, PC  
 C12R1.92)  
 CC

FEATURES  
 source Location/Qualifiers  
 FT 1..27  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCGACCCCAACTACTC 20  
 Db 4 TTGGCGACCCCAACTACTC 23

RESULT 10  
 BD000274  
 LOCUS 27 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.

ACCESSION BD000274.1 GI:18623353  
 VERSION JP 2000279200-A/12  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 27)  
 AUTHORS Lynen,J.M. and Gorman,K.M.  
 TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof  
 PATENT: JP 2000279200-A 12 10-OCT-2000;  
 ORTHO CLINICAL DIAGNOSTICS INC

COMMENT  
 JOURNAL  
 OS Artificial Sequence  
 PN JP 2000279200-A/12

PD 10-OCT-2000  
 PF 03-FEB-2000 JP 2000032656  
 PR 03-FEB-1999 US 60/118497  
 PI JEFFREY M LYNN, KEVIN M GORMAN  
 PC C1201/68, C12N15/09/(C12N15/09, C12R1.92), C12N15/00, (C12N15/00, C12R1.92)  
 CC  
 FH  
 FT source Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCGACCCCAACTACTC 20  
 Db 4 TTGGCGACCCCAACTACTC 23

RESULT 11  
 AX803705  
 LOCUS 28 bp DNA linear PAT 24-NOV-2003  
 DEFINITION Sequence 68 from Patent EP1331267.  
 ACCESSION AX803705  
 VERSION AX803705.1 GI:38502247  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified

REFERENCE 1  
 AUTHORS Frank,B.L., Goodchild,J., Hamlin,H.A., Kulkuskie,R.E.,  
 TITLE Oligonucleotides specific for Hepatitis C Virus  
 JOURNAL  
 PATENT: EP 1331267-A 68 30-JUL-2003;  
 HYBRIDON, INC. (US)

FEATURES  
 source Location/Qualifiers  
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 /organism="unidentified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCGACCCCAACTACTC 20  
 Db 1 TTGGCGACCCCAACTACTC 20

RESULT 12  
 AX803711  
 LOCUS 28 bp DNA linear PAT 24-NOV-2003  
 DEFINITION Sequence 74 from Patent EP1331267.  
 ACCESSION AX803711  
 VERSION AX803711.1 GI:38502253  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified

REFERENCE 1  
 AUTHORS Frank,B.L., Goodchild,J., Hamlin,H.A., Kulkuskie,R.E.,  
 TITLE Oligonucleotides specific for Hepatitis C Virus  
 JOURNAL  
 PATENT: EP 1331267-A 74 30-JUL-2003;

FEATURES HYBRIDON, INC. (US)  
source Location/Qualifiers  
1..28  
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/mol\_type="unassigned DNA"  
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ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
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5 TTCCGACCCCAACTACTC 24

RESULT 13  
BD183048 29 bp DNA linear PAT 17-JUN-2003  
LOCUS Nucleic acids for grouping hepatitis C virus and method for group  
DEFINITION ing hepatitis C virus using the same.  
ACCESSION BD183048  
VERSION BD183048.1 GI:31875248  
KEYWORDS JP 2002345467-A/20.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Mukai, M., Teunoda, K. and Hikiji, K.  
TITLE Nucleic acids for grouping hepatitis C virus and method for group  
JOURNAL ing hepatitis C virus using the same  
PATENT: JP 2002345467-A 20 03-DEC-2002;  
SRL INC  
COMMENT OS Artificial Sequence  
PN JP 2002345467-A/20  
PD 03-DEC-2002  
PF 17-APR-2001 JP 2001118810  
PI MASAKAZU MUKAI, KOICHI TSUNODA, KAZUMASA HIKIJI PC  
C12N15/09, C12Q1/68, G01N33/56, C12N15/00 CC Nucleic Acid  
Used as signal-amplifying probe which hybridizes CC  
with a  
CC region in HCV 5'-UTR region  
FH key Location/Qualifiers  
FT source 1..29  
/organism="Artificial Sequence".  
Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
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26 TTCCGACCCCAACTACTC 7

RESULT 14  
AR004396 33 bp DNA linear PAT 04-DEC-1998  
LOCUS Sequence 50 from patent US 5747244.  
DEFINITION AR004396  
ACCESSION AR004396  
VERSION AR004396.1 GI:3965275  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 33)

AUTHORS Sheridan, P., Chang, C.-A., Running, J. and Urdea, M.S.  
TITLE Nucleic acid probes immobilized on polystyrene surfaces  
JOURNAL Patent: US 5747244-A 50 05-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
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10 TTCCGACCCCAACTACTC 29

RESULT 15  
AR064935 33 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 60 from patent US 5849481.  
DEFINITION AR064935  
ACCESSION AR064935  
VERSION AR064935.1 GI:5995151  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Urdea, M.S., Horn, T., Chang, C.-A., Warner, B. and Fultz, T.J.  
TITLE Nucleic acid hybridization assays employing large comb-type  
JOURNAL branched polynucleotides  
PATENT: US 5849481-A 60 15-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
10 TTCCGACCCCAACTACTC 29

RESULT 16  
AR097188 33 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 126 from patent US 6071693.  
DEFINITION AR097188  
ACCESSION AR097188  
VERSION AR097188.1 GI:12805918  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Cha, T.-A., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.  
TITLE HCV genomic sequences for diagnostics and therapeutics  
JOURNAL Patent: US 6071693-A 126 06-JUN-2000;  
FEATURES Location/Qualifiers  
source 1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20

Db 10 TTGCGACCCCAACTACTC 29

RESULT 17  
LOCUS AR130686 33 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 126 from patent US 6190864.  
ACCESSION AR130686  
VERSION AR130686.1 GI:14119011  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS Cha,T.-A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.  
TITLE HCV genomic sequences for diagnostics and therapeutics  
JOURNAL Patent: US 6190864-A 126 20-FEB-2001;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 10 TTGCGACCCCAACTACTC 29

RESULT 18  
LOCUS AR172035 33 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 126 from patent US 6297370.  
ACCESSION AR172035  
VERSION AR172035.1 GI:17910985  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS Cha,T.-A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.  
TITLE HCV genomic sequences for diagnostics and therapeutics  
JOURNAL Patent: US 6297370-A 126 02-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 10 TTGCGACCCCAACTACTC 29

RESULT 19  
LOCUS BD189152 33 bp DNA linear PAT 17-JUL-2003  
DEFINITION HCV Genomic Sequences For Diagnostics And Therapeutics.  
ACCESSION BD189152  
VERSION BD189152.1 GI:32998891  
KEYWORDS JP 2003009891-A/126.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 33)

Db 10 TTGCGACCCCAACTACTC 29

Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 10 TTGCGACCCCAACTACTC 29

RESULT 20  
LOCUS BD189299 33 bp DNA linear PAT 17-JUL-2003  
DEFINITION HCV Genomic Sequences For Diagnostics And Therapeutics.  
ACCESSION BD189299  
VERSION BD189299.1 GI:32999038  
KEYWORDS JP 2003009892-A/126.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Adair,M.S., Cha,T., Irvine,B., Kolberg,J. and Beal,E.  
TITLE HCV Genomic Sequences For Diagnostics And Therapeutics  
JOURNAL Patent: JP 2003009892-A 126 14-JAN-2003;  
COMMENT Chiron Corporation  
OS Artificial Sequence  
PN JP 2003009892-A/126  
PR 14-JAN-2003  
PF 10-MAY-2002 JP 2002134999  
PR 08-MAY-1991 US 697326  
PI Michael S Adair, tai-ann cha, bruce irvine, janice kolberg, eileen  
PI beal  
CC synthetic construct  
FH Key Location/Qualifiers.  
FEATURES Location/Qualifiers  
source 1..33  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 10 TTGCGACCCCAACTACTC 29

RESULT 21  
LOCUS BD189446 33 bp DNA linear PAT 17-JUL-2003



DEFINITION HCV Genomic Sequences For Diagnostics And Therapeutics.  
ACCESSION BD189446  
VERSION BD189446.1 GI:32899185  
KEYWORDS JP 2003009893-A/126.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Adair,M.S., Cha,T., Beal,E., Irvine,B. and Kolberg,J.  
TITLE HCV Genomic Sequences For Diagnostics And Therapeutics  
JOURNAL Patent: JP 2003009893-A 126 14-JAN-2003;  
Chiron Corporation  
COMMENT OS Artificial Sequence  
PN JP 2003009893-A/126  
PD 14-JAN-2003  
PF 10-MAY-2002 JP 2002135000  
PR 08-MAY-1991 US 697326  
PI michael s adair,tai-ann cha,eileen beal,bruce irvine,janice  
PI kolberg  
CC synthetic construct  
FH key Location/Qualifiers.  
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source Location/Qualifiers  
1..33  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGACCCCAACTACTC 20  
DB 10 TTCCGGACCCCAACTACTC 29  
RESULT 22  
LOCUS 182871 33 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 50 from patent US 5712383.  
ACCESSION 182871  
VERSION 182871.1 GI:3211168  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Sheridan,P., Chang,C.-A., Running,J. and Urdea,M.S.  
TITLE Process for immobilizing nucleic acid probes on polystyrene  
surfaces  
JOURNAL Patent: US 5712383-A 50 27-JAN-1998;  
FEATURES  
source Location/Qualifiers  
1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGACCCCAACTACTC 20  
DB 10 TTCCGGACCCCAACTACTC 29  
RESULT 23  
LOCUS AR153179 40 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 181 from patent US 6235480.  
ACCESSION AR153179  
VERSION AR153179.1 GI:15120711

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 40)  
AUTHORS Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,  
Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,  
Olson,R.J., Wood,K.V. and Welch,R.  
TITLE Detection of nucleic acid hybrids  
JOURNAL Patent: US 6235480-A 181 22-MAY-2001;  
FEATURES  
source Location/Qualifiers  
1..40  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGACCCCAACTACTC 20  
DB 29 TTCCGGACCCCAACTACTC 10  
RESULT 24  
LOCUS AR163348 40 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 43 from patent US 6270974.  
ACCESSION AR163348  
VERSION AR163348.1 GI:16233929  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 40)  
AUTHORS Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,  
Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,  
Olson,R.J., Wood,K.V. and Welch,R.  
TITLE Exogenous nucleic acid detection  
JOURNAL Patent: US 6270974-A 43 07-AUG-2001;  
FEATURES  
source Location/Qualifiers  
1..40  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGACCCCAACTACTC 20  
DB 29 TTCCGGACCCCAACTACTC 10  
RESULT 25  
LOCUS BD242950 40 bp DNA linear PAT 17-JUL-2003  
DEFINITION Method for assaying the presence of target nucleic acid sequence  
and its application.  
ACCESSION BD242950  
VERSION BD242950.1 GI:33052720  
KEYWORDS JP 2002536981-A/43.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 40)  
AUTHORS Shultz,J.W., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,  
Rhodes,R.B., Andrews,C.A., Hartnett,J.R., Gu,T., Olson,R.J.,  
Wood,K.V. and Welch,R.  
TITLE Method for assaying the presence of target nucleic acid sequence  
and its application

JOURNAL Patent: JP 2002536981-A 43 05-NOV-2002;  
 FROMEGA CORP  
 COMMENT Hepatitis virus (hepatitis C virus)  
 OS JP 2002536981-A/43  
 PN 05-NOV-2002  
 PD 18-FEB-2000 JP 2000599902  
 PR 18-FEB-1999 US 09/252436,21-JUL-1999 US 09/358972 PR  
 27-SEP-1999 US 09/406147  
 P1 JOHN W SHULTZ,MARTIN K LEWIS,DONNA LEIPPE,MICHELLE MANDREKAR,  
 DANIEL KEPHART,RICHARD B RHODES,CHRISTINE ANN ANDREWS,JAMES R  
 HARTNETT,  
 P1 TRENT GU,RYAN J OLSON,KEITH V WOOD ROY WELCH  
 PC C1201/68,C12N15/09,C12Q1/48,G01N21/78,G01N33/02,G01N33/483,PC  
 G01N33/53  
 CC Method for assaying the presence of target nucleic acid CC  
 CC sequence and its  
 CC application  
 CC Key Location/Qualifiers  
 FT source 1..40 /organism='Hepatitis virus (hepatitis C FT  
 FT virus)' Location/Qualifiers  
 1..40 /organism='unidentified'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 29 TTGGGACCCCAACTACTC 10

RESULT 26  
 AR533156 40 bp DNA linear PAT 08-OCT-2004  
 LOCUS Sequence 181 from patent US 6730479.  
 ACCESSION AR533156  
 VERSION AR533156.1 GI:53922709  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 40)  
 SHULTZ,J.W., LEWIS,M.K., LEIPPE,D., MANDREKAR,M., KEPHART,D.,  
 RHODES,R.B., ANDREWS,C.A., HARTNETT,J.R., GU,T., OLSON,R.J.,  
 WOOD,K.V. and WELCH,R.  
 TITLE Detection of nucleic acid hybrids  
 JOURNAL Patent: US 6730479-A 181 04-MAY-2004;  
 FEATURES Location/Qualifiers  
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 /organism='unknown'  
 /mol\_type='genomic DNA'

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 29 TTGGGACCCCAACTACTC 10

RESULT 27  
 I44581 46 bp DNA linear PAT 07-OCT-1997  
 LOCUS Sequence 10 from patent US 5635352.  
 DEFINITION

ACCESSION I44581  
 VERSION I44581.1 GI:2469294  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 46)  
 URDEA,M.S., FULTZ,T., WARNER,B.D. and COLLINS,M.  
 TITLE Solution phase nucleic acid sandwich assays having reduced  
 background noise  
 JOURNAL Patent: US 5635352-A 10 03-JUN-1997;  
 FEATURES Location/Qualifiers  
 1..46  
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 /mol\_type='unassigned DNA'

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 10 TTGGGACCCCAACTACTC 29

RESULT 28  
 I70986 46 bp DNA linear PAT 03-APR-1998  
 LOCUS Sequence 10 from patent US 5681697.  
 ACCESSION I70986  
 VERSION I70986.1 GI:3007121  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 46)  
 URDEA,M.S., FULTZ,T., WARNER,B.D. and COLLINS,M.  
 TITLE Solution phase nucleic acid sandwich assays having reduced  
 background noise and kits therefor  
 JOURNAL Patent: US 5681697-A 10 28-OCT-1997;  
 FEATURES Location/Qualifiers  
 1..46  
 /organism='unknown'  
 /mol\_type='unassigned DNA'

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 10 TTGGGACCCCAACTACTC 29

RESULT 29  
 AX397948 50 bp DNA linear PAT 27-MAY-2002  
 LOCUS Sequence 26 from Patent WO0220054.  
 ACCESSION AX397948  
 VERSION AX397948.1 GI:21260805  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 REFERENCE 1  
 THOMAS,H.C., TAYLOR-ROBINSON,S.D., KARAYIANNIS,P. and FORTON,D.M.  
 TITLE Methods of treatment and diagnosis of HCV infection in CNS based on  
 magnetic resonance spectroscopy  
 JOURNAL Patent: WO 0220054-A 26 14-MAR-2002;  
 IMPERIAL COLLEGE OF SCIENCE, TECHNOLOGY AND MEDICINE (GB)

FEATURES  
source 1.50  
Location/Qualifiers  
/organism="Hepatitis C virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11103"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
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31 TTCCGACCCCAACTACTC 12

RESULT 30  
AX397960/c 50 bp DNA linear PAT 27-MAY-2002  
LOCUS Sequence 38 from Patent WO0220054.  
ACCESSION AX397960  
VERSION AX397960.1 GI:21260815  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1  
Thomas, H.C., Taylor-Robinson, S.D., Karayiannis, P. and Forston, D.M.  
AUTHORS Methods of treatment and diagnosis of HCV infection in CNS based on  
TITLE Magnetic resonance spectroscopy  
JOURNAL Patent: WO 0220054-A 38 14-MAR-2002;  
IMPERIAL COLLEGE OF SCIENCE, TECHNOLOGY AND MEDICINE (GB)  
FEATURES  
source 1.50  
Location/Qualifiers  
/organism="Hepatitis C virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11103"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
31 TTCCGACCCCAACTACTC 12

RESULT 31  
BD183034 57 bp DNA linear PAT 17-JUN-2003  
LOCUS Nucleic acids for grouping hepatitis C virus and method for group  
DEFINITION ing hepatitis C virus using the same.  
ACCESSION BD183034  
VERSION BD183034.1 GI:31875234  
KEYWORDS JP 2002345467-A/6.  
SOURCE unidentified  
ORGANISM unidentified  
1 (bases 1 to 57)  
REFERENCE Mukai, M., Tsumoda, K. and Hiki, K.  
AUTHORS Nucleic acids for grouping hepatitis C virus and method for group  
TITLE ing hepatitis C virus using the same  
JOURNAL Patent: JP 2002345467-A 6 03-DEC-2002;  
SRL INC  
OS Hepatitis virus (hepatitis C virus)  
PN JP 2002345467-A/6  
PD 03-DEC-2002  
PF 17-APR-2001 JP 2001118810  
PI MASAKAZU MUKAI, KOICHI TSUMODA, KAZUMASA HIKI, PI  
C12N15/09, C12N15/53, C12N15/56, C12N15/00 CC Nucleic  
acids for grouping hepatitis C virus and method for CC

group ing  
CC hepatitis C virus using the same  
FH Key Location/Qualifiers  
FT source 1.57  
FT /organism="Hepatitis virus (hepatitis C FT  
virus)"

FEATURES  
source 1.57  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
46 TTCCGACCCCAACTACTC 27

RESULT 32  
AX616614/c 60 bp DNA linear PAT 20-FEB-2003  
LOCUS Sequence 1 from Patent EP1262566.  
ACCESSION AX616614  
VERSION AX616614.1 GI:28447591  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1  
Amorose, D.A., Shannon, K.W., Collins, P.J. and Wolber, P.K.  
AUTHORS Composite polynucleotide arrays  
TITLE Patent: EP 1262566-A 1 04-DEC-2002;  
JOURNAL Agilent Technologies, Inc. (US)  
FEATURES  
source 1.60  
Location/Qualifiers  
/organism="Hepatitis C virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11103"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
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24 TTCCGACCCCAACTACTC 5

RESULT 33  
AR338416 108 bp DNA linear PAT 17-AUG-2003  
LOCUS Sequence 31 from patent US 6569647.  
DEFINITION AR338416  
ACCESSION AR338416  
VERSION AR338416.1 GI:33725188  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
1 (bases 1 to 108)  
REFERENCE Zhang, D.Y., Brandwein, M. and Hsu, T.C.H.  
AUTHORS Nucleic acid amplification method: ramification-extension  
TITLE amplification method (RAM)  
JOURNAL Patent: US 6569647-A 31 27-MAY-2003;  
FEATURES Location/Qualifiers  
source 1.108  
/organism="unknown"  
/mol\_type="genomic DNA"

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ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TTCCGACCCCAACTACTC 20
|||||
4 TTCCGACCCCAACTACTC 23

RESULT 34
AR353611      108 bp  DNA  linear  PAT 17-AUG-2003
LOCUS      Sequence 31 from patent US 6593086.
DEFINITION AR353611
ACCESSION  AR353611
VERSION    AR353611.1  GI:33759642
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 108)
AUTHORS   Zhang,D.Y.
TITLE     Nucleic acid amplification methods
JOURNAL   Patent: US 6593086-A 31 15-JUL-2003;
FEATURES   Location/Qualifiers
            source      /organism="Unknown"
                        /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TTCCGACCCCAACTACTC 20
|||||
4 TTCCGACCCCAACTACTC 23

RESULT 35
BD069495      108 bp  DNA  linear  PAT 27-AUG-2002
LOCUS      Nucleic acid amplification method: Ramification-extension
DEFINITION BD069495
ACCESSION  BD069495
VERSION    BD069495.1  GI:22615098
KEYWORDS   JP 2001514483-A/31.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 108)
AUTHORS   Zhang,D.Y., Brandwein,M. and Hsu,H.T.C.H.
TITLE     Nucleic acid amplification method: Ramification-extension
JOURNAL   Patent: JP 2001514483-A 31 11-SEP-2001;
FEATURES   Location/Qualifiers
            source      /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TTCCGACCCCAACTACTC 20
|||||
4 TTCCGACCCCAACTACTC 23

RESULT 36
BD083967      108 bp  DNA  linear  PAT 27-AUG-2002
LOCUS      Nucleic acid amplification method: Hybridization signal
DEFINITION BD083967
ACCESSION  BD083967
VERSION    BD083967.1  GI:22629577
KEYWORDS   JP 2001521373-A/31.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 108)
AUTHORS   Zhang,D.Y. and Brandwein,M.
TITLE     Nucleic acid amplification method: Hybridization signal
JOURNAL   Patent: JP 2001521373-A 31 06-NOV-2001;
FEATURES   Location/Qualifiers
            source      /organism="unidentified"
                        /mol_type="genomic DNA"
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ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TTCCGACCCCAACTACTC 20
|||||
4 TTCCGACCCCAACTACTC 23

RESULT 37
BD183033      126 bp  DNA  linear  PAT 17-JUN-2003
LOCUS      Nucleic acids for grouping hepatitis C virus and method for group
DEFINITION ing hepatitis C virus using the same.
ACCESSION  BD183033
VERSION    BD183033.1  GI:31875233
KEYWORDS   JP 200234567-A/5.
SOURCE     unidentified
ORGANISM   unidentified

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source      1. .108
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ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TTCCGACCCCAACTACTC 20
|||||
4 TTCCGACCCCAACTACTC 23

RESULT 37
BD183033      126 bp  DNA  linear  PAT 17-JUN-2003
LOCUS      Nucleic acids for grouping hepatitis C virus and method for group
DEFINITION ing hepatitis C virus using the same.
ACCESSION  BD183033
VERSION    BD183033.1  GI:31875233
KEYWORDS   JP 200234567-A/5.
SOURCE     unidentified
ORGANISM   unidentified

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REFERENCE 1 (bases 1 to 126)
AUTHORS Mukai, M., Tsunoda, K. and Hiki, J. K.
TITLE Nucleic acids for grouping hepatitis C virus and method for group
JOURNAL ing hepatitis C virus using the same
SRL INC Patent: JP 2002345467-A 5 03-DEC-2002;
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002345467-A/5
PD 03-DEC-2002
PF 17-APR-2001 JP 2001118810
PI MASAKAZU MUKAI, KOICHI TSUNODA, KAZUMASA HIKI, PC
C12N15/09, C12O1/68, G01N33/53, G01N33/566, C12N15/00 CC Nucleic
acids for grouping hepatitis C virus and method for CC
group ing
CC hepatitis C virus using the same
FH Key Location/Qualifiers
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/organism='Hepatitis virus (hepatitis C FT
virus)';
location/Qualifiers
1..126
/organism='unidentified'
/mol_type='genomic DNA'
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20
|||||
DB 115 TTCCGACCCCAACTACTC 96

RESULT 38
AF282631/c 139 bp RNA linear VRL 01-MAR-2001
LOCUS Hepatitis C virus isolate H069 clone 1 5' non-coding region
DEFINITION
sequence.
ACCESSION AF282631
VERSION AF282631.1 GI:10764494
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris, K.A. and Teo, C.G.
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing
JOURNAL gradient gel electrophoresis
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 20579439
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris, K.A. and Teo, C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK

FEATURES
source location/Qualifiers
1..139
/organism='Hepatitis C virus'
/mol_type='genomic RNA'
/isolate='H069'
/db_xref='taxon:11103'
/clone='I'
1..139
/note='5' non-coding region'

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Query Match 100.0%; Score 20; DB 14; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20
|||||
DB 116 TTCCGACCCCAACTACTC 97

RESULT 40
AF282633/c 139 bp RNA linear VRL 01-MAR-2001
LOCUS Hepatitis C virus isolate H071 clone 1 5' non-coding region
DEFINITION
sequence.
ACCESSION AF282633
VERSION AF282633.1 GI:10764496
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris, K.A. and Teo, C.G.
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing
JOURNAL gradient gel electrophoresis
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 20579439
REFERENCE 2 (bases 1 to 139)

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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20
|||||
DB 116 TTCCGACCCCAACTACTC 97

RESULT 39
AF282632 139 bp RNA linear VRL 01-MAR-2001
LOCUS Hepatitis C virus isolate H069 clone 11 5' non-coding region
DEFINITION
sequence.
ACCESSION AF282632
VERSION AF282632.1 GI:10764495
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris, K.A. and Teo, C.G.
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing
JOURNAL gradient gel electrophoresis
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 20579439
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris, K.A. and Teo, C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK

FEATURES
source location/Qualifiers
1..139
/organism='Hepatitis C virus'
/mol_type='genomic RNA'
/isolate='H069'
/db_xref='taxon:11103'
/clone='I'
1..139
/note='5' non-coding region'

ORIGIN
Query Match 100.0%; Score 20; DB 14; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20
|||||
DB 116 TTCCGACCCCAACTACTC 97

RESULT 40
AF282633/c 139 bp RNA linear VRL 01-MAR-2001
LOCUS Hepatitis C virus isolate H071 clone 1 5' non-coding region
DEFINITION
sequence.
ACCESSION AF282633
VERSION AF282633.1 GI:10764496
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris, K.A. and Teo, C.G.
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing
JOURNAL gradient gel electrophoresis
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 20579439
REFERENCE 2 (bases 1 to 139)

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AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H071"  
/db\_xref="taxon:11103"  
/clone="I1"  
1.139  
misc\_feature  
/note="5' non-coding region"

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 41  
AF282634/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H071 clone II 5' non-coding region  
DEFINITION  
ACCESSION AF282634  
VERSION AF282634.1 GI:10764497  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H071"  
/db\_xref="taxon:11103"  
/clone="I1"  
1.139  
misc\_feature  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 42  
AF282635/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS

DEFINITION Hepatitis C virus isolate H075 clone I 5' non-coding region  
sequence.  
ACCESSION AF282635  
VERSION AF282635.1 GI:10764498  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H075"  
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/clone="I1"  
1.139  
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/note="5' non-coding region"

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 43  
AF282637/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H075 clone III 5' non-coding region  
DEFINITION  
ACCESSION AF282637  
VERSION AF282637.1 GI:10764500  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H075"  
/db\_xref="taxon:11103"

misc\_feature 1..139  
/note="5' non-coding region"  
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Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
116 TTCCGACCCCAACTACTC 97

RESULT 44  
AF282638/139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H075 clone IV 5' non-coding region  
DEFINITION  
ACCESSION AF282638  
VERSION AF282638.1 GI:10764501  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
source 1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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/db\_xref="taxon:11103"  
/clone="IV"  
1..139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
116 TTCCGACCCCAACTACTC 97

RESULT 45  
AF282639/139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H058 clone I 5' non-coding region  
DEFINITION  
ACCESSION AF282639  
VERSION AF282639.1 GI:10764502  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.

TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
source 1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H058"  
/db\_xref="taxon:11103"  
/clone="I"  
1..139  
/note="5' non-coding region"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
116 TTCCGACCCCAACTACTC 97

RESULT 46  
AF282640/139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H858 clone II 5' non-coding region  
DEFINITION  
ACCESSION AF282640  
VERSION AF282640.1 GI:10764503  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
source 1..139  
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/mol\_type="genomic RNA"  
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/clone="II"  
1..139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
116 TTCCGACCCCAACTACTC 97

Db 116 TTGGGACCCCAACTACTC 97

RESULT 47  
AF282641/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H858 clone III 5' non-coding region  
DEFINITION  
AF282641  
ACCESSION AF282641.1 GI:10764504  
VERSION  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
SHT, UK

FEATURES  
source 1. .139  
Location/Qualifiers  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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/clone="III"  
misc\_feature 1. .139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
116 TTGGGACCCCAACTACTC 97

Db 116 TTGGGACCCCAACTACTC 97

RESULT 48  
AF282642/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone I 5' non-coding region  
DEFINITION  
AF282642  
ACCESSION AF282642.1 GI:10764505  
VERSION  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
SHT, UK

FEATURES  
source 1. .139  
Location/Qualifiers  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="I"  
misc\_feature 1. .139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
116 TTGGGACCCCAACTACTC 97

Db 116 TTGGGACCCCAACTACTC 97

RESULT 49  
AF282643/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone II 5' non-coding region  
DEFINITION  
AF282643  
ACCESSION AF282643.1 GI:10764506  
VERSION  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
SHT, UK

FEATURES  
source 1. .139  
Location/Qualifiers  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="II"  
misc\_feature 1. .139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
116 TTGGGACCCCAACTACTC 97

Db 116 TTGGGACCCCAACTACTC 97

RESULT 50  
AF282644/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone IV 5' non-coding region  
DEFINITION  
AF282644  
ACCESSION AF282644.1 GI:10764507  
VERSION  
KEYWORDS



SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK  
FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="IV"  
1..139  
/note="5' non-coding region"  
misc\_feature  
/note="5' non-coding region"  
ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 116 TTCCGACCCCAACTACTC 97  
RESULT 51  
AF282645 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone V 5' non-coding region  
DEFINITION  
sequence.  
ACCESSION AF282645  
VERSION AF282645.1 GI:10764508  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK  
FEATURES  
source Location/Qualifiers  
1..139  
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/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="V"  
1..139  
/note="5' non-coding region"  
misc\_feature  
/note="5' non-coding region"  
ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 116 TTCCGACCCCAACTACTC 97  
RESULT 52  
AF282646 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone VI 5' non-coding region  
DEFINITION  
sequence.  
ACCESSION AF282646  
VERSION AF282646.1 GI:10764509  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK  
FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="VI"  
1..139  
/note="5' non-coding region"  
misc\_feature  
/note="5' non-coding region"  
ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 116 TTCCGACCCCAACTACTC 97  
RESULT 53  
AY003921 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD244 clone I 5' non-coding region,  
partial sequence.  
DEFINITION  
sequence.  
ACCESSION AY003921  
VERSION AY003921.1 GI:9858202  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

misc\_feature  
/note="5' non-coding region"  
ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 116 TTCCGACCCCAACTACTC 97  
RESULT 52  
AF282646 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone VI 5' non-coding region  
DEFINITION  
sequence.  
ACCESSION AF282646  
VERSION AF282646.1 GI:10764509  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK  
FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
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1..139  
/note="5' non-coding region"  
misc\_feature  
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ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 116 TTCCGACCCCAACTACTC 97  
RESULT 53  
AY003921 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD244 clone I 5' non-coding region,  
partial sequence.  
DEFINITION  
sequence.  
ACCESSION AY003921  
VERSION AY003921.1 GI:9858202  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

misc\_feature  
/note="5' non-coding region"  
ORIGIN

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match  
1 TTGCGACCCACACTACTC 20  
116 TTGCGACCCACACTACTC 97

RESULT 54  
AY003922/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD244 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003922  
VERSION AY003922.1 GI:9858203  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match  
1 TTGCGACCCACACTACTC 20  
116 TTGCGACCCACACTACTC 97

RESULT 55  
AY003923/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD244 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003923  
VERSION AY003923.1 GI:9858204  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="III"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match  
1 TTGCGACCCACACTACTC 20  
116 TTGCGACCCACACTACTC 97

RESULT 56  
AY003924/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD244 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003924  
VERSION AY003924.1 GI:9858205  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139

misc\_feature /organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="IV"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
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116 TTGGGACCCCAACTACTC 97

Db

RESULT 57  
AY003925/c 139 bp ss-RNA linear VRL 01-MAR-2001  
DEFINITION Hepatitis C virus isolate BD244 clone V 5' non-coding region,  
partial sequence.  
ACCESSION AY003925  
VERSION AY003925.1 GI:9858206  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:11103"  
/clone="V"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
116 TTGGGACCCCAACTACTC 97

Db

RESULT 58  
AY003928/c 139 bp ss-RNA linear VRL 01-MAR-2001  
DEFINITION Hepatitis C virus isolate BD244 clone VIII 5' non-coding region,  
partial sequence.  
ACCESSION AY003928  
VERSION AY003928.1 GI:9858209  
KEYWORDS

SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1..139  
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/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="VIII"  
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<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
116 TTGGGACCCCAACTACTC 97

Db

RESULT 59  
AY003929/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD259 clone I 5' non-coding region,  
partial sequence.  
DEFINITION  
ACCESSION AY003929  
VERSION AY003929.1 GI:9858210  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD259"  
/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1b"  
<1..>139  
/note="5' non-coding region"

misc\_feature

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCCACACTACTC 20  
116 TTGGCGACCCACACTACTC 97

Db

RESULT 60  
AY003930/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD259 clone II 5' non-coding region,  
partial sequence.  
ACCESSION AY003930  
VERSION AY003930.1 GI:9858211  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1.139  
/organism="Hepatitis C virus"  
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/db\_xref="taxon:11103"  
/clone="I1"  
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<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCCACACTACTC 20  
116 TTGGCGACCCACACTACTC 97

Db

RESULT 61  
AY003932 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD268 clone I 5' non-coding region,  
partial sequence.  
ACCESSION AY003932  
VERSION AY003932.1 GI:9858213  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis

JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="I1"  
/note="genotype: 1b"  
<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCCACACTACTC 20  
116 TTGGCGACCCACACTACTC 97

Db

RESULT 62  
AY003933/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD268 clone II 5' non-coding region,  
partial sequence.  
ACCESSION AY003933  
VERSION AY003933.1 GI:9858214  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1.139  
/organism="Hepatitis C virus"  
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/db\_xref="taxon:11103"  
/clone="I1"  
/note="genotype: 1b"  
<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCCACACTACTC 20  
116 TTGGCGACCCACACTACTC 97

Db

Db 116 TTGGGACCCCAACTACTC 97

RESULT 63  
AY003934/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003934  
VERSION AY003934.1 GI:9858215  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="IV"  
/note="genotype: 1b"  
misc\_feature <1. .>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
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Db 116 TTGGGACCCCAACTACTC 97

RESULT 64  
AY003935/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003935  
VERSION AY003935.1 GI:9858216  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

5HT, UK

FEATURES  
source 1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="IV"  
/note="genotype: 1b"  
misc\_feature <1. .>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 65  
AY003936/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003936  
VERSION AY003936.1 GI:9858217  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1. .139  
/organism="Hepatitis C virus"  
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/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="V"  
/note="genotype: 1b"  
misc\_feature <1. .>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 66  
AY003937/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone VI 5' non-coding region,  
DEFINITION partial sequence.

ACCESSION AY003937  
VERSION AY003937.1 GI:9858218  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
SHT, UK

FEATURES  
source Location/Qualifiers  
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/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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/clone="VI"  
/note="genotype: 1b"  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
Db 116 TTGCGACCCCACTACTC 97

RESULT 67  
AY003938 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone VII 5' non-coding region,  
Partial sequence.  
ACCESSION AY003938  
VERSION AY003938.1 GI:9858219  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
SHT, UK

FEATURES  
source Location/Qualifiers  
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/mol\_type="genomic RNA"  
/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="VI"  
/note="genotype: 1b"  
/note="5' non-coding region"

misc\_feature  
/note="genotype: 1b"  
<1..>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
Db 116 TTGCGACCCCACTACTC 97

RESULT 68  
AY003939 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone I 5' non-coding region,  
Partial sequence.  
ACCESSION AY003939  
VERSION AY003939.1 GI:9858220  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
SHT, UK

FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD424"  
/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 3a"  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
Db 116 TTGCGACCCCACTACTC 97

RESULT 69  
AY003940 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone II 5' non-coding region,  
Partial sequence.  
ACCESSION AY003940  
VERSION AY003940.1 GI:9858221  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)

AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD424"  
/db\_xref="taxon:11103"  
/clone="11"  
/note="genotype: 3a"  
<1..>139  
/note="5' non-coding region"

misc\_feature  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
|||||  
Db 116 TTGCGACCCCACTACTC 97

RESULT 70  
AY003941/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003941  
VERSION AY003941.1 GI:9858222  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepcivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
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/isolate="BD424"  
/db\_xref="taxon:11103"  
/clone="11"  
/note="genotype: 3a"  
<1..>139  
/note="5' non-coding region"

misc\_feature  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
|||||  
Db 116 TTGCGACCCCACTACTC 97

RESULT 71  
AY003942/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003942  
VERSION AY003942.1 GI:9858223  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepcivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1..139  
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/mol\_type="genomic RNA"  
/isolate="BD424"  
/db\_xref="taxon:11103"  
/clone="11"  
/note="genotype: 3a"  
<1..>139  
/note="5' non-coding region"

misc\_feature  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
|||||  
Db 116 TTGCGACCCCACTACTC 97

RESULT 72  
AY003943/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003943  
VERSION AY003943.1 GI:9858224  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepcivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.

Qy 1 TTGCGACCCCACTACTC 20  
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Db 116 TTGCGACCCCACTACTC 97

RESULT 71  
AY003942/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003942  
VERSION AY003942.1 GI:9858223  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepcivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
|||||  
Db 116 TTGCGACCCCACTACTC 97

RESULT 72  
AY003943/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003943  
VERSION AY003943.1 GI:9858224  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepcivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.

TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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/note="5' non-coding region"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
Db 116 TTGCGACCCACACTACTC 97

RESULT 73  
AY003944/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD426 clone I 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003944  
VERSION AY003944.1 GI:9858225  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.  
AUTHORS Direct Submission  
TITLE Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
JOURNAL Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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misc\_feature  
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/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
Db 116 TTGCGACCCACACTACTC 97

RESULT 74  
AY003945/c

LOCUS AY003945 139 bp ss-RNA linear VRL 01-MAR-2001  
DEFINITION Hepatitis C virus isolate BD426 clone II 5' non-coding region,  
partial sequence.  
ACCESSION AY003945  
VERSION AY003945.1 GI:9858226  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.  
AUTHORS Direct Submission  
TITLE Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
JOURNAL Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"

LOCUS AY003980 139 bp ss-RNA linear VRL 01-MAR-2001  
DEFINITION Hepatitis C virus isolate IDU189 clone I 5' non-coding region,  
partial sequence.  
ACCESSION AY003980  
VERSION AY003980.1 GI:9858294  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.  
AUTHORS Direct Submission  
TITLE Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
JOURNAL Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
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/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"



/isolate="IDU189"  
/db\_xref="taxon:11103"  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
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116 TTGGGACCCCACTACTC 97

Db 116 TTGGGACCCCACTACTC 97

RESULT 76  
AY003981/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone II 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003981  
VERSION AY003981.1 GI:9858295  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
1..139  
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/mol\_type="genomic RNA"  
/isolate="IDU189"  
/db\_xref="taxon:11103"  
/clone="I"  
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/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
|||||  
116 TTGGGACCCCACTACTC 97

Db 116 TTGGGACCCCACTACTC 97

RESULT 77  
AY003982 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003982  
VERSION AY003982.1 GI:9858296  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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/isolate="IDU189"  
/db\_xref="taxon:11103"  
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/note="5' non-coding region"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
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116 TTGGGACCCCACTACTC 97

Db 116 TTGGGACCCCACTACTC 97

RESULT 78  
AY003983/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003983  
VERSION AY003983.1 GI:9858297  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="IDU189"  
/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
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 116 TTGCGACCCACACTACTC 97

Db

RESULT 79  
 AY003984/c 139 bp ss-RNA linear VRL 01-MAR-2001  
 LOCUS Hepatitis C virus isolate IDU189 clone V 5' non-coding region,  
 DEFINITION partial sequence.  
 ACCESSION AY003984  
 VERSION AY003984.1 GI:9858298  
 KEYWORDS Hepatitis C virus  
 SOURCE Hepatitis C virus  
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
 AUTHORS Harris, K.A. and Teo, C.G.  
 TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
 JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
 MEDLINE 20579439  
 PUBMED 11139197

REFERENCE  
 AUTHORS Harris, K.A. and Teo, C.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
 Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
 SHT, UK

FEATURES  
 source Location/Qualifiers  
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 /mol\_type="genomic RNA"  
 /isolate="IDU189"  
 /db\_xref="taxon:11103"  
 /clone="V"  
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 /note="5' non-coding region"

ORIGIN  
 Query Match 100.0%; Score 20; DB 14; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
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 116 TTGCGACCCACACTACTC 97

Db

RESULT 80  
 AY003985/c 139 bp ss-RNA linear VRL 01-MAR-2001  
 LOCUS Hepatitis C virus isolate IDU189 clone VI 5' non-coding region,  
 DEFINITION partial sequence.  
 ACCESSION AY003985  
 VERSION AY003985.1 GI:9858299  
 KEYWORDS Hepatitis C virus  
 SOURCE Hepatitis C virus  
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
 AUTHORS Harris, K.A. and Teo, C.G.  
 TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
 JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
 MEDLINE 20579439

PUBMED 11139197  
 REFERENCE 2 (bases 1 to 139)  
 AUTHORS Harris, K.A. and Teo, C.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
 Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
 SHT, UK

FEATURES  
 source Location/Qualifiers  
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 /clone="VI"  
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 <1..>139  
 /note="5' non-coding region"

ORIGIN  
 Query Match 100.0%; Score 20; DB 14; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
 |||||  
 116 TTGCGACCCACACTACTC 97

Db

RESULT 81  
 AY003986/c 139 bp ss-RNA linear VRL 01-MAR-2001  
 LOCUS Hepatitis C virus isolate IDU189 clone VII 5' non-coding region,  
 DEFINITION partial sequence.  
 ACCESSION AY003986  
 VERSION AY003986.1 GI:9858300  
 KEYWORDS Hepatitis C virus  
 SOURCE Hepatitis C virus  
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
 AUTHORS Harris, K.A. and Teo, C.G.  
 TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
 JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
 MEDLINE 20579439  
 PUBMED 11139197

REFERENCE  
 AUTHORS Harris, K.A. and Teo, C.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
 Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
 SHT, UK

FEATURES  
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 /clone="VII"  
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 /note="5' non-coding region"

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
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 116 TTGCGACCCACACTACTC 97

Db

RESULT 82  
AY003987/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone VII 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003987  
VERSION AY003987.1 GI:9858301  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
1139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
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/clone="VII"  
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/note="5' non-coding region"

ORIGIN  
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Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
Db 116 TTCCGGACCCCAACTACTC 97

RESULT 83  
AY003989/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone I 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003989  
VERSION AY003989.1 GI:9858303  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
1139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
Location/Qualifiers  
1..139  
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/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

source 1..139  
/organism="Hepatitis C virus"  
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<1..>139  
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ORIGIN  
misc\_feature  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
Db 116 TTCCGGACCCCAACTACTC 97

RESULT 84  
AY003990/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone II 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003990  
VERSION AY003990.1 GI:9858304  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
1139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
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/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="IDU191"  
/db\_xref="taxon:11103"  
/clone="II"  
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ORIGIN  
misc\_feature  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
Db 116 TTCCGGACCCCAACTACTC 97

RESULT 85  
AY003992/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003992  
VERSION AY003992.1 GI:9858306

KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
source Location/Qualifiers  
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/organism="Hepatitis C virus"  
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/db\_xref="taxon:11103"  
/clone="IV"  
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<1..>139  
/note="5' non-coding region"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGAGCCCAACTACTC 20  
116 TTGCGAGCCCAACTACTC 97

Db 116 TTGCGAGCCCAACTACTC 97

RESULT 86  
AY003993/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003993  
VERSION AY003993.1 GI:9858307  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
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Db 116 TTGCGAGCCCAACTACTC 97

RESULT 87  
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ACCESSION AY003995  
VERSION AY003995.1 GI:9858309  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

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DEFINITION partial sequence.  
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VERSION AY003996.1 GI:9858310  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing

JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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LOCUS Hepatitis C virus isolate IDU230 clone III 5' non-coding region,  
DEFINITION partial sequence.  
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VERSION AY003997.1 GI:9858311  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
MEDLINE 11139197  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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Db 116 TTGGGACCCCAACTACTC 97

RESULT 90  
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LOCUS Hepatitis C virus isolate IDU230 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003998  
VERSION AY003998.1 GI:9858312  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
MEDLINE 11139197  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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Db 116 TTGGGACCCCAACTACTC 97

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LOCUS Hepatitis C virus isolate IDU230 clone VI 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004000  
VERSION AY004000.1 GI:9858314  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
MEDLINE 11139197  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,

JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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RESULT 91  
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LOCUS Hepatitis C virus isolate IDU230 clone VI 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004000  
VERSION AY004000.1 GI:9858314  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
MEDLINE 11139197  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,

Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers

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Db 116 TTGCGACCCCAACTACTC 97

RESULT 92  
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LOCUS Hepatitis C virus isolate IDU230 clone VII 5' non-coding region.  
DEFINITION partial sequence.  
ACCESSION AY004001 GI:9858315  
VERSION AY004001.1 GI:9858315  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis

JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001).  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Direct Submission

JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers

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Db 116 TTGCGACCCCAACTACTC 97

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LOCUS Hepatitis C virus isolate IDU23 clone I 5' non-coding region.  
DEFINITION

partial sequence.

ACCESSION AY004007 GI:9858321  
VERSION AY004007.1 GI:9858321  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis

JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001).  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Direct Submission

JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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DEFINITION partial sequence.

ACCESSION AY004008 GI:9858322  
VERSION AY004008  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis

JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001).  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
TITLE Direct Submission

JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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Db 116 TTCGGACCCACACTACTC 97

RESULT 95  
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LOCUS Hepatitis C virus isolate IDU323 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004009  
VERSION AY004009.1 GI:9858323  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
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REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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LOCUS Hepatitis C virus isolate IDU323 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004010  
VERSION AY004010.1 GI:9858324  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
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REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 1139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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Db 116 TTCGGACCCACACTACTC 97

RESULT 97  
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LOCUS Hepatitis C virus isolate IDU323 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004011  
VERSION AY004011.1 GI:9858325  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 1139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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Db

RESULT 98  
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LOCUS Hepatitis C virus isolate IDU323 clone VI 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004012  
VERSION AY004012.1 GI:9858326  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
REFERENCE 1139197  
2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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Db

RESULT 99  
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LOCUS Hepatitis C virus isolate IDU323 clone VII 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004013  
VERSION AY004013.1 GI:9858327  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 20579439  
REFERENCE 1139197  
2 (bases 1 to 139)

AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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116 TTGCGACCCCACTACTC 97

Db

RESULT 100  
AF506651/c 157 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate KGV130 5' untranslated region, partial  
DEFINITION sequence.  
ACCESSION AF506651  
VERSION AF506651.1 GI:20977995  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
2 (bases 1 to 157)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
630559, Russia

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LOCUS Sequence 6 from Patent WO0144266.  
DEFINITION AX172758  
ACCESSION AX172758  
VERSION AX172758.1 GI:14597854



KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
KEYWORDS other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Karn,J.C. and Walker,S.C.  
TITLE Nucleic acid compounds and screening assays using the same  
JOURNAL Patent: WO 0144266-A 6 21-JUN-2001;  
Ribotargets Limited (GB)  
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LOCUS AY147807/c  
DEFINITION Hepatitis C virus isolate 3-1C 5' untranslated region, partial  
sequence.  
ACCESSION AY147807  
VERSION AY147807.1 GI:24935230  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 164)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 164)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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ACCESSION AY344037  
VERSION AY344037.1 GI:37790676  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 164)  
AUTHORS Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.  
TITLE Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
JOURNAL Arch. Virol. 149 (5), 1015-1026 (2004)  
PUBMED 15098115  
REFERENCE 2 (bases 1 to 164)  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUN-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
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DEFINITION Hepatitis C virus isolate KGV123 5' untranslated region, partial  
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ACCESSION AF506628  
VERSION AF506628.1 GI:20977972  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
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RESULT 105  
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DEFINITION  
ACCESSION AY147800 GI:24935223  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus genotypes and Hepatitis Delta virus types in Turkish patients with hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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162 TTGGCGACCCCAACTACTC 143

Db

RESULT 106  
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DEFINITION  
ACCESSION AY147801  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus genotypes and Hepatitis Delta virus types in Turkish patients with hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,

Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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RESULT 107  
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LOCUS Hepatitis C virus isolate 3-01 5' untranslated region, partial  
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ACCESSION AY147802  
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KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus genotypes and Hepatitis Delta virus types in Turkish patients with hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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RESULT 108  
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DEFINITION  
ACCESSION AY147803

VERSION AY147803.1 GI:24935226  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
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KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
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REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
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ACCESSION AY147805  
VERSION AY147805.1 GI:24935228  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
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LOCUS AY147806/C  
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ACCESSION AY147806  
VERSION AY147806.1 GI:24935229  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
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AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
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Db 162 TTCCGACCCCAACTACTC 143  
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DEFINITION  
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ACCESSION AY147808 GI:24935231  
VERSION AY147808  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
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Db 162 TTCCGACCCCAACTACTC 143  
RESULT 113  
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LOCUS Hepatitis C virus isolate 1-11 5' untranslated region, partial  
DEFINITION  
sequence.

ACCESSION AY147809  
VERSION AY147809.1 GI:24935232  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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ACCESSION AY147810 GI:24935233  
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SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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RESULT 115  
AY147811/c 165 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 1-15 5' untranslated region, partial  
DEFINITION  
ACCESSION AY147811 GI:24935234  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey

FEATURES  
source 1..165  
/organism="Hepatitis C virus"  
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Qy 1 TTCCGACCCCAACTACTC 20  
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162 TTCCGACCCCAACTACTC 143

RESULT 116  
AY147812/c 165 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 1-16 5' untranslated region, partial  
DEFINITION  
ACCESSION AY147812  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey

FEATURES  
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/note="genotype: 1b"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
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162 TTCCGACCCCAACTACTC 143

RESULT 117  
AY147813/c 165 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 1-04 5' untranslated region, partial  
DEFINITION  
ACCESSION AY147813 GI:24935236  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey

FEATURES  
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/organism="Hepatitis C virus"  
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/note="genotype: 1b"  
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ORIGIN  
5'UTR  
<1..>165

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Qy 1 TTCCGACCCCAACTACTC 20  
|||||  
162 TTCCGACCCCAACTACTC 143

RESULT 118  
AY147814/c 165 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 1-05 5' untranslated region, partial  
DEFINITION

sequence.  
ACCESSION AY147814 GI:24935237  
VERSION AY147814.1  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus genotypes and Hepatitis Delta virus types in Turkish patients with hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute of Hepatology, Ankara University, Cebecl, Ankara 06100, Turkey  
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/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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/note="genotype: 1b"  
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Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGCGACCCCAACTACTC 20  
Db 162 TTGCGACCCCAACTACTC 143  
RESULT 119  
AY147815 165 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 1-07 5' untranslated region, partial  
DEFINITION  
SEQUENCE  
AY147815  
ACCESSION AY147815.1 GI:24935238  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus genotypes and Hepatitis Delta virus types in Turkish patients with hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute of Hepatology, Ankara University, Cebecl, Ankara 06100, Turkey  
FEATURES  
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/mol\_type="genomic RNA"  
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/db\_xref="taxon:11103"  
/note="genotype: 1b"  
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Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGCGACCCCAACTACTC 20  
Db 162 TTGCGACCCCAACTACTC 143  
RESULT 120  
AY147816 165 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 1-09 5' untranslated region, partial  
DEFINITION  
SEQUENCE  
AY147816  
ACCESSION AY147816.1 GI:24935239  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus genotypes and Hepatitis Delta virus types in Turkish patients with hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T., Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute of Hepatology, Ankara University, Cebecl, Ankara 06100, Turkey  
FEATURES  
source 1..165  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="1-09"  
/db\_xref="taxon:11103"  
/note="genotype: 1b"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGCGACCCCAACTACTC 20  
Db 162 TTGCGACCCCAACTACTC 143  
RESULT 121  
AY344028 165 bp RNA linear VRL 23-APR-2004  
LOCUS Hepatitis C virus isolate SL3-S7 5' UTR.  
DEFINITION  
ACCESSION AY344028  
VERSION AY344028.1 GI:3790667  
KEYWORDS  
SOURCE  
ORGANISM  
Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bhattacharyya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R., Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.  
TITLE Phylogenetic conservation of the stem-loop III structure of the 5' untranslated region of Hepatitis C virus RNA among natural variants in samples collected from Southern India  
JOURNAL Arch. Virol. 149 (5), 1015-1026 (2004)

PUBMED 15098115  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India

FEATURES  
source Location/Qualifiers  
1..165 /organism="Hepatitis C virus"  
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/isolate="SL3-S17"  
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ORIGIN  
5'UTR

Query Match 100.0%; Score 20; DB 14; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
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148 TTGGGACCCCAACTACTC 129

RESULT 122  
AY344029 165 bp RNA linear VRL 23-APR-2004  
LOCUS Hepatitis C virus isolate SL3-S10 5' UTR.  
DEFINITION AY344029  
ACCESSION AY344029 GI:37790668  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
2 (bases 1 to 165)  
Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.,  
Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)  
15098115  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India

FEATURES  
source Location/Qualifiers  
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/isolate="SL3-S10"  
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ORIGIN  
5'UTR

Query Match 100.0%; Score 20; DB 14; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
148 TTGGGACCCCAACTACTC 129

RESULT 123  
AY344030 165 bp RNA linear VRL 23-APR-2004  
LOCUS Hepatitis C virus isolate SL3-S16 5' UTR.  
DEFINITION AY344030  
ACCESSION AY344030

VERSION AY344030.1 GI:37790669  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
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Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.,  
Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)  
15098115  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India

FEATURES  
source Location/Qualifiers  
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ORIGIN  
5'UTR

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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
148 TTGGGACCCCAACTACTC 129

RESULT 124  
AY344031 165 bp RNA linear VRL 23-APR-2004  
LOCUS Hepatitis C virus isolate SL3-S17 5' UTR.  
DEFINITION AY344031  
ACCESSION AY344031 GI:37790670  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
2 (bases 1 to 165)  
Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.,  
Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)  
15098115  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India

FEATURES  
source Location/Qualifiers  
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ORIGIN  
5'UTR

Query Match 100.0%; Score 20; DB 14; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCAACTACTC 20  
Db 148 TTGGCGACCCCAACTACTC 129

## RESULT 125

LOCUS AY344032 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S24 5' UTR.  
ACCESSION AY344032  
VERSION AY344032.1 GI:37790671  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

1 (bases 1 to 165)

REFERENCE Bhattacharyya, S., Mapa, K., Prabhavathi, S., Sudhamani, S.R.,  
AUTHORS Menon, P.K., John, K.P., Shivaram, C., Amarnath, S. and Das, S.,  
TITLE Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)

JOURNAL 15098115  
PUBMED 2 (bases 1 to 165)  
REFERENCE Bhattacharyya, S., Srinivasan, P., Mapa, K. and Das, S.  
AUTHORS Direct Submission  
TITLE Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India

## FEATURES

source Location/Qualifiers  
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/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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/db\_xref="taxon:11103"  
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## ORIGIN

5'UTR

Query Match 100.0%; Score 20; DB 14; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCAACTACTC 20  
Db 148 TTGGCGACCCCAACTACTC 129

## RESULT 126

LOCUS AY344033 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S24 5' UTR.  
ACCESSION AY344033  
VERSION AY344033.1 GI:37790672  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

1 (bases 1 to 165)

REFERENCE Bhattacharyya, S., Mapa, K., Prabhavathi, S., Sudhamani, S.R.,  
AUTHORS Menon, P.K., John, K.P., Shivaram, C., Amarnath, S. and Das, S.,  
TITLE Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)

JOURNAL 15098115  
PUBMED 2 (bases 1 to 165)  
REFERENCE Bhattacharyya, S., Srinivasan, P., Mapa, K. and Das, S.  
AUTHORS Direct Submission

## TITLE

Direct Submission

## JOURNAL

Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India

FEATURES Location/Qualifiers  
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/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="SL3-S24"  
/db\_xref="taxon:11103"  
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## ORIGIN

5'UTR

Query Match 100.0%; Score 20; DB 14; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCAACTACTC 20  
Db 148 TTGGCGACCCCAACTACTC 129

## RESULT 127

LOCUS AY344034 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S25 5' UTR.  
ACCESSION AY344034  
VERSION AY344034.1 GI:37790673  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

1 (bases 1 to 165)

REFERENCE Bhattacharyya, S., Mapa, K., Prabhavathi, S., Sudhamani, S.R.,  
AUTHORS Menon, P.K., John, K.P., Shivaram, C., Amarnath, S. and Das, S.,  
TITLE Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)

JOURNAL 15098115  
PUBMED 2 (bases 1 to 165)  
REFERENCE Bhattacharyya, S., Srinivasan, P., Mapa, K. and Das, S.  
AUTHORS Direct Submission  
TITLE Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India

## FEATURES

source Location/Qualifiers  
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## ORIGIN

5'UTR

Query Match 100.0%; Score 20; DB 14; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCAACTACTC 20  
Db 148 TTGGCGACCCCAACTACTC 129

## RESULT 128

LOCUS AY344035 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S26 5' UTR.  
ACCESSION AY344035  
VERSION AY344035.1 GI:37790674  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus

## TITLE



Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirius.

REFERENCE  
1 (bases 1 to 165)  
Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R., Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.  
Phylogenetic conservation of the stem-loop III structure of the 5' untranslated region of Hepatitis C virus RNA among natural variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)

JOURNAL  
PUBMED  
15098115

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

2 (bases 1 to 165)  
Bhattacharya,S., Srinivasan,P., Mapa,K. and Das,S.  
Direct Submission  
Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian Institute of Science, C.V. Raman Street, Bangalore, Karnataka 560012, India

FEATURES  
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/db\_xref="taxon:11103"  
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ORIGIN  
5'UTR

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Qy 1 TTGGGACCCCAACTACTC 20  
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Db 148 TTGGGACCCCAACTACTC 129

RESULT 129  
AF506648/c 166 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate KGV124 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506648.1 GI:20977992  
VERSION AF506648  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirius.  
REFERENCE  
AUTHORS 1 (bases 1 to 166)  
Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
2 (bases 1 to 166)  
Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
AUTHORS Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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/organism="Hepatitis C virus"  
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Db 159 TTGGGACCCCAACTACTC 140

RESULT 130  
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LOCUS Hepatitis C virus isolate KGV127 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506649.1 GI:20977993  
VERSION AF506649  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirius.  
REFERENCE  
AUTHORS 1 (bases 1 to 166)  
Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
2 (bases 1 to 166)  
Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
AUTHORS Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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Db 159 TTGGGACCCCAACTACTC 140

RESULT 131  
AF506642 167 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG126 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506642.1 GI:20977986  
VERSION AF506642  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirius.  
REFERENCE  
AUTHORS 1 (bases 1 to 167)  
Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
2 (bases 1 to 167)  
Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
AUTHORS Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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161 TTGGGACCCCAACTACTC 142

Db 161 TTGGGACCCCAACTACTC 142

RESULT 132  
AF506684/c 167 bp RNA linear VRL 20-MAY-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate RIG106 5' untranslated region, partial  
sequence.  
AF506684  
AF506684.1 GI:20978028  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 167)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Genetic variability of hepatitis C virus in Western Siberia  
REFERENCE 2 (bases 1 to 167)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
630559, Russia

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161 TTGGGACCCCAACTACTC 142

Db 161 TTGGGACCCCAACTACTC 142

RESULT 133  
AF506682/c 168 bp RNA linear VRL 20-MAY-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate RIG83 5' untranslated region, partial  
sequence.  
AF506682  
AF506682.1 GI:20978026  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 168)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Genetic variability of hepatitis C virus in Western Siberia  
REFERENCE 2 (bases 1 to 168)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.

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Location/Qualifiers  
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162 TTGGGACCCCAACTACTC 143

Db 162 TTGGGACCCCAACTACTC 143

RESULT 134  
AF506695/c 169 bp RNA linear VRL 20-MAY-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate VOI3 5' untranslated region, partial  
sequence.  
AF506695  
AF506695.1 GI:20978039  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 169)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Genetic variability of hepatitis C virus in Western Siberia  
REFERENCE 2 (bases 1 to 169)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
630559, Russia

FEATURES  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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162 TTGGGACCCCAACTACTC 143

Db 162 TTGGGACCCCAACTACTC 143

RESULT 135  
AY146006/c 170 bp RNA linear VRL 12-NOV-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate KGV474 5' UTR, partial sequence.  
AY146006  
AY146006.1 GI:24935134  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 170)

AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE The prevalence and genetic variability of hepatitis C virus  
JOURNAL Isolates in Western Siberia  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 170)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Direct Submission  
Submitted (29-AUG-2002) Inst. Molecular Biology, State Research  
Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559,  
Russia

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RESULT 136  
AF506691/C 171 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG96 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506691  
VERSION AF506691  
KEYWORDS AF506691.1 GI:20978035  
SOURCE  
ORGANISM  
Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 171)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
2 (bases 1 to 171)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
630559, Russia  
FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 165 TTGGGACCCCAACTACTC 146

RESULT 137  
AY545673/C 172 bp RNA linear VRL 09-MAR-2004  
LOCUS

DEFINITION Hepatitis C virus isolate IR-1269 5' UTR.  
ACCESSION AY545673.1 GI:45120596  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 172)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi  
Arzenani,M., Adeli,A. and Sarrafi Pouroushani,R.  
JOURNAL Direct Submission  
Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
FEATURES  
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QY 1 TTGGGACCCCAACTACTC 20  
DB 130 TTGGGACCCCAACTACTC 111

RESULT 138  
AY545676/C 173 bp RNA linear VRL 09-MAR-2004  
LOCUS Hepatitis C virus isolate IR-1806 5' UTR.  
DEFINITION  
ACCESSION AY545676  
VERSION AY545676.1 GI:45120599  
KEYWORDS  
SOURCE  
ORGANISM  
Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 173)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi  
Arzenani,M., Adeli,A. and Sarrafi Pouroushani,R.  
JOURNAL Direct Submission  
Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
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DB 131 TTGGGACCCCAACTACTC 112

RESULT 139  
AY545678/C 172 bp RNA linear VRL 09-MAR-2004  
LOCUS

LOCUS AY545678 173 bp RNA linear VRL 09-MAR-2004  
 DEFINITION Hepatitis C virus isolate IR-2026 5' UTR.  
 ACCESSION AY545678  
 VERSION AY545678.1 GI:44975239  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Hepacivirus.  
 REFERENCE 1 (bases 1 to 173)  
 AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi  
 Arzenani,M., Adeli,A. and Sarrafi Pouroushani,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
 12 Farvardin, Tehran 69 13164, Iran  
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 131 TTGCGACCCCAACTACTC 112  
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 LOCUS AF506673  
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 sequence.  
 ACCESSION AF506673  
 VERSION AF506673.1 GI:20978017  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Hepacivirus.  
 REFERENCE 1 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
 Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
 630559, Russia  
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Db 167 TTGCGACCCCAACTACTC 148  
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 AF506685/c 174 bp RNA linear VRL 20-MAY-2002  
 LOCUS AF506685/c  
 DEFINITION Hepatitis C virus isolate RI676 5' untranslated region, partial  
 sequence.  
 ACCESSION AF506685  
 VERSION AF506685.1 GI:20978029  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Hepacivirus.  
 REFERENCE 1 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
 Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
 630559, Russia  
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 168 TTGCGACCCCAACTACTC 149  
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 RESULT 142  
 AF506692/c 174 bp RNA linear VRL 20-MAY-2002  
 LOCUS AF506692/c  
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 sequence.  
 ACCESSION AF506692  
 VERSION AF506692.1 GI:20978036  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Hepacivirus.  
 REFERENCE 1 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
 Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
 630559, Russia  
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Db	168 TTCCGACCCCAACTACTC 149	
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DEFINITION	Hepatitis C virus isolate RIG98 5' untranslated region, partial sequence.	
ACCESSION	AF506693	
VERSION	AF506693.1	GI:20978037
KEYWORDS		
SOURCE	Hepatitis C virus	
ORGANISM	Hepatitis C virus	
REFERENCE	1 (bases 1 to 174)	
AUTHORS	Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.	
TITLE	Genetic variability of hepatitis C virus in western Siberia	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 174)	
AUTHORS	Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.	
TITLE	Direct Submission	
JOURNAL	Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia	
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Matches	20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 144		
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DEFINITION	Hepatitis C virus isolate IR-1747 5' UTR.	
ACCESSION	AY523463	
VERSION	AY523463.1	GI:41352544
KEYWORDS		
SOURCE	Hepatitis C virus	
ORGANISM	Hepatitis C virus	
REFERENCE	1 (bases 1 to 174)	
AUTHORS	Almadijpour,M.H., Kevani Aminah,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Foroushani,R.	
TITLE	Hepatitis C virus 5' untranslated region sequences among Iranian HCV infected subjects	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 174)	
AUTHORS	Almadijpour,M.H., Kevani Aminah,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Foroushani,R.	

FEATURES	source
TITLE	Direct Submission
JOURNAL	Submitted (08-JAN-2004) Biotechnology, Pasteur of Iran, 12
AUTHORS	Farvardin, Tehran, 69 13164, Iran
LOCATION/Qualifiers	1. .174
ORGANISM	/organism="Hepatitis C virus"
DEFINITION	/mol_type="genomic RNA"
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VERSION	/db_xref="taxon:11103"
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REFERENCE	<1. .>174
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DEFINITION	
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VERSION	
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DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
REFERENCE	

SOURCE  
Hepatitis C virus  
ORGANISM  
Hepatitis C virus  
REFERENCE  
1 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M.H., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Hepatitis C virus 5' untranslated region sequences among Iranian HCV infected subjects  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M.H., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (08-JAN-2004) Biotechnology, Pasteur of Iran, 12 Farvardin, Tehran, 69 13164, Iran  
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OY  
1 TTGGGACCCACACTACTC 20  
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DB 133 TTGGGACCCACACTACTC 114

RESULT 147  
AY523466 174 bp RNA linear VRL 02-FEB-2004  
LOCUS  
DEFINITION  
Hepatitis C virus isolate IR-1411 5' UTR.  
ACCESSION  
AY523466  
VERSION  
AY523466.1 GI:41352547  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Hepatitis C virus  
REFERENCE  
1 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M.H., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Hepatitis C virus 5' untranslated region sequences among Iranian HCV infected subjects  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M.H., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (08-JAN-2004) Biotechnology, Pasteur of Iran, 12 Farvardin, Tehran, 69 13164, Iran  
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OY  
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DB 132 TTGGGACCCACACTACTC 113

RESULT 148  
AY545671 174 bp RNA linear VRL 09-MAR-2004  
LOCUS  
DEFINITION  
Hepatitis C virus isolate IR-0613 5' UTR.  
ACCESSION  
AY545671  
VERSION  
AY545671.1 GI:45120594  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Hepatitis C virus  
REFERENCE  
1 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (09-FEB-2004) Biotechnology, Pasteur Institute of Iran, 12 Farvardin, Tehran 69 13164, Iran  
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OY  
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DB 132 TTGGGACCCACACTACTC 113

RESULT 149  
AY545672 174 bp RNA linear VRL 09-MAR-2004  
LOCUS  
DEFINITION  
Hepatitis C virus isolate IR-0652 5' UTR.  
ACCESSION  
AY545672  
VERSION  
AY545672.1 GI:45120595  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Hepatitis C virus  
REFERENCE  
1 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran, 12 Farvardin, Tehran 69 13164, Iran  
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QY 1 TTGGGACCCCACTACTC 20  
|||||  
Db 132 TTGGGACCCCACTACTC 113

RESULT 150  
AY545674/c 174 bp RNA linear VRL 09-MAR-2004  
LOCUS Hepatitis C virus isolate IR-1733 5' UTR.  
DEFINITION AY545674  
ACCESSION AY545674.1 GI:45120597  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 174)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Fourooshani,R.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
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QY 1 TTGGGACCCCACTACTC 20  
|||||  
Db 132 TTGGGACCCCACTACTC 113

RESULT 151  
AY545675/c 174 bp RNA linear VRL 09-MAR-2004  
LOCUS Hepatitis C virus isolate IR-1743 5' UTR.  
DEFINITION AY545675  
ACCESSION AY545675.1 GI:45120598  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 174)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Fourooshani,R.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
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Db 132 TTGGGACCCCACTACTC 113

RESULT 152  
AY545677/c 174 bp RNA linear VRL 09-MAR-2004  
LOCUS Hepatitis C virus isolate IR-1883 5' UTR.  
DEFINITION AY545677  
ACCESSION AY545677.1 GI:45120600  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 174)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Fourooshani,R.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
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QY 1 TTGGGACCCCACTACTC 20  
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Db 132 TTGGGACCCCACTACTC 113

RESULT 153  
AF506661/c 175 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG81 5' untranslated region, partial  
DEFINITION AF506661  
ACCESSION AF506661.1 GI:20978005  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 175)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 175)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
FEATURES  
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5'UTR /country="Russia"  
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QY 1 TTGGGACCCCAACTACTC 20  
169 TTGGGACCCCAACTACTC 150

RESULT 154  
AF506645/c 176 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG78 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506645  
VERSION AF506645  
KEYWORDS GI:20977989  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
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QY 1 TTGGGACCCCAACTACTC 20  
170 TTGGGACCCCAACTACTC 151

RESULT 155  
AF506658/c 176 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG100 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506658  
VERSION AF506658  
KEYWORDS GI:20978002  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission

JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
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QY 1 TTGGGACCCCAACTACTC 20  
170 TTGGGACCCCAACTACTC 151

RESULT 156  
AF506694/c 176 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG99 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506694  
VERSION AF506694  
KEYWORDS GI:20978038  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
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170 TTGGGACCCCAACTACTC 151

RESULT 157  
AY145948/c 176 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate GAY149 5' UTR, partial sequence.  
DEFINITION  
ACCESSION AY145948  
VERSION AY145948  
KEYWORDS GI:24935076  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;



REFERENCE 1 Hepacivirus.  
AUTHORS 1 (bases 1 to 176)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL The prevalence and genetic variability of hepatitis C virus  
AUTHORS isolates in Western Siberia  
TITLE Unpublished  
JOURNAL 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research  
AUTHORS Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559,  
JOURNAL Russia

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QY 1 TTGCGAGCCCACTACTC 20  
DB 131 TTGCGAGCCCACTACTC 112

RESULT 158  
LOCUS AY145951 176 bp RNA linear VRL 12-NOV-2002  
DEFINITION Hepatitis C virus isolate GA236 5' UTR, partial sequence.  
ACCESSION AY145951  
VERSION AY145951.1 GI:24935079  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE The prevalence and genetic variability of hepatitis C virus  
JOURNAL isolates in Western Siberia  
AUTHORS Unpublished  
JOURNAL 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research  
AUTHORS Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559,  
JOURNAL Russia

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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
DB 131 TTGCGAGCCCACTACTC 112

RESULT 159

LOCUS HCV6329 176 bp RNA linear VRL 25-MAY-1998  
DEFINITION Hepatitis C virus type 1b 5'UTR, isolate c94.6, partial.  
ACCESSION AJ006329  
VERSION AJ006329.1 GI:3152994  
KEYWORDS  
SOURCE Hepatitis C virus type 1b  
ORGANISM Hepatitis C virus type 1b  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1  
AUTHORS del Campo Terron,S., Moreno Garoz,N., Telleria Oriols,D. and  
TITLE Virus C de Hepatitis en pacientes transplantados de hígado  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 176)  
TITLE del Campo Terron,S.  
JOURNAL Direct Submission  
Submitted (18-MAY-1998) del Campo Terron S., Gastroenterología,  
Hospital Ramon y Cajal, CTRA Colmenar Km 9.1 Madrid, E-28034, SPAIN

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
DB 166 TTGCGAGCCCACTACTC 147

RESULT 160  
LOCUS AF506677 177 bp RNA linear VRL 20-MAY-2002  
DEFINITION Hepatitis C virus isolate KGV69 5' untranslated region, partial  
sequence.  
ACCESSION AF506677  
VERSION AF506677.1 GI:20978021  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 177)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Direct Submission  
Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
AUTHORS Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
JOURNAL 630559, Russia

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 170 TTGGGAGCCCACTACTC 151

RESULT 161  
 AF506680/c 177 bp RNA linear VRL 20-MAY-2002  
 LOCUS Hepatitis C virus isolate KGV70 5' untranslated region, partial  
 DEFINITION  
 ACCESSION AF506680  
 VERSION AF506680  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 177)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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 /db\_xref="taxon:11103"  
 /country="Russia"  
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 Best Local Similarity 100.0%; Pred. No. 0.14;  
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QY 1 TTGGGAGCCCACTACTC 20  
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 170 TTGGGAGCCCACTACTC 151

Db 170 TTGGGAGCCCACTACTC 151

RESULT 162  
 AF506686/c 177 bp RNA linear VRL 20-MAY-2002  
 LOCUS Hepatitis C virus isolate RIG75 5' untranslated region, partial  
 DEFINITION  
 ACCESSION AF506686  
 VERSION AF506686  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 177)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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Db 170 TTGGGAGCCCACTACTC 151

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 AF506680/c 177 bp RNA linear VRL 07-NOV-2003  
 LOCUS Hepatitis C virus isolate S21 5' noncoding region, partial  
 DEFINITION  
 ACCESSION AF506680  
 VERSION AF506680  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
 AUTHORS Lole,K.S., Jha,J.A., Shrotri,S.P., Tandon,B.N., Prasad,V.G. and Arankalle,V.A.  
 TITLE Comparison of hepatitis C virus genotyping by 5' noncoding region- and core-based reverse transcriptase PCR assay with sequencing and use of the assay for determining subtype distribution in India  
 JOURNAL J. Clin. Microbiol. 41 (11), 5240-5244 (2003)  
 MEDLINE 22967393  
 PUBMED 14605173

ORIGIN  
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 170 TTGGGAGCCCACTACTC 151

Db 170 TTGGGAGCCCACTACTC 151

RESULT 164  
 AF463460/c 178 bp RNA linear VRL 29-JAN-2002  
 LOCUS Hepatitis C virus isolate TM37 5'UTR, partial sequence.  
 DEFINITION  
 ACCESSION AF463460  
 VERSION AF463460  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 177)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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QY 1 TTGGGAGCCCACTACTC 20  
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 170 TTGGGAGCCCACTACTC 151

Db 170 TTGGGAGCCCACTACTC 151

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 174 TTCCGACCCCAACTACTC 155

RESULT 165  
AF463462/C 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN28 5'UTR, partial sequence.  
DEFINITION AF463462  
ACCESSION AF463462.1 GI:18390062  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Best Local Similarity 100.0%; Pred. No. 0.14;  
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DB 171 TTCCGACCCCAACTACTC 152

RESULT 166  
AF463463/C 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN28 5'UTR, partial sequence.  
DEFINITION AF463463  
ACCESSION AF463463.1 GI:18390063  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
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DB 172 TTCCGACCCCAACTACTC 153

RESULT 167  
AF463464/C 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN4 5'UTR, partial sequence.  
DEFINITION AF463464  
ACCESSION AF463464.1 GI:18390064  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Db 172 TTGCGACCCCAACTACTC 153

RESULT 168  
AF463466/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN34 5'UTR, partial sequence.  
ACCESSION AF463466  
VERSION AF463466.1 GI:18390066  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
1 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
Unpublished  
2 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
Direct Submission  
Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Db 172 TTGCGACCCCAACTACTC 153

RESULT 169  
AF463467/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN16 5'UTR, partial sequence.  
ACCESSION AF463467  
VERSION AF463467.1 GI:18390067  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
1 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
Unpublished  
2 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
Direct Submission  
Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Best Local Similarity 100.0%; Pred. No. 0.14;  
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Db 172 TTGCGACCCCAACTACTC 153

RESULT 170  
AF463468/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN20 5'UTR, partial sequence.  
ACCESSION AF463468  
VERSION AF463468.1 GI:18390068  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
1 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
Unpublished  
2 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
Direct Submission  
Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Db 172 TTGCGACCCCAACTACTC 153

RESULT 171  
AF463469/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN21 5'UTR, partial sequence.  
ACCESSION AF463469  
VERSION AF463469.1 GI:18390069  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi,A. and Triki,H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi,A. and Triki,H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Db 173 TTGGGACCCCACTACTC 154

RESULT 172  
AF463470 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN43 5'UTR, partial sequence.  
DEFINITION AF463470  
ACCESSION AF463470.1 GI:18390070  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi,A. and Triki,H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi,A. and Triki,H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Db 172 TTGGGACCCCACTACTC 153

RESULT 173  
AF463471 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN23 5'UTR, partial sequence.  
DEFINITION AF463471  
ACCESSION AF463471.1 GI:18390071  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi,A. and Triki,H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi,A. and Triki,H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Db 172 TTGGGACCCCACTACTC 153

RESULT 174  
AF463472 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN2 5'UTR, partial sequence.  
DEFINITION AF463472  
ACCESSION AF463472.1 GI:18390072  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi,A. and Triki,H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi,A. and Triki,H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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172 TTGCGACCCCAACTACTC 153

RESULT 175  
AF463474/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN14 5'UTR, partial sequence.  
DEFINITION AF463474  
ACCESSION AF463474  
VERSION AF463474.1 GI:18390074  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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ORIGIN 5'UTR  
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172 TTGCGACCCCAACTACTC 153

RESULT 176  
AF463475/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN24 5'UTR, partial sequence.  
DEFINITION AF463475  
ACCESSION AF463475  
VERSION AF463475.1 GI:18390075  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.

TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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ORIGIN 5'UTR  
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172 TTGCGACCCCAACTACTC 153

RESULT 177  
AF463476/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN31 5'UTR, partial sequence.  
DEFINITION AF463476  
ACCESSION AF463476  
VERSION AF463476.1 GI:18390076  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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ORIGIN 5'UTR  
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QY 1 TTGCGACCCCAACTACTC 20  
172 TTGCGACCCCAACTACTC 153

RESULT 178  
AF463477/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN33 5'UTR, partial sequence.  
DEFINITION AF463477  
ACCESSION AF463477  
VERSION AF463477.1 GI:18390077  
KEYWORDS

SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 171 TTGGGACCCCACTACTC 152

RESULT 179  
AF463478 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN15 5'UTR, partial sequence.  
DEFINITION AF463478  
ACCESSION AF463478.1 GI:18390078  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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/note="genotype: 1b"  
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Query Match 100.0%; Score 20; DB 14; Length 178;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 171 TTGGGACCCCACTACTC 152

Db 172 TTGGGACCCCACTACTC 153

RESULT 180  
AF463479 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN42 5'UTR, partial sequence.  
DEFINITION AF463479  
ACCESSION AF463479.1 GI:18390079  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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1..178  
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/db\_xref="taxon:11103"  
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/note="genotype: 1b"  
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ORIGIN  
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Query Match 100.0%; Score 20; DB 14; Length 178;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 173 TTGGGACCCCACTACTC 154

RESULT 181  
AF463480 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN18 5'UTR, partial sequence.  
DEFINITION AF463480  
ACCESSION AF463480.1 GI:18390080  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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/country="Tunisia"  
/note="genotype: 1b"  
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ORIGIN  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCCAACTACTC 20  
172 TTCCGACCCCAACTACTC 153

RESULT 182  
AF463486/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN5 5'UTR, partial sequence.  
DEFINITION AF463486  
ACCESSION AF463486.1 GI:18390086  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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ORIGIN  
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Oy 1 TTCCGACCCCAACTACTC 20  
172 TTCCGACCCCAACTACTC 153

RESULT 183  
AF463487/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN36 5'UTR, partial sequence.  
DEFINITION AF463487  
ACCESSION AF463487.1 GI:18390087  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished

2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCCAACTACTC 20  
172 TTCCGACCCCAACTACTC 153

RESULT 184  
AF463488/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN7 5'UTR, partial sequence.  
DEFINITION AF463488  
ACCESSION AF463488.1 GI:18390088  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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/note="genotype: 3a"

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Best Local Similarity 100.0%; Pred. No. 0.14;  
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Oy 1 TTCCGACCCCAACTACTC 20  
172 TTCCGACCCCAACTACTC 153

RESULT 185  
AF463489/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN1 5'UTR, partial sequence.  
DEFINITION AF463489  
ACCESSION AF463489



VERSION AF463489.1 GI:18390089  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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/note="genotype: 4"  
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OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 173 TTCCGACCCCAACTACTC 154

RESULT 186  
AF463491/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN22 5'UTR, partial sequence.  
DEFINITION AF463491  
ACCESSION AF463491  
VERSION AF463491.1 GI:18390091  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 171 TTCCGACCCCAACTACTC 152

RESULT 187  
AY145950/c 179 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate GMA195 5' UTR, partial sequence.  
DEFINITION AY145950  
ACCESSION AY145950  
VERSION AY145950.1 GI:24935078  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 179)  
AUTHORS Shustov, A. V., Gavrilova, I. V. and Netesov, S. V.  
TITLE The prevalence and genetic variability of hepatitis C virus isolates in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 179)  
AUTHORS Shustov, A. V., Gavrilova, I. V. and Netesov, S. V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
source Location/Qualifiers  
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/organism="Hepatitis C virus"  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
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Db 134 TTCCGACCCCAACTACTC 115

RESULT 188  
AY145973/c 180 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate KGV299 5' UTR, partial sequence.  
DEFINITION AY145973  
ACCESSION AY145973  
VERSION AY145973.1 GI:24935101  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 180)  
AUTHORS Shustov, A. V., Gavrilova, I. V. and Netesov, S. V.  
TITLE The prevalence and genetic variability of hepatitis C virus isolates in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 180)  
AUTHORS Shustov, A. V., Gavrilova, I. V. and Netesov, S. V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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/mol\_type="genomic RNA"

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/country="Russia"
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Db     135 TTCGCAGCCCACAATACTC 116
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RESULT	189				
LOCUS	AY190502/c				
DEFINITION	AY190502	180 bp	RNA	linear	VRL 07-NOV-2003
DESCRIPTION	Hepatitis C virus isolate S38 5' noncoding region, partial sequence.				

ACCESSION	AY190502	
VERSION	AY190502.1	GI:37779535
KEYWORDS		
SOURCE	Hepatitis C virus	
ORGANISM	Hepatitis C virus	

REFERENCE	1 (bases 1 to 180)
AUTHORS	Iole, K.S., Jha, J.A., Shrotri, S.P., Tandon, B.N., Prasad, V.G. and Aravindan, R.

TITLE	Comparison of hepatitis C virus genotyping by 5' noncoding region and core-based reverse transcriptase PCR assay with sequencing and use of the assay for determining subtype distribution in India
JOURNAL	J. Clin. Microbiol. 41 (11), 5240-5244 (2003)
ISSN	0095-1136
ARTICLE	5240-5244

REFERENCE  
AUTHORS  
2 (bases 1 to 180)  
Iole, K.S., Jha, J.A., Shrotri, S.P., Tandon, B.N., Mohan Prasad, V.G. and Aravindan, V. A.

JOURNAL	Submitted (04-BEC-2002)	Hepatitis Division, National Institute of Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES	location/Qualifiers	
SOURCE	1	180

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/virion
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/isolate="S38"
/db_xref="taxon:11103"
/country="India"

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				Indels

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RESULT 190	AF134750/c	181 bp	RNA	linear	VRL 01-SEP-2000
LOCUS	AF134750				
DEFINITION	Hepatitis C virus isolate NY-1	5'	non-coding region.		
ACCSSION	AF134750				

VERSION	AF134750.1	GI:9956918
KEYWORDS	.	
SOURCE	Hepatitis C virus	
ORGANISM	Hepatitis C virus	

**REFERENCES**

HANCOCK, J. 1968. Non-positive strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

1 (bases 1 to 181)

AUTHORS Jha, J. and Arankalle, V.A.  
 TITLE Phylogenetic Analysis of Indian HCV Indian Isolates  
 JOURNAL Unpublished  
 REFERENCE 2 (Bases 1 to 181)  
 AUTHORS Jha, J. and Arankalle, V.A.

**TITLE** Direct Submission  
**JOURNAL** Hepatitis Department, National Institute of  
Submitted (12-MAR-1999) Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
**FEATURES** Location/Qualifiers  
**SOURCE** 1. .181

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Best Local Similarity	100.0%	Pred. No. 0.14;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 TTGGGACCCCAACACTACTC 20
          |||||
Db      170 TTGGGACCCCAACACTACTC 151

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RESULT 191	AF134751/c	181 bp	RNA	linear	VRL 01-SEP-2000
LOCUS	AF134751				
DEFINITION	Hepatitis C virus isolate NIV-2	5'	non-coding region.		
ACCESSION	AF134751				

KEYWORDS	SOURCE	ORGANISM
Hepatitis C virus	.	Hepatitis C virus
Hepatitis C virus		Hepatitis C virus

REFERENCE  
Hepacivirus.  
1 (bases 1 to 181)  
Jha, J. and Arankalle, V. A.

JOURNAL	unpublished
REFERENCE	2 (bases 1 to 181)
AUTHORS	Jha, J. and Arankalle, V.A.

Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India

FEATURES	source	Location/Qualifiers
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Query Match	100.0%;	Score 20;	DB 14;	Length 181;
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			0;	Indels
				Gaps
				0

Db 170 TTGGGACCCAACTACTC 151

	AF134754	181 bp	PVA	linear	VOL. 01-SEP-2000
	AOCUS				
	RESULT 192				
	AF134754/C				

DEFINITION Hepatitis C virus isolate NIV-5 5' non-coding region.  
ACCESSION AF134754  
VERSION AF134754.1 GI:9956922  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
UNPUBLISHED  
REFERENCE 2 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
TITLE Direct Submission  
SUBMITTED (12-MAR-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune, Maharashtra 411001, India  
FEATURES  
source Location/Qualifiers  
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/country="India"  
misc\_feature 1..181  
/note="5' non-coding region"  
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Query Match 100.0%; Score 20; DB 14; Length 181;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGCGACCCCAACTACTC 20  
Db 170 TTGCGACCCCAACTACTC 151  
RESULT 193  
AF134756 181 bp RNA linear VRL 01-SEP-2000  
LOCUS AF134756  
DEFINITION Hepatitis C virus isolate NIV-7 5' non-coding region.  
ACCESSION AF134756  
VERSION AF134756.1 GI:9956924  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
UNPUBLISHED  
REFERENCE 2 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
TITLE Direct Submission  
SUBMITTED (12-MAR-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune, Maharashtra 411001, India  
FEATURES  
source Location/Qualifiers  
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misc\_feature 1..181  
/note="5' non-coding region"  
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Query Match 100.0%; Score 20; DB 14; Length 181;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 170 TTGCGACCCCAACTACTC 151  
RESULT 194  
AF134757 181 bp RNA linear VRL 01-SEP-2000  
LOCUS AF134757  
DEFINITION Hepatitis C virus isolate NIV-8 5' non-coding region.  
ACCESSION AF134757  
VERSION AF134757.1 GI:9956925  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
UNPUBLISHED  
REFERENCE 2 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
TITLE Direct Submission  
SUBMITTED (12-MAR-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune, Maharashtra 411001, India  
FEATURES  
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/country="India"  
misc\_feature 1..181  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGCGACCCCAACTACTC 20  
Db 170 TTGCGACCCCAACTACTC 151  
RESULT 195  
AF134758 181 bp RNA linear VRL 01-SEP-2000  
LOCUS AF134758  
DEFINITION Hepatitis C virus isolate NIV-9 5' non-coding region.  
ACCESSION AF134758  
VERSION AF134758.1 GI:9956926  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
UNPUBLISHED  
REFERENCE 2 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
TITLE Direct Submission  
SUBMITTED (12-MAR-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune, Maharashtra 411001, India  
FEATURES  
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/db\_xref="taxon:11103"  
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1..181  
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ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGCGACCCCAACTACTC 20  
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170 TTGGCGACCCCAACTACTC 151

Db 170 TTGGCGACCCCAACTACTC 151

RESULT 196  
AF134759/c 181 bp RNA linear VRL 01-SEP-2000  
LOCUS Hepatitis C virus isolate NIV-10 5' non-coding region.  
DEFINITION AF134759  
ACCESSION AF134759  
VERSION AF134759.1 GI:9956927  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 181)  
REFERENCE Jha,J. and Arankalle,V.A.  
AUTHORS Phylogenetic Analysis of Indian HCV Indian Isolates  
JOURNAL Unpublished  
2 (bases 1 to 181)  
REFERENCE Jha,J. and Arankalle,V.A.  
AUTHORS Direct Submission  
TITLE Submitted (12-MAR-1999) Hepatitis Department, National Institute of  
JOURNAL Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
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170 TTGGCGACCCCAACTACTC 151

Db 170 TTGGCGACCCCAACTACTC 151

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VERSION AF134760.1 GI:9956928  
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SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
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1 (bases 1 to 181)  
REFERENCE Jha,J. and Arankalle,V.A.  
AUTHORS Phylogenetic Analysis of Indian HCV Indian Isolates  
JOURNAL Unpublished  
2 (bases 1 to 181)  
REFERENCE Jha,J. and Arankalle,V.A.  
AUTHORS

TITLE Direct Submission  
JOURNAL Submitted (12-MAR-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 170 TTGGCGACCCCAACTACTC 151

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LOCUS Hepatitis C virus isolate NIV-12 5' non-coding region.  
DEFINITION AF158605  
ACCESSION AF158605  
VERSION AF158605.1 GI:9954158  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 181)  
REFERENCE Jha,J.A. and Arankalle,V.A.  
AUTHORS Phylogenetic Analysis of Indian HCV Isolates  
JOURNAL Unpublished  
2 (bases 1 to 181)  
REFERENCE Jha,J.A. and Arankalle,V.A.  
AUTHORS Direct Submission  
TITLE Submitted (11-JUN-1999) Hepatitis Department, National Institute of  
JOURNAL Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411001, India  
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ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 170 TTGGCGACCCCAACTACTC 151

RESULT 199  
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DEFINITION AF158607  
ACCESSION AF158607  
VERSION AF158607.1 GI:9954160  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

## REFERENCE

1 (bases 1 to 181)

AUTHORS Jha,J.A. and Arankalle,V.A.

TITLE Phylogenetic Analysis of Indian HCV Isolates

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 181)

AUTHORS Jha,J.A. and Arankalle,V.A.

TITLE Direct Submission

JOURNAL Submitted (11-JUN-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road,, Pune, Maharashtra 411001, India

## FEATURES

Location/Qualifiers

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB

170 TTGGGACCCACACTACTC 151

## RESULT 200

AF158608/C

## LOCUS

AF158608 181 bp RNA linear VRL 31-AUG-2000

DEFINITION Hepatitis C virus isolate NIV-35 5' non-coding region.

ACCESSION AF158608

VERSION AF158608.1 GI:9954161

## KEYWORDS

Hepatitis C virus

Hepatitis C virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

## ORGANISM

Hepacivirus.

1 (bases 1 to 181)

AUTHORS Jha,J.A. and Arankalle,V.A.

TITLE Phylogenetic Analysis of Indian HCV Isolates

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 181)

AUTHORS Jha,J.A. and Arankalle,V.A.

TITLE Direct Submission

JOURNAL Submitted (11-JUN-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road,, Pune, Maharashtra 411001, India

## FEATURES

Location/Qualifiers

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DB

170 TTGGGACCCACACTACTC 151

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:46 ; Search time 1923.68 Seconds  
(Without alignments)  
395.743 Million cell updates/sec

Title: US-08-887-505B-28

Perfect score: 20

Sequence: 1 TTTCGCGACCCCACTACTC 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

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3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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5	15	75.0	328	9	CL283937 ZMMBB062
6	15	75.0	395	9	AG306140 Mus muscu
7	15	75.0	457	1	AI891392 614021E04
8	15	75.0	468	8	AZ170379 SP_0116_A
9	15	75.0	479	2	BF610107 NXSL_054
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21	15	75.0	854	4	BG441796 GA_Ea001
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23	15	75.0	873	8	CC096047 CSU-K34.1
24	15	75.0	876	9	CG117887 PUPO45TD

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34	14	70.0	267	1	BG988270 PMO-HT116
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37	14	70.0	302	2	BH109364 BH109364
38	14	70.0	315	5	BH640525 mgcw012XL
39	14	70.0	319	9	CG124493 PUUC62TD
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43	14	70.0	351	9	CG845406 OG4AB34TV
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45	14	70.0	365	5	BF752355 BF752355
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52	14	70.0	457	9	CG059179 PUUCW72TB
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55	14	70.0	475	5	CG845394 OG4AB34TH
56	14	70.0	482	5	BQ741880 BQ741880
57	14	70.0	491	8	BH219227 1006085D0
58	14	70.0	496	7	CK148694 AGT-30-G1
59	14	70.0	504	7	CK747642 nad03--6cs
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70	14	70.0	566	9	CE261393 C1gr-g88-
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91	14	70.0	637	8	CC383900 PUPO45TD
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93	14	70.0	642	4	BQ646828 BQ646828
94	14	70.0	642	5	BO415743 GA_ED010
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96	14	70.0	658	9	BX202031 Dario rer
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102	14	70.0	665	7	CF351008	CF351008	C 175	14	70.0	952	2	BE957748	BE957748	601653861
103	14	70.0	667	7	CF350992	r166b12.y	C 176	14	70.0	955	9	CG218509	CG218509	OCMKR46TV
104	14	70.0	668	7	CF351019	r166a04.y	C 177	14	70.0	965	9	CG126611	CG126611	PURFSN84TB
105	14	70.0	668	7	CF351064	r166d01.y	C 178	14	70.0	974	6	BZ463975	BZ463975	BONGX86TR
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124	14	70.0	713	9	CG197500	CG197500	C 197	14	70.0	1187	8	BM921441	BM921441	AGENCOURT
125	14	70.0	716	9	CG197500	CG197500	C 198	14	70.0	1260	5	CL105095	CL105095	CH261-185
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127	14	70.0	718	9	CG197500	CG197500	C 200	14	70.0	1277	9	CC294903	CC294903	602313372
128	14	70.0	721	5	BM0971958	BM0971958	C 201	14	70.0	1293	8	AG451724	AG451724	Mus muscu
129	14	70.0	728	9	AG407958	AG407958	C 202	14	70.0	1422	5	BM913543	BM913543	AGENCOURT
130	14	70.0	733	7	CF437404	CF437404	C 203	14	70.0	1620	5	BG680217	BG680217	102406880
131	14	70.0	743	7	CF437404	CF437404	C 204	14	70.0	1784	4	BZ081108	BZ081108	1K980C05
132	14	70.0	746	9	CG067495	CG067495	C 205	14	70.0	2467	8	BH865462	BH865462	SALK_0985
133	14	70.0	747	2	BF864639	BF864639	C 206	14	70.0	51	6	CD959220	CD959220	SCU_215
134	14	70.0	749	2	AG575296	AG575296	C 207	14	70.0	62	2	BF596777	BF596777	sue2e06.y
135	14	70.0	753	9	CC889635	CC889635	C 208	14	70.0	97	2	BS0496	BS0496	CIT-HSP-446
136	14	70.0	754	5	BM407445	BM407445	C 209	14	70.0	103	8	CC140738	CC140738	NDL_68A1
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138	14	70.0	760	9	BM172443	BM172443	C 211	14	70.0	137	9	AY356181	AY356181	AY356181
139	14	70.0	762	2	BF613334	BF613334	C 212	14	70.0	138	2	BG589794	BG589794	AY356181
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143	14	70.0	779	8	AZ187767	AZ187767	C 216	14	70.0	174	7	BY164355	BY164355	EST197636
144	14	70.0	783	8	BZ822648	BZ822648	C 217	14	70.0	174	7	BY164355	BY164355	EST197636
145	14	70.0	785	8	BZ468932	BZ468932	C 218	14	70.0	175	7	BY164355	BY164355	EST197636
146	14	70.0	791	8	BZ477400	BZ477400	C 219	14	70.0	187	1	AA140212	AA140212	sh001-13m
147	14	70.0	793	5	BU852379	BU852379	C 220	14	70.0	192	8	BZ766812	BZ766812	AM0354_Sa
148	14	70.0	793	5	BU852379	BU852379	C 221	14	70.0	195	9	CE643940	CE643940	0011177AAN
149	14	70.0	800	9	CF449870	CF449870	C 222	14	70.0	200	7	FL4348	FL4348	m75e12.y
150	14	70.0	801	7	CC860424	CC860424	C 223	14	70.0	227	4	BY1788376	BY1788376	SALK_1407
151	14	70.0	802	9	CC615199	CC615199	C 224	14	70.0	239	8	BZ761454	BZ761454	ATT55260 AC
152	14	70.0	806	9	CG155334	CG155334	C 225	14	70.0	240	2	BB284873	BB284873	sa970a06
153	14	70.0	809	2	BF669895	BF669895	C 226	14	70.0	240	8	CC012253	CC012253	SAUK_0005
154	14	70.0	811	2	BF669895	BF669895	C 227	14	70.0	242	4	CC012253	CC012253	BB284873
155	14	70.0	811	2	BF669895	BF669895	C 228	14	70.0	242	4	CC012253	CC012253	BB284873
156	14	70.0	812	9	CNSO100Q	CNSO100Q	C 229	14	70.0	245	7	R73288	R73288	PUDHNS9TD
157	14	70.0	815	8	BZ822645	BZ822645	C 230	14	70.0	245	2	BB568455	BB568455	119110TB T
158	14	70.0	827	9	CG459141	CG459141	C 231	14	70.0	249	9	CC793874	CC793874	y192d03.x1
159	14	70.0	829	9	CG112064	CG112064	C 232	14	70.0	251	5	BX618332	BX618332	BB568455
160	14	70.0	846	9	CG086099	CG086099	C 233	14	70.0	255	2	AW768172	AW768172	BB568455
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162	14	70.0	856	7	CO38423	CO38423	C 235	14	70.0	261	8	CE362184	CE362184	602318508
163	14	70.0	861	9	CG007611	CG007611	C 236	14	70.0	265	2	AG256373	AG256373	602318508
164	14	70.0	865	2	BF680379	BF680379	C 237	14	70.0	267	7	CR375570	CR375570	602318508
165	14	70.0	883	9	CG226100	CG226100	C 238	14	70.0	270	7	H91101	H91101	602318508
166	14	70.0	888	9	CG366406	CG366406	C 239	14	70.0	272	6	CD632973	CD632973	602318508
167	14	70.0	893	8	BZ817229	BZ817229	C 240	14	70.0	273	8	BH112512	BH112512	602318508
168	14	70.0	906	7	CG0921238	CG0921238	C 241	14	70.0	274	2	BB239183	BB239183	602318508
169	14	70.0	916	7	CG126612	CG126612	C 242	14	70.0	274	2	BB239183	BB239183	602318508
170	14	70.0	929	9	CG388749	CG388749	C 243	14	70.0	274	2	BB468791	BB468791	602318508



244	13	65.0	274	9	BX895783	Arabiidops	C 317	13	65.0	359	5	BY163348
245	13	65.0	276	2	BBS56937	BBS56937	C 318	13	65.0	359	5	BY168257
246	13	65.0	278	1	AV204039	AV204039	C 319	13	65.0	359	8	CC090509
247	13	65.0	278	2	BF639610	BF639610	C 320	13	65.0	360	2	BE700909
248	13	65.0	278	2	AM435286	AM435286	C 321	13	65.0	360	2	BY172283
249	13	65.0	278	6	CD632972	CD632972	C 322	13	65.0	360	6	CD632962
250	13	65.0	278	9	CG446185	CG446185	C 323	13	65.0	361	5	BY071519
251	13	65.0	284	7	CN749542	CN749542	C 324	13	65.0	361	5	BY171614
252	13	65.0	285	8	AZ622366	AZ622366	C 325	13	65.0	361	6	CD632958
253	13	65.0	287	6	CD565074	CD565074	C 326	13	65.0	361	7	CP116778
254	13	65.0	288	2	BBS52495	BBS52495	C 327	13	65.0	362	5	BY165906
255	13	65.0	292	2	BF368261	BF368261	C 328	13	65.0	362	5	BY229212
256	13	65.0	293	2	BF406446	BF406446	C 329	13	65.0	362	6	CD632960
257	13	65.0	294	2	BBS43313	BBS43313	C 329	13	65.0	362	6	CD632960
258	13	65.0	298	6	CB610688	CB610688	C 330	13	65.0	363	5	BY173332
259	13	65.0	299	6	CR499941	CR499941	C 331	13	65.0	364	5	BY056240
260	13	65.0	300	6	CA145108	CA145108	C 332	13	65.0	364	5	BY168197
261	13	65.0	301	3	CNS08WY7	CNS08WY7	C 333	13	65.0	364	5	BY181823
262	13	65.0	301	6	CA145023	CA145023	C 334	13	65.0	364	5	BY181823
263	13	65.0	302	8	AO904839	AO904839	C 335	13	65.0	365	5	BY039430
264	13	65.0	304	1	AV749354	AV749354	C 336	13	65.0	366	5	BY215356
265	13	65.0	304	4	BY982651	BY982651	C 337	13	65.0	366	5	BY215356
266	13	65.0	312	5	BY325997	BY325997	C 338	13	65.0	367	5	BY055994
267	13	65.0	314	9	CC939349	CC939349	C 339	13	65.0	367	5	BY171557
268	13	65.0	319	5	BY317827	BY317827	C 340	13	65.0	368	6	BY775308
269	13	65.0	319	9	CR073901	CR073901	C 341	13	65.0	369	2	BE321493
270	13	65.0	323	4	BU039290	BU039290	C 342	13	65.0	370	1	AL929635
271	13	65.0	323	5	BY169676	BY169676	C 343	13	65.0	370	5	BY042553
272	13	65.0	324	2	BY140352	BY140352	C 344	13	65.0	370	5	BY160201
273	13	65.0	329	2	BF379628	BF379628	C 345	13	65.0	370	5	BY319579
274	13	65.0	329	5	BY344856	BY344856	C 346	13	65.0	372	5	BY041278
275	13	65.0	329	5	BY346900	BY346900	C 347	13	65.0	372	5	BY318107
276	13	65.0	332	5	BY313545	BY313545	C 348	13	65.0	373	5	BY045845
277	13	65.0	332	9	CE706030	CE706030	C 349	13	65.0	373	5	BY168894
278	13	65.0	333	5	BY324287	BY324287	C 350	13	65.0	374	5	BY320059
279	13	65.0	334	5	BY334856	BY334856	C 351	13	65.0	374	5	BY320120
280	13	65.0	335	2	BF927238	BF927238	C 352	13	65.0	374	6	CD632938
281	13	65.0	336	5	BY341371	BY341371	C 353	13	65.0	375	2	BB738422
282	13	65.0	339	5	BY065311	BY065311	C 354	13	65.0	375	5	BY047524
283	13	65.0	339	5	BY315647	BY315647	C 355	13	65.0	375	5	BY079221
284	13	65.0	339	6	CD632961	CD632961	C 356	13	65.0	375	6	CD632936
285	13	65.0	339	6	CD632969	CD632969	C 357	13	65.0	376	5	BY011294
286	13	65.0	340	5	BY327969	BY327969	C 358	13	65.0	376	6	CD632934
287	13	65.0	340	5	BY345044	BY345044	C 359	13	65.0	377	4	BM076491
288	13	65.0	341	5	BY048322	BY048322	C 360	13	65.0	378	5	BY171163
289	13	65.0	341	5	CD632968	CD632968	C 361	13	65.0	379	4	BM383458
290	13	65.0	342	2	AM488723	AM488723	C 362	13	65.0	379	5	BY320095
291	13	65.0	342	5	BY310507	BY310507	C 363	13	65.0	380	7	243379
292	13	65.0	343	5	BY310204	BY310204	C 364	13	65.0	381	3	CNS08UX2
293	13	65.0	347	5	BY042555	BY042555	C 365	13	65.0	383	5	BY172682
294	13	65.0	347	5	BY319239	BY319239	C 366	13	65.0	383	5	CB840599
295	13	65.0	347	5	BY334167	BY334167	C 367	13	65.0	385	5	BY155290
296	13	65.0	348	8	BH382625	BH382625	C 368	13	65.0	387	5	BY046933
297	13	65.0	350	8	BZ315397	BZ315397	C 369	13	65.0	388	5	BP659175
298	13	65.0	351	5	BY325348	BY325348	C 370	13	65.0	390	5	BY002112
299	13	65.0	352	5	BY035237	BY035237	C 371	13	65.0	393	8	CC095028
300	13	65.0	352	5	BY131807	BY131807	C 372	13	65.0	393	2	BE428707
301	13	65.0	352	5	BY163415	BY163415	C 373	13	65.0	397	1	AA855818
302	13	65.0	352	6	CD632971	CD632971	C 374	13	65.0	401	1	AU306485
303	13	65.0	353	5	BY318513	BY318513	C 375	13	65.0	401	5	BY044461
304	13	65.0	354	5	BY313567	BY313567	C 376	13	65.0	402	1	AA051401
305	13	65.0	354	6	CD632937	CD632937	C 377	13	65.0	403	1	BF074116
306	13	65.0	354	6	CD632939	CD632939	C 378	13	65.0	403	7	CF087529
307	13	65.0	354	6	CD632967	CD632967	C 379	13	65.0	403	8	AZ489698
308	13	65.0	354	6	CD632970	CD632970	C 380	13	65.0	403	9	CE138536
309	13	65.0	355	5	BY073274	BY073274	C 381	13	65.0	404	5	BY313269
310	13	65.0	357	5	BY173850	BY173850	C 382	13	65.0	404	6	CB812156
311	13	65.0	357	6	CD632959	CD632959	C 383	13	65.0	405	1	BY159700
312	13	65.0	357	6	CD632966	CD632966	C 384	13	65.0	409	1	AI662221
313	13	65.0	358	5	BY162404	BY162404	C 385	13	65.0	409	2	BF451829
314	13	65.0	358	5	BY162625	BY162625	C 386	13	65.0	409	6	CB770170
315	13	65.0	358	6	CD632963	CD632963	C 387	13	65.0	410	1	AA458782
316	13	65.0	358	8	AQ769948	AQ769948	C 388	13	65.0	411	1	AI091792
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C 392	13	65.0	412	8	AZ895545	AZ895545	465	471	4	BG771129	BG771129
C 393	13	65.0	413	8	CO736681	CO736681	466	471	8	BZ418383	BZ418383
C 394	13	65.0	414	5	BO813816	BO813816	467	472	4	B1537154	B1537154
C 395	13	65.0	414	7	CF944141	CF944141	468	473	6	CD632954	CD632954
C 396	13	65.0	415	8	BH787879	BH787879	469	473	6	BM336370	BM336370
C 397	13	65.0	416	2	BF602603	BF602603	470	476	4	AU285533	AU285533
C 398	13	65.0	416	2	BF602738	BF602738	471	476	4	BI211145	BI211145
C 399	13	65.0	416	2	BB845184	BB845184	472	476	8	AZ218637	AZ218637
C 400	13	65.0	416	5	BY166678	BY166678	473	477	5	BU087552	BU087552
C 401	13	65.0	419	7	AA856394	AA856394	474	478	3	CR699294	CR699294
C 402	13	65.0	419	7	R77324	R77324	475	479	1	AL805031	AL805031
C 403	13	65.0	420	5	BY060383	BY060383	476	480	6	CB479348	CB479348
C 404	13	65.0	420	5	CG398611	CG398611	477	481	2	BE651293	BE651293
C 405	13	65.0	421	2	AM522374	AM522374	478	481	2	BF604425	BF604425
C 406	13	65.0	421	7	HO1106	HO1106	479	484	8	BZ424437	BZ424437
C 407	13	65.0	423	5	BY241256	BY241256	480	485	1	AV852924	AV852924
C 408	13	65.0	423	7	AM740542	AM740542	481	485	6	CA296622	CA296622
C 409	13	65.0	425	2	AM743590	AM743590	482	485	9	TAB7D01F	TAB7D01F
C 410	13	65.0	426	7	CK988465	CK988465	483	487	7	CF197155	CF197155
C 411	13	65.0	427	8	BH029503	BH029503	484	488	2	BE105778	BE105778
C 412	13	65.0	428	5	BY154329	BY154329	485	489	1	AI037618	AI037618
C 413	13	65.0	428	8	AO523785	AO523785	486	490	9	CE540312	CE540312
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C 415	13	65.0	429	2	BF420420	BF420420	488	491	5	BX103797	BX103797
C 416	13	65.0	430	8	BH379894	BH379894	489	492	8	AO721877	AO721877
C 417	13	65.0	431	4	BG988250	BG988250	490	493	7	CF362658	CF362658
C 418	13	65.0	431	4	BY181034	BY181034	491	495	1	AL602429	AL602429
C 419	13	65.0	432	5	BY040305	BY040305	492	496	7	CF571235	CF571235
C 420	13	65.0	432	7	CR878272	CR878272	493	497	8	BZ303129	BZ303129
C 421	13	65.0	432	8	AO737306	AO737306	494	497	8	AY613871	AY613871
C 422	13	65.0	433	5	BK640357	BK640357	495	500	3	BF452277	BF452277
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C 424	13	65.0	436	8	BY167306	BY167306	497	506	9	CNS0275A	CNS0275A
C 425	13	65.0	436	8	BZ270970	BZ270970	498	507	1	AI510089	AI510089
C 426	13	65.0	437	1	AL346770	AL346770	499	507	4	BG784081	BG784081
C 427	13	65.0	437	1	CK607551	CK607551	500	507	4	BM253598	BM253598
C 428	13	65.0	438	7	CN798528	CN798528	501	507	6	CD548174	CD548174
C 429	13	65.0	440	8	CC312975	CC312975	502	507	6	CD632948	CD632948
C 430	13	65.0	441	5	BX766490	BX766490	503	509	7	BM154341	BM154341
C 431	13	65.0	441	5	BP593537	BP593537	504	509	7	CM490828	CM490828
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C 433	13	65.0	442	2	BE374201	BE374201	506	511	4	BF946965	BF946965
C 434	13	65.0	444	5	BY252149	BY252149	507	512	8	AI515450	AI515450
C 435	13	65.0	446	2	BM641330	BM641330	508	512	8	AZ489691	AZ489691
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686	13	65.0	619	4	BJ318939	BY318939
687	13	65.0	619	6	BY743707	BY743707
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689	13	65.0	619	9	FR0007492	FR0007492
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694	13	65.0	622	8	CA959176	CA959176
695	13	65.0	622	8	AO249286	AO249286
696	13	65.0	622	8	AG094968	AG094968
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698	13	65.0	624	8	AO801662	AO801662
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703	13	65.0	627	2	BE376814	BE376814
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721	13	65.0	639	1	AV352209	AV352209
722	13	65.0	639	1	AZ211889	AZ211889
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739	13	65.0	651	9	BY743057	BY743057
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754	13	65.0	657	6	CD925858	G750.118P

  

755	13	65.0	658	6	BY754472	BY754472
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## ALIGNMENTS

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RESULT 1
CV350260 597 bp mRNA linear EST 27-SEP-2004
LOCUS MR2-SN0006-050600-002-b11 SN0006 Homo sapiens cDNA, mRNA sequence.
DEFINITION CV350260
ACCESSION CV350260
VERSION CV350260.1 GI:52700315
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

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TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. http://www.ludwig.org.br.
Location/Qualifiers
1. 597

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FEATURES
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ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 597;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTGGCAGCCCACTACTC 20
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RESULT 2
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LOCUS NL1-DJ12C Human NotI clones Homo sapiens genomic, genomic survey
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DEFINITION A0938853
ACCESSION A0938853
VERSION A0938853.1 GI:7215231
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Zabarovsky, E.R., Gizatullin, R., Podowski, R.M., Zabarovsky, V.V.,
Kie, L., Muravenko, O.V., Kozirev, S., Petrenko, L., Skobeleva, N.,
Li, J., Protopopov, A., Kashuba, V., Ernberg, I., Winberg, G. and
Wahlestedt, C.
TITLE NotI clones in the analysis of the human genome
JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)
MEDLINE 20175728
PUBMED 10710430
COMMENT Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.
Location/Qualifiers
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## FEATURES

## ORIGIN

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RESULT 3
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LOCUS rswpbd_002823.y1 swp Bombyx mori cDNA, mRNA sequence.
DEFINITION CX560425
ACCESSION CX560425
VERSION CX560425.1 GI:40944879
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori

```

```

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```

Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Bombycoidea; Bombycidae; Bombyx.  
1 (bases 1 to 586)

REFERENCE  
AUTHORS  
Xia, Q., Zhou, Z., Lu, C., Cheng, D., Dai, F., Li, B., Zhao, P., Zha, X.,  
Cheng, T., Chai, C., Pan, G., Xu, J., Liu, C., Lin, Y., Qian, J., Hou, Y.,  
Wu, Z., Li, G., Pan, M., Li, C., Shen, Y., Lan, X., Yuan, L., Li, T.,  
Xu, H., Yang, G., Wan, Y., Zhu, Y., Yu, M., Shen, W., Wu, D., Xiang, Z.,  
Yu, J., Wang, J., Li, R. Q., Shi, J. P., Li, H., Li, G. Y., Su, J. N.,  
Wang, X. L., Li, G. Q., Zhang, Z. J., Wu, Q. F., Li, J., Zhang, Q. P., Wei, N.,  
Xu, J. Z., Sun, H. B., Dong, L., Liu, D. Y., Zhao, S. L., Zhao, X. L.,  
Meng, Q. S., Lan, F. D., Huang, X. G., Li, Y. Z., Fang, F., Li, C. F.,  
Li, D. W., Sun, Y. Q., Zhang, Z. P., Yang, Z., Huang, Y. Q., Xi, Y., Qi, Q. H.,  
He, D. D., Huang, H. Y., Zhang, X. W., Wang, Z. Q., Li, W. J., Cao, Y. Z.,  
Mang, J., Ye, J., Ji, H., Li, S. T., Ni, P. X., Zhang, J. G., Zhang, Y.,  
Zhang, H. K., Ye, C., Wang, J., Wong, G. K. S. and Yang, H. M.  
A draft sequence for the genome of the domesticated silkworm  
(Bombyx mori)  
Unpublished (2004)  
Contact: Zhonghui Xiang  
Southwest Agricultural University  
Chongqing Baibei  
Tel: 86-23-68251123  
Fax: 86-23-68251128  
Email: xzh@swau.cq.cn.  
Location/Qualifiers

FEATURES  
source  
1..586  
/organism="Bombyx mori"  
/mol\_type="mRNA"  
/strain="Dazhao (P50)"  
/db\_xref="taxon:7091"  
/seq="mixed"  
/dev\_stage="Embryo (unfertilized)"  
/clone\_lib="swp"  
/note="Vector: pBluescript II SK(+)"

## ORIGIN

Query Match 80.0%; Score 16; DB 7; Length 586;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGGGACCCCAACTA 17  
|||||  
Db 217 TTGGGACCCCAACTA 232

RESULT 4  
CC876242 293 bp DNA linear GSS 29-JUL-2003  
LOCUS ZMMBB0194M08.r ZMMBB Zea mays genomic clone ZMMBB0194M08 3',  
DEFINITION genomic survey sequence.  
ACCESSION CC876242  
VERSION CC876242.1 GI:33306164  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 293)  
Yu, Y., Kim, H. R., Hatfield, J., Soderlund, C., Bharti, A. K., Messing, J.  
and Wing, R.  
Sequencing of the maize genome  
Unpublished (2003)  
Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088 USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: T7

BACKWARD: M13r  
Plate: 0194 row: M column: 08  
Seq primer: M13r  
Class: BAC ends.  
Location/Qualifiers

FEATURES  
source  
1..293  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBB0194M08"  
/lab\_host="DH10B"  
/clone\_lib="ZMMBBb"  
/note="Vector: pBeloBAC1; Site\_1: HindIII; Site\_2:  
HindIII; Zea mays L. sep. mays"

ORIGIN  
Query Match 75.0%; Score 15; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 11e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAAC 15  
|||||  
Db 251 TTGGGACCCCAAC 237

RESULT 5  
CU283937 328 bp DNA linear GSS 10-FEB-2004  
LOCUS ZMMBB0625L20f ZMMBB (HindIII) Zea mays genomic clone  
DEFINITION ZMMBB0625L20 5', genomic survey sequence.  
ACCESSION CU283937  
VERSION CU283937.1 GI:42498324  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 328)  
Bharti, A. K., Young, S., Kavchok, S., Kiefer, G., Bronzino, A. C.,  
Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.  
Sequencing of the maize genome at PGIR (2003c)  
Unpublished (2003)  
Contact: Bharti, A. K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Freilichuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 126.  
Location/Qualifiers

FEATURES  
source  
1..328  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBB0625L20"  
/lab\_host="E. coli DH10B"  
/clone\_lib="ZMMBB (HindIII)"  
/note="Vector: pCUGf; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
Query Match 75.0%; Score 15; DB 9; Length 328;  
Best Local Similarity 100.0%; Pred. No. 11e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAAC 15  
|||||

Db 244 TTCGGACCCACAC 230

RESULT 6  
AG306140/c 395 bp DNA linear GSS 02-JUN-2004  
LOCUS AG306140  
DEFINITION Mus musculus molossinus DNA, clone:MSM91-086P16.T7, genomic survey  
sequence.

ACCESSION AG306140  
VERSION AG306140.1 GI:47879094  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE BAC end Sequences of Library MSM91  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 395)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: hattori@gsc.riken.jp URL: http://ngp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the mouse BAC library MSM91. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsubura Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp  
PRIMERS

ORIGIN  
Sequencing : T7  
LIBRARY  
Vector : PBAC3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI

FEATURES  
source  
1..395  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSM91-086P16.T7"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_lib="MSM91 Mouse Male BAC Library"

ORIGIN  
Query Match 75.0%; Score 15; DB 9; Length 395;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGGACCCACACTA 17  
|||||  
Db 336 CCGGACCCACACTA 322

RESULT 7  
AI891392/c 457 bp mRNA linear EST 27-JUL-1999  
LOCUS AI891392  
DEFINITION 614021B04.x1 614 - root cDNA library from Walbot Lab Zea mays cDNA,  
mRNA sequence.  
ACCESSION AI891392  
VERSION AI891392.1 GI:5597294  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE 1 (bases 1 to 457)  
AUTHORS Walbot, V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
JOURNAL University  
COMMENT Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 614021 row: E column: 04.

FEATURES  
source  
1..457  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W23"  
/db\_xref="taxon:4577"  
/tissue\_type="root"  
/dev\_stage="3-4 days old"  
/lab\_host="XLOIR"  
/clone\_lib="614 - root cDNA library from Walbot Lab"  
/note="Organ: root; Vector: pBluescriptII SK+; Site 1:  
EcoRI; Site 2: XhoI; 3-4 days old root tissue from Walbot  
Lab (LM)"

ORIGIN  
Query Match 75.0%; Score 15; DB 1; Length 457;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGGACCCACACTA 17  
|||||  
Db 298 CCGGACCCACACTA 284

RESULT 8  
AZ170379 468 bp DNA linear GSS 29-AUG-2000  
LOCUS AZ170379  
DEFINITION SP 0116 A1 G11 T7A Strongylocentrotus purpuratus, purple sea  
urchin, sperm genomic BAC library Strongylocentrotus purpuratus  
genomic clone Plate=116 Col=21 Row=W, genomic survey sequence.  
ACCESSION AZ170379  
VERSION AZ170379.1 GI:8340747  
KEYWORDS GSS.  
SOURCE Strongylocentrotus purpuratus  
ORGANISM Strongylocentrotus purpuratus  
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
Echinoidea; Euechinoidea; Echinacea; Echinoida;  
Strongylocentrotidae; Strongylocentrotus.  
1 (bases 1 to 468)  
Cameron, R.A., Mahairas, G., Raetz, J.P., Martinez, P., Biondi, T.R.,  
Swartzell, S., Wallace, J.C., Pouska, A.J., Livingston, B.T.,  
Wray, G.A., Ettensohn, C.A., Lettrach, H., Britten, R.J., Davidson, E.H.  
and Hood, L.  
A sea urchin genome project: sequence scan, virtual map, and  
additional resources  
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
10920195  
Contact: Cameron, R.A., Davidson, E.H., Hood, L.  
Division of Biology 156-29  
California Institute of Technology  
Pasadena California 91125, USA  
Tel: (626) 395-8421  
Fax: (626) 793-3047  
Email: acameron@caltech.edu  
Plate: 116 row: M column: 21  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 468.



## FEATURES

Location/Qualifiers

1..468  
/organism="Strongylocentrotus purpuratus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7668"  
/clone\_plate=116 Col=21 Row=M  
/clone\_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"  
/note="Organ: sperm; Vector: BAC3.6; BAC clones in E-Coli DH10B"

## ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACTC 20  
DB 407 GACCCACACTACTC 421

## RESULT 9

BF610107/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BF610107 479 bp mRNA linear EST 07-MAY-2003  
NXSI\_054\_G10\_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA  
clone NXSI\_054\_G10\_5', mRNA sequence.  
BF610107  
BF610107.1 GI:11778429  
EST.  
Pinus taeda (loblolly pine)  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
1 (bases 1 to 479)  
Sederoff, R.  
Molecular Basis of Wood Formation in the Pine Megagenome  
Unpublished (2000)  
Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron\_sederoff@ncsu.edu, jerri\_johnson@ncsu.edu  
Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further  
information.  
Seq primer: T3.

## FEATURES

source

Location/Qualifiers  
1..479  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NXSI\_054\_G10"  
/tissue\_type="Xylem"  
/cell\_type="Side"  
/dev\_stage="Juvenile"  
/lab\_host="XLI-BIue"  
/clone\_lib="NXSI (Nsf Xylem Side wood Inclined)"  
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:  
XhoI. The library is from early (spring) wood, taken from  
three six-year old trees (three different genotypes), in  
the juvenile phase. These trees were induced to form side  
wood by bending to a 45 degree angle and tying them to the  
ground. Differentiating xylem was harvested from the sides  
of the inclined stems, and a mixture of all three  
genotypes was used for the library. oligo-dt primed cDNA  
was directionally cloned into the EcoRI-XhoI Bluescript SK  
vector arms. NOTE: The sequences contain a 'cDNA adapter'  
between the EcoRI site and the start of the EST. The  
adapter sequence is 'AATTCGCGACGAG'."

## ORIGIN

Query Match 75.0%; Score 15; DB 2; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACTC 20  
DB 18 GACCCACACTACTC 4

## RESULT 10

AM037206

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AM037206 496 bp mRNA linear EST 15-SEP-1999  
614021B04.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,  
mRNA sequence.  
AM037206  
AM037206.1 GI:5895960  
EST.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 496)  
Walbot, V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 614021 row: B column: 04.

## FEATURES

source

Location/Qualifiers  
1..496  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W23"  
/db\_xref="taxon:4577"  
/tissue\_type="root"  
/dev\_stage="3-4 days old"  
/lab\_host="XLOLR"  
/clone\_lib="614 - root cDNA library from Walbot Lab"  
/note="Organ: root; Vector: pBluescriptII SK+; Site 1:  
EcoRI; Site 2: XhoI; 3-4 days old root tissue from Walbot  
Lab (LM) "

## ORIGIN

Query Match 75.0%; Score 15; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGACCCACACTA 17  
DB 168 GCGGACCCACACTA 182

## RESULT 11

AZ170708

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AZ170708 549 bp DNA linear GSS 29-AUG-2000  
SP 0117.AL.H09.T7A Strongylocentrotus purpuratus, purple sea  
urchin, sperm genomic BAC library Strongylocentrotus purpuratus  
genomic clone Plate=117 Col=17 Row=0, genomic survey sequence.  
AZ170708  
AZ170708.1 GI:8341076  
GSS.  
Strongylocentrotus purpuratus  
Strongylocentrotus purpuratus  
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
Echinoidea; Euechinoidea; Echinacea; Echinoida;

REFERENCE 1 (bases 1 to 549)  
 AUTHORS Cameron, R.A., Mahaires, G., Raet, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehnach, H., Britten, R.J., Davidson, E.H., and Hood, L.  
 TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
 MEDLINE 20402566  
 PUBMED 10920195  
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L  
 Division of Biology 156-29  
 California Institute of Technology  
 Pasadena California 91125, USA  
 Tel: (626) 395-8421  
 Fax: (626) 793-3047  
 Email: acameron@caltech.edu  
 Plate: 117 row: O column: 17  
 Seq primer: 17  
 Class: BAC ends  
 High quality sequence stop: 549.  
 Location/Qualifiers  
 1..549  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7668"  
 /clone="Plate:117 Col:17 Row:O"  
 /clone\_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"  
 /note="Organ: sperm; Vector: BAC3.6; BAC clones in E-Coli DH10B"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 394 GACCCACACTACTC 408  
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 |||||

RESULT 12  
 CA772709/c 599 bp mRNA linear EST 03-DEC-2002  
 LOCUS 1083102.y1 HR85 islet Homo sapiens cDNA IMAGE:6133106 5',  
 DEFINITION mRNA sequence.  
 CA772709  
 ACCESSION CA772709.1 GI:26009976  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 599)  
 Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K., Lemishka, I., Scarsce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tesgareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Other\_ESTs: 1083102.x1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@wustl.edu)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 492.  
 Location/Qualifiers  
 1..599  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6133106"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"  
 /clone\_lib="HR85 islet"  
 /note="Organ: Pancreas; Vector: pRiuescript SK(-); Site:1;  
 NotI, Site:2; XhoI, cDNA made by oligo-dT priming.  
 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permut Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."

ORIGIN  
 Query Match 75.0%; Score 15; DB 6; Length 599;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 CGCGACCCACACTA 17  
 |||||  
 |||||

RESULT 13  
 CL934496 616 bp DNA linear GSS 14-SEP-2004  
 LOCUS OA\_ABA0044F03.r OA\_Aba Oryza australiensis genomic clone  
 DEFINITION OA\_ABA0044F03 3', genomic survey sequence.  
 CL934496  
 ACCESSION CL934496.1 GI:52063100  
 VERSION  
 KEYWORDS GSS.  
 SOURCE Oryza australiensis  
 ORGANISM Oryza australiensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eubartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 616)  
 Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
 Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
 OMAP Project  
 Unpublished (2004)  
 Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Plate: 0044 row: F column: 03  
 Seq primer: CAC TCA TTA GGC ACC CCA  
 Class: BAC ends.  
 Location/Qualifiers  
 1..616  
 /organism="Oryza australiensis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4532"  
 /clone="OA\_ABA0044F03"  
 /tissue\_type="young leaves"

TITLE  
 JOURNAL  
 COMMENT

/lab host="DH10B T1 phage resistant"  
/clone\_lib="OA\_Aba"  
/note="Vector: pGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 616;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACTC 20  
|||  
Db 140 GACCCAACTACTC 154

RESULT 14  
AQ325164/c 624 bp DNA linear GSS 08-JAN-1999  
LOCUS mgxb0020P04r CUGI Rice Blast BAC library Magnaporthe grisea genomic  
DEFINITION clone mgxb0020P04r, genomic survey sequence.  
ACCESSION AQ325164.1 GI:4117016  
VERSION  
KEYWORDS  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM  
REFERENCE 1 (bases 1 to 624)  
AUTHORS Yu, Y.; Zhu, H.; Boyd, C.A.; Gaudette, B.; Gayle, A.; Kingsbury, R.;  
Phillips, K.; Sasinowski, M.; Wing, R.A. and Dean, R.A.  
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea  
Genome  
JOURNAL Unpublished (1998)  
COMMENT Contact: Dean RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson University, Clemson, SC 29634  
Tel: 864 656 5737  
Fax: 864 656 4293  
Email: rdean@clemson.edu  
Seq primer: GGAACAGCTATGACCATG  
Class: BAC ends  
High quality sequence stop: 395.  
Location/Qualifiers

FEATURES  
source  
1..624  
/organism="Magnaporthe grisea"  
/mol\_type="genomic DNA"  
/strain="70-15"  
/db\_xref="taxon:148305"  
/clone="mgxb0020P04r"  
/issue\_type="Protoplasts"  
/lab\_host="E. coli DH10B"  
/clone\_lib="CUGI Rice Blast BAC library"  
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;  
Rice blast is one of the most devastating fungal diseases  
of rice world wide. It is a filamentous ascomycete with  
a haploid genome (n=7) of approximately 40 Mbp. Rice  
blast is an important model fungal pathogen for studying  
numerous aspects of the fungal-host interaction. In  
order to facilitate genome wide analysis, a BAC library  
containing 9216 clones with an average insert size of 130  
kbp was constructed. This library represents greater  
than 25X genome coverage. High density colony filters  
are available upon request."

ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 624;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACTC 20  
|||  
Db 248 GACCCAACTACTC 234

RESULT 15  
AQ286947/c 635 bp DNA linear GSS 03-DEC-1998  
LOCUS mgxb0015C17r CUGI Rice Blast BAC library Magnaporthe grisea genomic  
DEFINITION clone mgxb0015C17r, genomic survey sequence.  
ACCESSION AQ286947  
VERSION AQ286947.1 GI:3948033  
KEYWORDS  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM  
REFERENCE 1 (bases 1 to 635)  
AUTHORS Yu, Y.; Zhu, H.; Boyd, C.A.; Gaudette, B.; Gayle, A.; Kingsbury, R.;  
Phillips, K.; Sasinowski, M.; Wing, R.A. and Dean, R.A.  
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea  
Genome  
JOURNAL Unpublished (1998)  
COMMENT Contact: Dean RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson University, Clemson, SC 29634  
Tel: 864 656 5737  
Fax: 864 656 4293  
Email: rdean@clemson.edu  
Seq primer: GGAACAGCTATGACCATG  
Class: BAC ends  
High quality sequence start: 18  
High quality sequence stop: 464.  
Location/Qualifiers

FEATURES  
source  
1..635  
/organism="Magnaporthe grisea"  
/mol\_type="genomic DNA"  
/strain="70-15"  
/db\_xref="taxon:148305"  
/clone="mgxb0015C17r"  
/issue\_type="Protoplasts"  
/lab\_host="E. coli DH10B"  
/clone\_lib="CUGI Rice Blast BAC library"  
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;  
Rice blast is one of the most devastating fungal diseases  
of rice world wide. It is a filamentous ascomycete with  
a haploid genome (n=7) of approximately 40 Mbp. Rice  
blast is an important model fungal pathogen for studying  
numerous aspects of the fungal-host interaction. In  
order to facilitate genome wide analysis, a BAC library  
containing 9216 clones with an average insert size of 130  
kbp was constructed. This library represents greater  
than 25X genome coverage. High density colony filters  
are available upon request."

ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 635;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACTC 20  
|||  
Db 271 GACCCAACTACTC 257

RESULT 16  
B2247695 650 bp DNA linear GSS 12-OCT-2002  
LOCUS CH230-408D6 TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone  
DEFINITION CH230-408D6, genomic survey sequence.  
ACCESSION B2247695  
VERSION B2247695.1 GI:23908877  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus  
1 (bases 1 to 650)  
Zhao, S., Shetty, U., Shatsman, S., Tsagaye, G., Geer, K.,  
Shvartsbeyn, A., Gebregiorgis, E., Overton, L., Russell, D., Chen, D.,  
Ri99s, F., de Jong, P. and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 MboI segment  
Unpublished (1999)  
Other GSSs: CH230-408D6.TV8  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/or ordering information.htm). BAC end  
page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 408 row: D column: 6  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source  
Location/Qualifiers

1..650  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SNHsd/MCW"  
/db\_xref="taxon:10116"  
/clone="CH230-408D6"  
/sex="Female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 2"  
/note="Vector: pPARAC1.3; Site\_1: MboI; Site\_2: MboI;  
CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by  
Pieter de Jong"

Query Match 75.0%; Score 15; DB 8; Length 650;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GACCCAACTACTCTC 20  
Dd 423 GACCCAACTACTCTC 437

RESULT 17  
LOCUS CG319811 721 bp DNA linear GSS 26-AUG-2003  
DEFINITION OGV551TV\_ZM\_0.7.1.5\_KB\_Zea\_mays\_genomic\_clone\_ZMM5MA0523105,  
genomic survey sequence.  
ACCESSION CG319811.  
VERSION CG319811.1 GI:34237077  
KEYWORDS GSS  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 721)  
Whiteley, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, V.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGV551TV  
Contact: Cathy Whiteley  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Fax: 301-838-0208  
Email: whiteley@tigr.org  
Seq primer: TP  
Class: sheared ends.  
Location/Qualifiers

1..721  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZMM5MA0523105"  
/clone="ZM\_0.7.1.5\_KB"  
/note="Vector: pBCK-; Site\_1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 721;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACTCTC 20  
Dd 41 GACCCAACTACTCTC 55

RESULT 18  
LOCUS CV435578/c 784 bp mRNA linear EST 29-SEP-2004  
DEFINITION 59138.1 Suspension culture Solanum tuberosum cDNA clone 59138 5',  
mRNA sequence.  
ACCESSION CV435578  
VERSION CV435578.1 GI:52844868  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 784)  
Pflum, B., Rothwell, C., Sardana, R., Griffiths, R., Laque, M., De  
Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.  
Generation of ESTs from potato suspension cultures  
Unpublished (2004)  
Contact: Barry Pflum  
The Canadian Potato Genome Project - BioAtlantech  
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
Email: bflum@bioatlantech.nb.ca  
Seq primer: T3.  
Location/Qualifiers

FEATURES  
source

1..784  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultiivar="Shepody"  
/db\_xref="taxon:4113"  
/clone="59138"  
/tissue\_type="Callus-derived suspension culture"  
/lab\_host="XL10-Gold"  
/clone\_lib="Suspension culture"  
/note="Vector: pBluescript II SK(+) XR; Site\_1: EcoRI;  
Site\_2: XhoI; supplier: Developmental series. Callus was  
induced from Shepody. Clone 1756, sterile stem sections by  
culture on Callus Induction Medium (CIM), comprised of MS  
medium (pH 5.6) containing 10 mg/L thiamine-HCL, .01 mg/L  
kinetin and 3 mg/L 2,4-D solidified with .8% (w/v)  
phytagar. Suspensions were induced by placing flasks from  
the plates into 125 ml Erlenmeyer flasks with liquid CIM  
(no phytagar) at a density of 10% (w/v) in volumes of  
approximately 30-35 ml. Cells were subcultured weekly by  
transfer to fresh media, with the density remaining at 10%  
(w/v) and the volume remaining around 30 ml. Cells were  
collected for RNA isolations and library construction 5  
days after subculture."

ORIGIN

Query Match 75.0%; Score 15; DB 7; Length 784;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACTACT 19  
 |||||  
 Db 632 CGACCAACTACT 618

RESULT 19  
 CL907067 787 bp DNA linear GSS 14-SEP-2004  
 LOCUS OA\_ABA0005M21.f OA\_ABA Oryza australiensis genomic clone  
 DEFINITION OA\_ABA0005M21.5, genomic survey sequence.  
 ACCESSION CL907067  
 VERSION CL907067.1 GI:52015946  
 KEYWORDS GSS.  
 SOURCE Oryza australiensis  
 ORGANISM Oryza australiensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Erihartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 787)  
 REFERENCE Klm.H., Yu.Y., Stum.D., Yost.D., Rao.K., Luo.M., Jetty.R.,  
 Koldra.D., Muller.C., Hatfield.J., Soderlund.C. and Wing.R.  
 AUTHORS OMAP Project  
 TITLE Unpublished (2004)  
 JOURNAL Contact: Rod A. Wing  
 COMMENT Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TC4 CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Plate: 0005 ROW: M COLUMN: 21  
 Seq primer: TAA TAC GAC TCA CTA TAG GG  
 Class: BAC ends.

FEATURES  
 source  
 1..787  
 /organism="Oryza australiensis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4532"  
 /clone="OA\_ABA0005M21"  
 /issue\_type="Young leaves"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="OA\_Aba"  
 /note="Vector: pGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCAACTACTC 20  
 |||||  
 Db 731 GACCAACTACTC 745

RESULT 20  
 BG299847 798 bp mRNA linear EST 18-OCT-2001  
 LOCUS HVSME0022B19f Hordeum vulgare seedling shoot EST library  
 DEFINITION HVCDNA0001 (Cold stress) Hordeum vulgare subsp. vulgare cDNA clone  
 HVSME0022B19f, mRNA sequence.  
 ACCESSION BG299847  
 VERSION BG299847.2 GI:16256940  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE  
 AUTHORS Wing.R., Close.T.J., Kleinhofs.A., Wise.R., Begum.D., Friesch.D.,  
 Yu.Y., Henry.D., Palmer.M., Rambo.T., Simmons.J., Oates.R.,  
 Choi.D.W., Fenton.R.D. and Main.D.  
 TITLE Development of a genetically and physically anchored EST resource  
 for barley genomics: Morex cold-stressed seedling shoot cDNA  
 library  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 21, 2001 this sequence version replaced gi:13087684.  
 CONTACT: Wing RA  
 CLEMSON UNIVERSITY GENOMICS INSTITUTE  
 100 JORDAN HALL, CLEMSON, SC 29634, USA  
 TEL: 864 656 7288  
 FAX: 864 656 4293  
 EMAIL: rwing@clermson.edu  
 TOTAL HQ BASES = 280  
 SEQ PRIMER: AATTACCTCCTCAAGG  
 HIGH QUALITY SEQUENCE STOP: 628.

FEATURES  
 source  
 1..798  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Morex"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="HVSME0022B19f"  
 /issue\_type="Seedling shoot"  
 /lab\_host="TTC121"  
 /clone\_lib="Hordeum vulgare seedling shoot EST library  
 HVCDNA0001 (Cold stress)"  
 /note="Vector: LambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
 Seeds were surface sterilized then germinated under aseptic  
 conditions in the dark at room temperature on filter paper  
 with water, nystatin and cefotaxime in covered  
 crystallization dishes. Five-day old seedlings were  
 incubated at 50C for 2 days. Shoots were then harvested,  
 total RNA was prepared, poly(A) RNA was purified, one  
 primary unamplified cDNA library was made, and 600000 pfu  
 were in vivo excised to give plasmid library  
 phagemids. These steps were performed in the TU Close  
 Laboratory at the University of California, Riverside  
 (Choi, Close, Fenton). Phagemids were plated and picked at  
 the Clemson University Genomics Institute (CUGI) (Begum,  
 Palmer, Friesch, Atkins and Wing). Plasmid DNA  
 preparations, DNA sequencing and sequence analysis were  
 performed at CUGI (Wing, Yu, Friesch, Henry, Simmons,  
 Oates, Rambo, Main). The sequence has been trimmed to  
 remove vector sequence and contains a minimum of 100 bases  
 of phred value 20 or above. For more details on library  
 preparation and sequence analysis see  
 http://www.genome.clemson.edu/projects/barley. To order  
 this clone see http://www.genome.clemson.edu/orders also  
 see Close TU, Wing R, Kleinhofs A, Wise R (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (http://wheat.pw.usda.gov/gsgpages/bgn/31/cover.html)"

ORIGIN  
 Query Match 75.0%; Score 15; DB 4; Length 798;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCGGACCAACT 16  
 |||||  
 Db 206 TCGGACCAACT 220

RESULT 21  
 BG441796/c

LOCUS BG441796 854 bp mRNA linear EST 15-MAR-2001  
 DEFINITION GA\_Ea0014L03f Gossypium arboreum 7-10 dpa fiber library Gossypium  
 arboreum cDNA clone GA\_Ea0014L03f, mRNA sequence.  
 ACCESSION BG441796  
 VERSION BG441796.1 GI:13351448  
 KEYWORDS EST.  
 SOURCE Gossypium arboreum  
 ORGANISM Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eustosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 854)  
 Wing, R.A., Fritsch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
 Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
 An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)  
 JOURNAL Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7268  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Seq primer: TAATACGACTCACTATAGG  
 High quality sequence start: 2  
 High quality sequence stop: 734.  
 Location/Qualifiers  
 1..854  
 /organism="Gossypium arboreum"  
 /mol\_type="mRNA"  
 /strain="AKA"  
 /cultivar="8400"  
 /db\_xref="taxon:29729"  
 /clone="GA\_Ea0014L03f"  
 /issue\_type="Fibers isolated from bolls harvested 7-10  
 dpa"  
 /lab\_host="E. coli"  
 /clone\_1lb="Gossypium arboreum 7-10 dpa fiber library"  
 /note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
 Query Match 75.0%; Score 15; DB 4; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGCGACCCGACAC 15  
 Db 596 TTCCGCGACCCGACAC 582

RESULT 22  
 CG463371 871 bp DNA linear GSS 17-SEP-2003  
 LOCUS PUJ099DB\_ZM\_0.6\_1.0\_KB\_Zea\_mays genomic clone ZMMBTa0598A18,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG463371  
 VERSION CG463371.1 GI:34848358  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 871)  
 Whitefaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and  
 Benneken, J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 JOURNAL Other\_GSSs: PUJ099TBB  
 COMMENT Contact: Cathy Whitefaw  
 TIGR

FEATURES  
 source  
 Location/Qualifiers  
 1..871  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBTa0598A18"  
 /clone\_1lb="ZM\_0.6\_1.0\_KB"  
 /note="Vector: pCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cor selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GACCCAACTACTC 20  
 Db 434 GACCCAACTACTC 420

RESULT 23  
 CC096047 873 bp DNA linear GSS 16-APR-2003  
 LOCUS CSU-K34.114P10.SP6 CSU-K34 Aedes aegypti genomic clone  
 DEFINITION CSU-K34.114P10, genomic survey sequence.  
 ACCESSION CC096047  
 VERSION CC096047.1 GI:23959126  
 KEYWORDS GSS.  
 SOURCE Aedes aegypti (yellow fever mosquito)  
 ORGANISM Aedes aegypti  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;  
 Stegomyia.  
 1 (bases 1 to 873)  
 Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.  
 End sequencing of Aedes aegypti BACs  
 Unpublished (2003)  
 JOURNAL Other\_GSSs: CSU-K34.114P10.T7  
 COMMENT Contact: Brendan Loftus  
 Department of Eukaryotic Genomics  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-3543  
 Fax: 301-838-0208  
 Email: emna@tigr.org  
 Library was provided by Susan Brown and Dennis Knudson at Colorado  
 State University.  
 Seq primer: SP6  
 Class: BAC ends.  
 Location/Qualifiers  
 1..873  
 /organism="Aedes aegypti"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7159"  
 /clone="CSU-K34.114P10"  
 /clone\_1lb="CSU-K34"  
 /note="Vector: pBAC3.6; Site\_1: EcoRI; Source DNA: Aedes  
 aegypti; strain unknown (derived from freshly hatched  
 larvae at the Virus Research Centre, Poona, India.  
 Reference: SINGH, K. R. P., 1967 Cell cultures derived  
 from larvae of Aedes albopictus (Skuse) and Aedes aegypti  
 (L.). Current Science 36: 506-508; ATC-10 cell line ATCC  
 CCL-125"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 873;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACTC 20  
|||||  
742 GACCCACACTACTC 728

Db 455 GACCCACACTACTC 469

RESULT 24  
CG117887 876 bp DNA linear GSS 20-AUG-2003  
LOCUS PUPOP4STD.ZM.0.6.1.0 KB Zea mays genomic clone ZMMBTa0697H18,  
DEFINITION genomic survey sequence.  
ACCESSION CG117887 GI:34001324  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 876)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennerzen,J.  
Bennetzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUPOP45TB  
Contact: Cathy WhiteLaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@tigr.org  
Seq primer: TF  
Class: sheared ends.  
FEATURES  
source location/Qualifiers  
1..876  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBTa0697H18"  
/clone\_lib="ZM\_0.6.1.0 KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cot selected genomic DNA library"

ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 876;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACTC 20  
|||||  
455 GACCCACACTACTC 469

Db 455 GACCCACACTACTC 469

RESULT 25  
BG422240 879 bp mRNA linear EST 14-MAR-2001  
LOCUS 602446874P1.NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4565315.5,  
DEFINITION mRNA sequence.  
ACCESSION BG422240 GI:13328746  
VERSION BG422240.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 879)  
Mammalia http://mgc.nci.nih.gov/.  
NIN-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: L16M1312 row: d column: 20  
High quality sequence stop: 668.  
location/Qualifiers  
1..879  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4565315"  
/clone\_lib="NIH\_MGC\_14"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: Kidney; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 75.0%; Score 15; DB 4; Length 879;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCACAC 15  
|||||  
856 TTCCGACCCACAC 870

Db 856 TTCCGACCCACAC 870

RESULT 26  
CC438014 942 bp DNA linear GSS 20-MAY-2003  
LOCUS PUHGJ10TD.ZM.0.6.1.0 KB Zea mays genomic clone ZMMBTa445A20,  
DEFINITION genomic survey sequence.  
ACCESSION CC438014 GI:30936685  
VERSION CC438014.1  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 942)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennetzen,J.  
Bennetzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUHGJ10TB  
Contact: Cathy WhiteLaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@tigr.org  
Seq primer: TF  
Class: sheared ends.  
FEATURES  
source location/Qualifiers  
1..942  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 942;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 713 GACCCACACTACTC 727  
 6 GACCCACACTACTC 20  
 |||||  
 /clone\_1ib="ZM 0.6 1.0 KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 942;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 713 GACCCACACTACTC 727  
 6 GACCCACACTACTC 20  
 |||||  
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 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

RESULT 27  
 BZ697242 945 bp DNA linear GSS 19-FEB-2003  
 LOCUS PUBMO20TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa089D15,  
 DEFINITION genomic survey sequence.  
 ACCESSION BZ697242  
 VERSION BZ697242.1 GI:28417089  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 945)  
 WhiteLaw.C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Bennecken,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

REFERENCE  
 AUTHORS  
 WhiteLaw.C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Bennecken,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
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 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

TITLE  
 JOURNAL  
 COMMENT  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 1..945  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_1ib="ZM 0.6 1.0 KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
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## ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 945;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 844 GACCCACACTACTC 858  
 6 GACCCACACTACTC 20  
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 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 945;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 844 GACCCACACTACTC 858  
 6 GACCCACACTACTC 20  
 |||||  
 /clone\_1ib="ZM 0.6 1.0 KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

RESULT 28  
 CG117886/c 955 bp DNA linear GSS 20-AUG-2003  
 LOCUS PUFOP45TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0697H18,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG117886  
 VERSION CG117886.1 GI:34001323  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 955)  
 WhiteLaw.C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Bennecken,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

REFERENCE  
 AUTHORS  
 WhiteLaw.C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Bennecken,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

TITLE  
 JOURNAL  
 COMMENT  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 1..955  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_1ib="ZM 0.6 1.0 KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 955;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 540 GACCCACACTACTC 526  
 6 GACCCACACTACTC 20  
 |||||  
 /clone\_1ib="ZM 0.6 1.0 KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 955;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 540 GACCCACACTACTC 526  
 6 GACCCACACTACTC 20  
 |||||  
 /clone\_1ib="ZM 0.6 1.0 KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

RESULT 29  
 CC438010/c 968 bp DNA linear GSS 20-MAY-2003  
 LOCUS PUGGJ10TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa445A20,  
 DEFINITION genomic survey sequence.  
 ACCESSION CC438010  
 VERSION CC438010.1 GI:30936679  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 968)  
 WhiteLaw.C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Bennecken,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

## ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 968;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 540 GACCCACACTACTC 526  
 6 GACCCACACTACTC 20  
 |||||  
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 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 968;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 540 GACCCACACTACTC 526  
 6 GACCCACACTACTC 20  
 |||||  
 /clone\_1ib="ZM 0.6 1.0 KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

FEATURES  
 source  
 1..968  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"

FEATURES  
 source  
 1..968  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"



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/clone="ZM8BTA445A20"
/clone_lib="ZM_0.6.1.0_KB"
/nc="Vector: PCR4-TOPO, Site 1: EcoRI, 0.6-1.0 kb high
cot selected genomic DNA library"

ORIGIN
Query Match      75.0%; Score 15; DB 8; Length 968;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GACCCACACTACTC 20
|||||
Db      621 GACCCACACTACTC 607

RESULT 30
BG962370      989 bp      mRNA      linear      EST 12-JUN-2001
LOCUS        602827180P1_NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4982250 5',
DEFINITION   mRNA sequence.
ACCESSION    BG962370.1 GI:14350007
VERSION      BG962370.1
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 989)
/clone_lib="nc:nci.nih.gov/"
/nc="NIH-MGC http://mgc.nci.nih.gov/"
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10984 row: 0 column: 19
High quality sequence stop: 616.
Location/Qualifiers
1. 989
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4982250"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_C024"
/nc="NIH-MGC http://mgc.nci.nih.gov/"
/nc="NIH-MGC http://mgc.nci.nih.gov/"
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match      75.0%; Score 15; DB 4; Length 989;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GCGACCCACACTAC 18
|||||
Db      841 GCGACCCACACTAC 855

RESULT 31
CG757040      1192 bp      DNA      linear      GSS 24-OCT-2003
LOCUS        P052-1-H01.2a Ppa EcORI BAC library Pristionchus pacificus genomic,
DEFINITION   genomic survey sequence.
ACCESSION    CG757040
VERSION      CG757040.1 GI:37985205

FEATURES
source

```

```

KEYWORDS
SOURCE      GSS.
ORGANISM    Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS     Srinivasan,J., Sinz,W., Jesse,T., Wiggers-perelbolle,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
JOURNAL     22835951
MEDLINE     12884007
PUBMED
COMMENT     Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany.
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1. 1192
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcORI BAC Library"
/nc="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN
Query Match      75.0%; Score 15; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GACCCACACTACTC 20
|||||
Db      597 GACCCACACTACTC 611

RESULT 32
BIS61676      1633 bp      mRNA      linear      EST 05-SEP-2001
LOCUS        603255804P1_NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5298097 5',
DEFINITION   mRNA sequence.
ACCESSION    BIS61676
VERSION      BIS61676.1 GI:15448990
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1633)
/clone_lib="nc:nci.nih.gov/"
/nc="NIH-MGC http://mgc.nci.nih.gov/"
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11754 row: h column: 02
High quality sequence stop: 126.
Location/Qualifiers
1. 1633
/organism="Homo sapiens"

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/mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5298097"  
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 /clone\_id="NH\_MGC\_97"  
 /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTVN-3', size selected for average insert size 2.2 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 75.0%; Score 15; DB 4; Length 1633;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCAACAC 15  
 |||||  
 Db 673 TTCCGACCAACAC 687

RESULT 33  
 BI049394 183 bp mRNA linear EST 15-JUN-2001  
 LOCUS CM2-GN0295-020101-656-c10 GN0295 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BI049394  
 VERSION BI049394.1 GI:14456924  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 183)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL MEDLINE 20202663  
 PUBMED 10737800

COMMENT  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&ct2=CM2-GN0295-020101-656-c10&ct3=2001-01-02&ct4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 30  
 High quality sequence stop: 180.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_id="GN0295"  
 /note="Organ: Placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning

## FEATURES

source

## ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCAACTACT 19  
 |||||  
 Db 151 GACCAACTACT 164

RESULT 34  
 BG988270 267 bp mRNA linear EST 13-JUN-2001  
 LOCUS PM0-HT1167-120101-001-G07 HT1167 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BG988270  
 VERSION BG988270.1 GI:14392340  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 267)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL MEDLINE 20202663  
 PUBMED 10737800

COMMENT  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&ct2=PM0-HT1167-120101-001-G07&ct3=2001-01-12&ct4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 8  
 High quality sequence stop: 77.  
 Location/Qualifiers  
 1..267  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_id="HT1167"  
 /note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## FEATURES

source

products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	3	CGGACCCCACT 16
Dp	3	CGGACCCCACT 16
RESULT 35		
AV269536		
LOCUS		
DEFINITION	musculus CDNA clone 493054J09 3', mRNA sequence.	
ACCESSION	AY269536	
VERSION	AY269536.1	GI:6257573
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Euharvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus. 1 (bases 1 to 276)	
AUTHORS	Konno,H., Aitawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Satou,K., Shibata,K., Shibaeta,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateono,M., Tomiinga,N., Tounoda,Y., Watanishi,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	
TITLE	Riken Mouse ESTs (Konno,H., et al. 1999)	
JOURNAL	unpublished (1999)	
COMMENT	Contact: Yoshihide Hayashizaki	

**FEATURES**

**SOURCE**

genome-resgsc.riken.jp/, URL: <http://genome-gsc.riken.jp/>, Iizawa, M., Matsuaki, M., Ozawa, K., Tanaka, T., Yoneda, Y., Saito, Y., Carninci, P., Muramatsu, M., Okazaki, Y. and Additional sequencing: A method for DNA sequencing using RNA sequencing. *Natl. Acad. Sci. U.S.A.* 95 (7), 3455-3460 (1998) Katsunari, T., Akiyama, J., Shibata, K., Iizawa, M., Kawai, J., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Yamaoka, Y. and Hayashizaki, Y. Gene expression analysis by high-throughput plasmid preparation and sequencing. *Nat. Genet.* 9 (5), 463-470 (1999) Iizawa, M., Tanaka, T., Okazaki, Y., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Efficient full-length cDNA cloning. *Methods Enzymol.* 303, 99-114 (2003) To visit our web site (<http://genome-rtc.riken.go.jp>) for details.

Location/Qualifiers

1. 276

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="4930543J09"

/sex="male"

/tissue\_type="testis"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_idb="RIKEN full-length enriched, adult male testis (DH10B)"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5', GAAGAGAAGATCCAGAGCTCTTTTTTTTTTTTTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAAGAGAATCTCAGATTAAATTAATTCCTCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pInscript KS(+) after bulk excision from Lambda FLC 1. Cloning sites, 5' end: SalI; 3' end: BamHI."

Query Match	70.0%	Score 14	DB 1	Length 276
Best Local Similarity	100.0%	Pred. No. 4.6e+02		
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	6	GACCCAACTACTACT 19		
Db	92	GACCCAACTACTACT 105		
RESULT 36				
CO213401/c				
LOCUS	CO213401	281 bp	mRNA	linear
DEFINITION	WS000928.B21_I24 IS-B-N-A-10 <i>Picea engelmannii</i> x <i>Picea sitchensis</i>			EST 22-JUN-2004
ACCESSION	CNNA clone WS000928_I24 3', mRNA sequence.			
VERSION	CO213401			
KEYWORDS	CO213401.1 GI:49025847			
SOURCE	EST.			
ORGANISM	<i>Picea engelmannii</i> x <i>Picea sitchensis</i>			
	<i>Picea engelmannii</i> x <i>Picea sitchensis</i>			

FEATURES

SOURCE

Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C.,  
 Riand, K. and Bohlmann, J.  
 The spruce transcriptome: Analysis of expressed sequence tags from  
 multiple cDNA libraries  
 Unpublished (2004)  
 Contact: Joerg Bohlmann  
 Genome BC forest genomics program  
 University of British Columbia  
 UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,  
 Vancouver, British Columbia, Canada, V6T 1Z3  
 Tel: 1-604-822-0282  
 Fax: 1-604-822-6097  
 Email: bohlmann@interchange.ubc.ca  
 Plate: MS00928 row: I column: 24  
 High quality sequence steps: 281.  
 Location/Qualifiers  
 1..281  
 /organism="Picea engelmannii x Picea sitchensis"  
 /mol\_type="mRNA"  
 /cultivar="Fal-1028"  
 /db\_xref="taxon:273280"  
 /clone="MS00928.124"  
 /sex="Hermaphrodite"  
 /lab\_host="E. coli DH10B cells"  
 /lab\_1ib="HS-B-N-A-10"  
 /note="Organ: Bark (with phloem and cambium attached) from  
 one year old clonal trees grown under greenhouse  
 conditions in standard potting soil mixture; Vector:  
 pluscript II SK (+) XR; Site 1: EcorI (5' end of cDNA) ;  
 Site 2: XhoI (3' end of cDNA); Bark was wounded using  
 razor blades along the entire length of the tree at 5 mm  
 intervals on opposite sides of the trunk. The same trees  
 were also sprayed with a 0.01% (v/v) methyl jasmonate  
 solution resuspended in 0.1% (v/v) tween 20 (~50mls per  
 tree). Bark tissue with phloem attached was harvested 3



FEATURES  
source  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcw019 row: L column: 23  
Seq primer: T3.  
Location/Qualifiers

1..315  
/organism="Magnaporthe grisea"  
/mol\_type="rRNA"  
/strain="CP987"  
/db\_xref="taxon:148305"  
/clone="mgcw019x123"  
/sex="Mati-1 hermaphrodite"  
/tissue\_type="Mycelium"  
/dev\_stage="Day 5 post-inoculation"  
/clone\_lib="RCM Lambda Zap Express Library"  
/note="Vector: pBluescript excised from Lambda Zap Express; Site\_1: EcoRI; Site\_2: XhoI; Day 5 post-inoculation mRNA prepared from Magnaporthe grisea grown at 23C in the dark with constant gyratory shaking 100 rpm in Vogel's minimal medium containing 0.5% isolated rice cell walls as the sole carbon source. Library provided by Sheng-Cheng Wu. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 315;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACT 19  
|||||  
Db 289 GACCCAACTACT 302

RESULT 39  
CG124493/c 319 bp DNA linear GSS 20-AUG-2003  
LOCUS PUGG62TD ZM 0.6 1.0 KB zea mays genomic clone ZMMBT0660L03,  
DEFINITION genomic survey sequence.  
ACCESSION CG124493 GI:34007930  
VERSION CG124493.1  
KEYWORDS GSS.  
SOURCE zea mays  
ORGANISM zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 319)  
Whiteaw,C.A., Quackenbush,J., Van Aken,S., Utecherack,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennerzen,J.

TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUGG62TRB  
CONTACT: Cathy Whiteaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteaw@tigr.org  
Seq primer: TP  
Class: sheared ends.

FEATURES  
source  
1..319  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"

/clone="ZMMBT0660L03"  
/clone\_lib="ZM 0.6 1.0 KB"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
COT selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 319;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTC 20  
|||||  
Db 202 ACCCAACTACTC 189

RESULT 40  
CL957629/c 336 bp DNA linear GSS 21-SEP-2004  
LOCUS OaIFCC036262 Oryza sativa Express Library Oryza sativa (Indica  
DEFINITION cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL957629 GI:52370011  
VERSION CL957629  
KEYWORDS GSS.  
SOURCE Oryza sativa (Indica cultivar-group)  
ORGANISM Oryza sativa (Indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 336)  
Ma,L., Wang,C.J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,  
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,  
Mong,G.K.S., Deng,X.W. and Wang,J.

An analysis of transcriptional regulation of the rice genome and  
its comparison to Arabidopsis  
Unpublished (2004)  
CONTACT: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.

FEATURES  
source  
1..336  
/organism="Oryza sativa (Indica cultivar-group)"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:39946"  
/clone\_lib="Oryza sativa Express Library"  
/note="Oryza sativa exon trapped genomic sequences "

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 336;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACTACT 18  
|||||  
Db 150 CGACCAACTACT 137

RESULT 41  
CA652219/c 337 bp mRNA linear EST 24-NOV-2002  
LOCUS wreln.pk0112.f12 wreln Triticum aestivum cDNA clone  
DEFINITION wreln.pk0112.f12 5' end, mRNA sequence.  
ACCESSION CA652219 GI:25230744  
VERSION CA652219.1  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 337)  
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
 Maio, G., Caraher, N. and Hanafey, M.K.  
 DuPont Wheat CNA Sequence  
 Unpublished (2002)  
 Contact: Scott V. Tingey  
 Crop Genetics  
 E. I. DuPont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingey@usa.dupont.com  
 Seq primer: M3.

FEATURES  
 source  
 1. .337  
 /location/Qualifiers  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4565"  
 /clone="wreln.pk0112.f12"  
 /tissue\_type="root"  
 /clone\_lib="wreln"  
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:  
 XhoI; Wheat (Triticum aestivum L.) root; normalized from  
 wre1 library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 6; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCAACACTACTC 20  
 |||||  
 221 ACCCAACACTACTC 208

Db 221 ACCCAACACTACTC 208

RESULT 42  
 CF435681 347 bp mRNA linear EST 04-SEP-2003  
 LOCUS EST672026 normalized cDNA library of onion Allium cepa cDNA clone  
 ACAB249, mRNA sequence.  
 CF435681  
 CF435681.1 GI:34458371  
 EST.  
 Allium cepa (onion)  
 Allium cepa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
 Allium.  
 1 (bases 1 to 347)  
 Havey, M.J., Cheung, F., Van Aken, S., Uterback, T. and Town, C.D.  
 Expressed Sequence Tags from a normalized library of mixed onion  
 tissues (Allium cepa)  
 Unpublished (2003)  
 Contact: Havey MJ  
 Department of Horticulture  
 USDA-ARS and University of Wisconsin  
 1575 Linden Drive, Madison, WI 53706, USA  
 Tel: 608-262-1830  
 Fax: 608-262-4743  
 Email: mhavey@facstaff.wisc.edu  
 TIGR sequence name ACAB249TR. For more information:  
 http://havey1ab.hort.wisc.edu  
 Seq primer: CAG GAA ACA GCT ATG ACC.  
 Location/Qualifiers  
 1. .347  
 /organism="Allium cepa"  
 /mol\_type="mRNA"  
 /cultural="Red Creole(bulbs), unknown(callus), Ebano &  
 Texas Legend(roots)"  
 /db\_xref="taxon:4679"  
 /clone="ACAB249"

FEATURES  
 source

/tissue\_type="Callus, roots, and young bulbs"  
 /clone\_lib="normalized cDNA library of onion"  
 /note="Vector: pCMVSPORT6.1-ccdb (Invitrogen); Site 1:  
 EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA  
 from callus, roots, and young bulbs were combined to  
 synthesize the library. Normalization to enrich for  
 low-copy transcripts was performed by proprietary  
 techniques of Invitrogen."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 347;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCAACACTACTC 20  
 |||||  
 145 ACCCAACACTACTC 158

Db 145 ACCCAACACTACTC 158

RESULT 43  
 CG845406 351 bp DNA linear GSS 13-NOV-2003  
 LOCUS CG845406/c  
 DEFINITION CG845406 ZM 0.7-1.5 KB Zea mays genomic clone ZMMBMA0803E20,  
 genomic survey sequence.  
 ACCESSION CG845406  
 VERSION CG845406.1 GI:38306110  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 351)  
 Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
 Other\_GSSs: CG4AB34TH  
 Contact: Cathy Whiteclaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteclaw@cigr.org  
 Seq primer: TF  
 Class: sheared ends.  
 Location/Qualifiers  
 1. .351  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA0803E20"  
 /clone\_lib="ZM 0.7-1.5 KB"  
 /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

FEATURES  
 source

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACA 14  
 |||||  
 89 TTGCGACCCACA 76

Db 89 TTGCGACCCACA 76

RESULT 44  
 BH282705 362 bp DNA linear GSS 30-NOV-2001  
 LOCUS BH282705/c  
 DEFINITION CH230-166L20, TU CHORI-230 Segment 1 Ratius norvegicus genomic clone  
 CH230-166L20, genomic survey sequence.

ACCESSION BH282705  
 VERSION BH282705.1 GI:17195107  
 KEYWORDS GSS.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 362)  
 Zhao,S., Shetty,J., Shatsman,S., Tsengaye,G., Geer,K.,  
 Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,  
 Riggs,P., de Jong,P. and Fraser,C.M.  
 Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
 Unpublished (1999)  
 Other\_GSSs: CH230-166L20.TV  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the rat BAC library CHORI-230  
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library  
 availability, please contact Plietier de Jong ([pdjong@mail.cho.org](mailto:pdjong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/or\\_exting\\_information.htm](http://www.chori.org/bacpac/or_exting_information.htm)). BAC end  
 pages: [http://www.tigr.org/tdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html)  
 Plate: 166 row: L column: 20  
 Seq primer: SP6  
 Class: BAC ends.  
 Location/Qualifiers  
 1..362  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /strain="BN/SnHsd/MCM"  
 /db\_xref="taxon:10116"  
 /clone="CH230-166L20"  
 /sex="Female"  
 /cell\_type="Brain"  
 /clone\_id="CHORI-230 Segment 1"  
 /note="Vector: PTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;  
 CHORI-230 Rat (BN/SnHsd/MCM) BAC library produced by  
 Plietier de Jong"  
 ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 TTGCGACCCACACA 14  
 |||||||||  
 |||||||||  
 Db 39 TTCGACCAACA 26  
 RESULT 45  
 BP752355 365 bp mRNA linear EST 15-JUN-2004  
 LOCUS BP752355  
 DEFINITION BP752355 partially normalized diploid tobacco CDNA library  
 Nicotiana sylvestris cDNA clone R-111\_F03, mRNA sequence.  
 ACCESSION BP752355  
 VERSION BP752355.1 GI:48761959  
 KEYWORDS EST.  
 SOURCE Nicotiana sylvestris (wood tobacco)  
 Nicotiana sylvestris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Solanales; Solanaceae; Nicotiana.  
 1 (bases 1 to 365)  
 Katoh,A., Yamaguchi,Y., Sano,H. and Hashimoto,T.  
 Analysis of expression sequence tags from Nicotiana sylvestris  
 Proc. Jpn. Acad. Ser. B 79, 151-154 (2003)  
 Contact: Takashi Hashimoto

<hr/>					
FEATURES					
source					
1. 365					
/organism="Nicotiana sylvestris"					
/mol_type="mRNA"					
/db_xref="taxon:4096"					
/clone="R-111_F03"					
/issue_type="mixture of wounded and un-wounded leaf"					
/dev_stage="2-month-old plant"					
/clone_lib="partially normalized diploid tobacco cDNA library"					
ORIGIN					
Query Match           70.0%; Score 14; DB 5; Length 365;					
Best Local Similarity 100.0%; Pred. No. 4.5e+02;					
Matches       14; Conservative   0; Mismatches   0; Indels     0; Gaps   0;					
OY	7	ACCCACACTACTC	20		
DB	169	ACCCACACTACTC	182		
RESULT 46					
BP751956                          366 bp      mRNA      linear   EST 15-JUN-2004					
LOCUS					
DEFINITION					
BP751956 partially normalized diploid tobacco cDNA library					
Nicotiana sylvestris cDNA clone R-101_G09, mRNA sequence.					
ACCESSION					
BP751956					
BP751956.1 GI:48761560					
EST.					
Nicotiana sylvestris (wood tobacco)					
Nicotiana sylvestris					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
asterids; lamids; Solanales; Solanaceae; Nicotiana.					
1 (bases 1 to 366)					
Karch, A., Yamaguchi, Y., Sano, H. and Hashimoto, T.					
Analysis of expression sequence tags from Nicotiana sylvestris					
Proc. Jpn. Acad. Ser. B 79, 151-154 (2003)					
Contact: Takashi Hashimoto					
Graduate School of Biological Sciences					
Nara Institute of Science and Technology					
Takayama 8916-5, Ikoma, Nara 630-0192, Japan					
Tel.: 81-743-72-5520					
Fax: 81-743-72-5529					
Email: hashimoto@bs.naist.jp.					
Location/Qualifiers					
1. 366					
/organism="Nicotiana sylvestris"					
/mol_type="mRNA"					
/db_xref="taxon:4096"					
/clone="R-101_G09"					
/issue_type="mixture of wounded and un-wounded leaf"					
/dev_stage="2-month-old plant"					
/clone_lib="partially normalized diploid tobacco cDNA library"					
ORIGIN					
Query Match           70.0%; Score 14; DB 5; Length 365;					
Best Local Similarity 100.0%; Pred. No. 4.5e+02;					
Matches       14; Conservative   0; Mismatches   0; Indels     0; Gaps   0;					
OY	7	ACCCACACTACTC	20		
DB	169	ACCCACACTACTC	182		
RESULT 47					

AA310704  
 LOCUS AA310704 385 bp mRNA linear EST 19-APR-1997  
 DEFINITION EST181516 Jurkat T-cells V Homo sapiens CDNA 5' end, mRNA sequence.  
 ACCESSION AA310704  
 VERSION AA310704.1 GI:1963053  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 385)  
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullmer,R.A.,  
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Whi,C.,  
 Clayton,R.A., Cline,T.R., Cotton,M.D., Barle-Hughes,J., Fine,L.D.,  
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.,  
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,B., Hinkle,P.S., Jr.,  
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
 Bedarik,D.P., Geol,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,  
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H.,  
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,  
 Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M., and Venter,J.C.  
 TITLE Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
 MEDLINE 96026280  
 PUBMED 7566098  
 COMMENT Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 FEATURES  
 source  
 1. 385  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (inhost):156734"  
 /db\_xref="taxon:9606"  
 /cell\_type="T-lymphocyte"  
 /clone\_lib="Jurkat T-cells V"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI"  
 ORIGIN  
 Query Match 70.0%; Score 14; DB 1; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GACCCACACTACT 19  
 |||||  
 60 GACCCACACTACT 73  
 |||||  
 RESULT 48  
 CA370296 418 bp mRNA linear EST 06-NOV-2002  
 LOCUS CA370296  
 DEFINITION 650428 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT22A11\_A\_A06 5',  
 mRNA sequence.  
 ACCESSION CA370296  
 VERSION CA370296.1 GI:24682780  
 KEYWORDS EST.

SOURCE  
 ORGANISM Oncorhynchus mykiss (rainbow trout)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 REFERENCE 1 (bases 1 to 418)  
 Rexroad,C.E. 3rd, Lee,Y., Keele,J.W., Karamyheva,S., Brown,G.,  
 Koop,B., Gahr,S.A., Palti,Y. and Quackenbush,J.  
 TITLE Sequence analysis of a rainbow trout cDNA library and creation of a  
 gene index  
 JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)  
 COMMENT Contact: Rexroad CE  
 USDA, ARS, National Center for Cool and Cold Water Aquaculture  
 11876 Leetown Road, Kearneysville, WV 25430, USA  
 Tel: 304 724 8340 x2129  
 Fax: 304 725 0351  
 Email: crexroad@nccwa.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alt option. Vector identified by  
 cross match v0.990329.  
 Seq primer: AGCGATACAAATTCACACAGGA.  
 FEATURES  
 source  
 1. 418  
 /organism="Oncorhynchus mykiss"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8022"  
 /clone="1RT22A11\_A\_A06"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="NCCWA 1RT"  
 /note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
 library made from pooled tissue from brain, gill, liver,  
 spleen, muscle, and kidney."  
 ORIGIN  
 Query Match 70.0%; Score 14; DB 6; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GACCCACACTACT 19  
 |||||  
 269 GACCCACACTACT 282  
 |||||  
 RESULT 49  
 BZ787299 432 bp DNA linear GSS 17-MAR-2003  
 LOCUS BZ787299  
 DEFINITION PURFK39TD ZM 0.6 1.0 KB Zea mays genomic clone ZMBB7A357G05.  
 ACCESSION BZ787299  
 VERSION BZ787299.1 GI:28980896  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 432)  
 Whiteaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennerzen,J.  
 TITLE Maize Genomics Consortium  
 JOURNAL Unpublished (2003)  
 COMMENT Other\_GSSs: PURFK39TB  
 Contact: Cathy Whiteaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteaw@tigr.org  
 Seq primer: TF  
 Class: sheared ends.  
 FEATURES  
 Location/Qualifiers



source

1. .432  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZM081A357G05"  
/clone\_lib="ZM 0.6 1.0 KB"  
/note="Vector: pCR4-TOPO, Site 1: EcoRI; 0.6-1.0 kb high  
cor selected genomic DNA library"

ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 432;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCCACACTA 17  
|||||  
158 GCGACCCACACTA 171

RESULT 50  
CFJ50979 447 bp mRNA linear EST 20-AUG-2003  
LOCUS r165g10.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG9959 PROTEIN. ;, mRNA  
SEQUENCE.  
CFJ50979.1 GI:33953561  
EST.  
Meloidogyne javanica (root-knot nematode)  
SOURCE Meloidogyne javanica  
ORGANISM Meloidogyne javanica (root-knot nematode)  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 447)  
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wyle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Taagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCam, R., Waterston, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
CONTACT: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified  
using Dynabeads (Dyna1) and mRNA eluted for first strand synthesis.  
First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added  
using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
strand and primers specific to SMART oligo and 3' end. Double  
stranded cDNA was digested using XhoI/NotI, fractionated on  
Chroma-spin 400 columns (Clontech) and ligated to digested  
pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
host cells. Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff Rousch. See  
www.nematode.net for additional project information.  
Seq primer: Sp6  
High quality sequence stop: 446.  
Location/Qualifiers  
1. .447  
/organism="Meloidogyne javanica"  
/mol\_type="mRNA"  
/db\_xref="taxon:6303"  
/issue\_type="whole organism"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Meloidogyne javanica J2 SMART pGEM"

source

1. .455  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-AE1-zf-c-12-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-AE1"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
information."

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 447;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGCGACCCACACA 14  
|||||  
118 TTGCGACCCACACA 131

RESULT 51  
A1706594 455 bp mRNA linear EST 03-JUN-1999  
LOCUS UI-R-AE1-zf-c-12-0-UI.s1 UI-R-AE1 Rattus norvegicus cDNA clone  
DEFINITION UI-R-AE1-zf-c-12-0-UI 3', mRNA sequence.  
A1706594  
A1706594.1 GI:4994494  
EST.  
Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 455)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
JOURNAL MEDLINE  
PUBMED 97044477  
8889548  
CONTACT: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Oligo-dT track not found. Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA library Preparation: M.B.  
Soares Lab Clone Distribution: Clones will be available through  
Research Genetics (www.resgen.com) The following repetitive  
elements were found in this cDNA sequence: 289-374,  
>ICGGnHSimple repeat  
Seq primer: M13 Forward  
POLYA=No.

polylinker, Site\_1: Not I; Site\_2: Eco RI; The UI-R-AB1 library is a normalized library constructed from 15 dpc rat ventricle. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dt track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Jim Lin, Department of Biology, University of Iowa.  
TAG\_SEQ=None found"

## ORIGIN

Query Match 70.0%; Score 14; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACTA 14  
|||||  
DB 435 TTCCGACCCACACTA 448

## RESULT 52

CG059179/c

LOCUS 457 bp DNA linear GSS 19-AUG-2003  
DEFINITION PUICW72TD ZM 0.6.1.0 Zea mays genomic clone ZMMBTa0639L23,  
genomic survey sequence.

CG059179

CG059179.1 GI:33931359

GSS.

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 457)

White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,

Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

Bennetzen, J.

Maize Genomics Consortium

Unpublished (2003)

Other GSSs: PUICW72TD

Contact: Cathy White, 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitec@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..457

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone\_lib="ZMMBTa0639L23"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high

Cot selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 457;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGACCCACACTA 17  
|||||  
DB 262 GCGACCCACACTA 249

## RESULT 53

CG059181

LOCUS 457 bp DNA linear GSS 19-AUG-2003  
DEFINITION PUICW72TD ZM 0.6.1.0 Zea mays genomic clone ZMMBTa0639L23,

genomic survey sequence.

CG059181

CG059181.1 GI:33931361

GSS.

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 457)

White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,

Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

Bennetzen, J.

Maize Genomics Consortium

Unpublished (2003)

Other GSSs: PUICW72TD

Contact: Cathy White, 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitec@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..457

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone\_lib="ZMMBTa0639L23"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high

Cot selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 457;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGACCCACACTA 17  
|||||  
DB 194 GCGACCCACACTA 207

## RESULT 54

AZ650597

LOCUS 462 bp DNA linear GSS 14-DEC-2000  
DEFINITION IM0520D24R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0520D24 R, genomic survey sequence.

AZ650597

AZ650597.1 GI:11785244

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 462)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tinsley, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0520 row: D column: 24  
 Seq primer: CACACAGGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 462.

## FEATURES

source

Location/Qualifiers  
 1. 462  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U9C1M0520D24"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid U9C1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[g147329072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Pred. No. 4.5e+02; Length 462;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
 |||||  
 Db 369 ACCCAACACTACTC 362

## RESULT 55

CG845394

LOCUS

DEFINITION CG845394 475 bp DNA linear GSS 13-NOV-2003  
 genomic survey sequence.

ACCESSION CG845394  
 VERSION CG845394.1 GI:38306098

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

## REFERENCE

AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 475)  
 Reanick A., Fraser C.M., Budiman M.A., Bedell J.A., Rohlfing T., Citek R.W., Nunberg A., Robbins D. and Lakey N.

TITLE Consortium for Maize Genomics  
 JOURNAL Unpublished (2002)  
 COMMENT Other GSSs: OG4AB34TV  
 Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

## FEATURES

source

Location/Qualifiers  
 1. 475  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZM0803E20"  
 /clone\_1lb="ZM 0.7.1.5\_KB"  
 /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Pred. No. 4.5e+02; Length 475;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
 |||||  
 Db 263 TTCCGACCCACACA 276

## RESULT 56

BQ741880/C

LOCUS

DEFINITION BQ741880 482 bp mRNA linear EST 02-JUL-2004  
 seg12a03.y1 Gm-cl045 Glycine max cDNA clone SOYBEAN CLONE ID:  
 Gm-cl045-4254 5', mRNA sequence.

ACCESSION BQ741880

VERSION BQ741880.1 GI:21888667

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

## REFERENCE

AUTHORS

1 (bases 1 to 482)  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritzer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.

TITLE Public Soybean EST Project

JOURNAL Unpublished (1999)

COMMENT Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. This clone is

available through: Biogenetic Services, 801 32nd Ave. Brookings, SD

57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

Seq primer: -40RP from Gibco

High quality sequence stop: 431.

## FEATURES

source

Location/Qualifiers  
 1. 482  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Williams 82"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl045-4254"  
 /tissue\_type="Hypocotyl, 9-10 day old etiolated seedlings"  
 /lab\_host="DH10B"  
 /clone\_1lb="Gm-cl045"  
 /note="Vector: pBluescriptII SK+, Site 1: EcoRI, Site 2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI

adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 482;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCAACACTACTC 19  
|||||  
184 GACCAACACTACTC 171

RESULT 57  
B29191 490 bp DNA linear GSS 13-OCT-1997  
LOCUS T28D21TF TAMU Arabidopsis thaliana genomic clone T28D21, genomic  
DEFINITION survey sequence.  
ACCESSION B29191 GI:2515157  
VERSION B29191.1 GI:2515157  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE  
AUTHORS Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. and Venter, J.C.

USE OF A BAC End Sequence Database To Identify Minimal Overlaps for Arabidopsis Genomic Sequencing  
TITLE Use of a BAC End Sequence Database To Identify Minimal Overlaps for Arabidopsis Genomic Sequencing  
JOURNAL Unpublished (1997)  
COMMENT Other GSSs: T28D21TR  
Contact: Steve Rounsley  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: rounsley@tigr.org  
Seq primer: M13-21  
Class: BAC ends  
High quality sequence stop: 490.

FEATURES  
source Location/Qualifiers  
1..490  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="T28D21"  
/sex="hermaphrodite"  
/clone\_lib="TAMU"  
/note="Vector: pBluescript II, Site 1: HindIII, Site 2: HindIII; Produced by Rod Wing"

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 490;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
|||||  
429 ACCCAACACTACTC 416

RESULT 58  
BH219227/c 491 bp DNA linear GSS 08-NOV-2001  
LOCUS BH219227

DEFINITION 1006085D03.x1 1006 - RescuedMu Grid G Zea mays genomic, genomic survey sequence.  
ACCESSION BH219227  
VERSION BH219227.1 GI:16813010  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 491)  
Walbot, V.

Maize genomic sequences found using engineered RescuedMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 723 8221  
Email: walbot@stanford.edu

Very probable ligation site found so sequence was trimmed.  
Post-ligation sequence submitted separately.  
Plate: 1006085 row: 20  
Class: transposon-tagged.

FEATURES  
source Location/Qualifiers  
1..491  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - RescuedMu Grid G"  
/note="Organ: leaf; Vector: RescuedMu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; RescuedMu is a 4.9 Kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuedMu, go to the web site 'www.zmbd.jastate.edu' and follow the links for 'RescuedMu', 'Grid G' was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 491;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
|||||  
103 ACCCAACACTACTC 90

RESULT 59  
CK148694/c 496 bp mRNA linear EST 01-JUN-2004  
LOCUS CK148694  
DEFINITION AGT-30-G10 Suppressive subtractive hybridization library Cicer arietinum cDNA clone AGT-30-G10 5', mRNA sequence.  
ACCESSION CK148694  
VERSION CK148694.1 GI:47832382  
KEYWORDS EST.  
SOURCE Cicer arietinum (chickpea)  
ORGANISM Cicer arietinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eutrosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.  
1 (bases 1 to 496)

**AUTHORS** Buhariwalla, H.K., Jayashree, B. and Crouch, J.H.  
**TITLE** Characterization of ESTs associated with drought tolerance from chickpea (*C. arietinum*) root tissue  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Buhariwalla HK  
 Swaminathan Applied Genomics Laboratory  
 International Crops Research Institute for the Semi-arid Tropics (ICRISAT)  
 Patancheru 502 324, Andhra Pradesh, India  
 Tel: +91 40 23296161  
 Fax: +91 40 23241239  
 Email: Buhariwalla@ICRISAT.EXCH.cgiar.org  
 Seq primer: T7

**FEATURES**  
**Source** High quality sequence stop: 496.  
 Location/Qualifiers

1..496  
 /organism="Cicer arietinum"  
 /mol\_type="mRNA"  
 /cultivar="ICC 4958"  
 /db\_xref="taxon:3827"  
 /clone="ACT-30-G10"  
 /issue\_type="Root"  
 /lab\_host="E.coli DH10B"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Site 2: EcoRI;  
 The suppression subtractive hybridization process was carried out using ICC 4958 as the tester and Amigari as the driver, the PCR products of the subtraction were cloned into the PCR4-TOPO cloning vector. The c-DNA inserts were amplified with M13 forward and reverse primers and subsequently sequenced with T7 primer from the 3' end."

**ORIGIN**

Query Match 70.0%; Score 14; DB 7; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 7 ACCCAACACTACTC 20  
 |||||  
**Db** 83 ACCCAACACTACTC 70

**RESULT 60**

CK747642

**LOCUS** nad03-6cs4-d09 Nad03 Nuphar advena cDNA clone nad03-6cs4-d09 5',  
 mRNA sequence.

**ACCESSION**

CK747642

**VERSION**

CK747642.1 GI:42638065

**KEYWORDS**

EST.

**SOURCE**

Nuphar advena

**ORGANISM**

Nuphar advena

**REFERENCE**

1 (bases 1 to 504)

**AUTHORS**

Leebens-Mack, J., Field, D., Arrington, J., Zahn, L., Kong, H.,  
 Druckenmiller, M., Landherr, L., Hu, Y., Ilut, D., Wall, K.,  
 Pluck, S., Chioresu, S., Albert, V., Doyle, J., Miller, W.,  
 Oppenheimer, D., Soltis, D., Soltis, P. and Rieseisen, G.  
 Generation of ESTs from early flower buds of Nuphar advena  
 Unpublished (2002)

**TITLE**

Unpublished (2002)

**JOURNAL**

Unpublished (2002)

**COMMENT**

Contact: Claude Leebens-Mack  
 Penn State University  
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn  
 State University, University Park, PA 16802, USA  
 Tel: 814 863 6413  
 Fax: 814 865 9131  
 Email: cwl3@psu.edu or jh100@psu.edu  
 The sequence provided is trimmed of vector and low quality regions.

**FEATURES**  
**Source** Full sequence and original trace file are available from the Plant  
 Genome Network website (http://pgn.cornell.edu)  
 Plate: nad03-6cs4 row: d column: 09  
 Seq primer: M13F.

Location/Qualifiers  
 1..504  
 /organism="Nuphar advena"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:77108"  
 /clone="nad03-6cs4-d09"  
 /issue\_type="flower buds"  
 /dev\_stage="<= 2.5mm"  
 /lab\_host="SOLR"  
 /clone\_lib="nad03"  
 /note="Vector: pBluescript SK (+/-); Site 1: EcoRI;  
 Site 2: XhoI; Only floral buds with diameter of 2.5 mm of  
 less were used for RNA isolation. This is a directionally  
 cloned, non-normalized library. Avg. insert length: 1134;  
 Primers: M13F and M13R; Antibiotic: 50 ug/ml Ampicillin;  
 Primary Titer: 286 pfu total; Amplified Titer: 3.2E10  
 pfu/ml; Mass Excised Titer: 5E10 total; This library has  
 been generated by the Floral Genome Project (FGP). The  
 Floral Genome Project is funded by NSF's Plant Genome  
 Research Program (DBI-0115684). More information about the  
 project can be obtained at http://fgp.bio.psu.edu"

**ORIGIN**

Query Match 70.0%; Score 14; DB 7; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 7 ACCCAACACTACTC 20  
 |||||  
**Db** 255 ACCCAACACTACTC 268

**RESULT 61**

BU964885

**LOCUS** nad03-6cs4-d09 Nad03 Nuphar advena cDNA clone nad03-6cs4-d09 5',  
 mRNA sequence.

**ACCESSION**

BU964885

**VERSION**

BU964885.1 GI:24205632

**KEYWORDS**

EST.

**SOURCE**

Glycine max (soybean)

**ORGANISM**

Glycine max

**REFERENCE**

1 (bases 1 to 507)

**AUTHORS**

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,  
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
 Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,  
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,  
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished (1999)

**TITLE**

Unpublished (1999)

**JOURNAL**

Unpublished (1999)

**COMMENT**

Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 When it has been determined, an EST from the other end of this  
 clone is listed in the 'Other ESTs on clone' field. This clone is  
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD  
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 450.  
 Location/Qualifiers

**FEATURES**

## source

1. 507  
 /organism="glycine max"  
 /mol\_type="mRNA"  
 /cultivar="JACK"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl036-12656"  
 /tissue\_type="somatic embryos cultured on MSD 20"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl036"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the life Technologies superscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

7 ACCCAACACTACTC 20  
 |||||  
 442 ACCCAACACTACTC 455

DB 442 ACCCAACACTACTC 455

## RESULT 62

BE474398/c

LOCUS

BE474398 512 bp mRNA linear EST 13-JUL-2004  
 sp3h05.y1 Gm-cl044 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-cl044-658 5', mRNA sequence.

ACCESSION

BE474398

VERSION

BE474398.1

KEYWORDS

EST.

SOURCE

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 512)

REFERENCE

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pepe, D., Harvey, N.,

Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterson, R., and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

CONTACT: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 266 1800

Fax: 314 266 1810

Email: est@wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800.423.4163; email: info@biogeneticservices.com) Insert Length: 854 Std Error: 0.00 High quality sequence stop: 363.

Location/Qualifiers

1. 512

## ORIGIN

Query Match 70.0%; Score 14; DB 2; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

6 GACCCACACTACT 19  
 |||||  
 23 GACCCACACTACT 10

DB 23 GACCCACACTACT 10

## RESULT 63

BU039555

LOCUS

BU039555 513 bp mRNA linear EST 26-AUG-2002  
 PP LEA0003C22F Peach developing fruit mesocarp Prunus persica cDNA

clone PP\_LEA0003C22F, mRNA sequence.

ACCESSION

BU039555

VERSION

BU039555.1

KEYWORDS

EST.

SOURCE

ORGANISM

Prunus persica (peach)

Prunus persica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 513)

REFERENCE

Callahan, A., Palmer, M., Main, D., Wing, R., and Abbott, A.

Peach Model Genome for Rosaceae

Unpublished (2002)

CONTACT: Abbott, A.

Dept of Genetics and Biochemistry

Clemson University

122 Long Hall, Clemson University, Clemson, SC 29634, USA

Tel: 864 656 3060

Fax: 864 656 6879

Email: aalbert@clemson.edu

Total High Quality bases = 13;

Seq primer: TATACGACTGACTATGAG

High quality sequence stop: 513.

Location/Qualifiers

1. 513

/organism="Prunus persica"

/mol\_type="mRNA"

/cultivar="Loring"  
 /db\_xref="taxon:3760"  
 /clone="PP\_LEA0003C22F"  
 /tissue\_type="Mesocarp"  
 /lab\_host="E. coli"  
 /clone\_lib="Peach developing fruit mesocarp"  
 /note="Vector: pBluescript II SK(-); Site 1: EcoRI; Site 2: XhoI; authority=Prunus persica L. Batsch; The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or

## ORIGIN

above. For more details on library preparation and sequence analysis go to <http://www.genome.clemson.edu/projects/peach>. To order this clone go to <http://www.genome.clemson.edu/orders>

Query Match 70.0%; Score 14; DB 5; Length 513;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GACCCACACTACT 18  
|||||  
Db 280 GACCCACACTACT 293

RESULT 64  
B1786794/c 525 bp mRNA linear EST 08-JUL-2004  
LOCUS sa153d09.y1 Gm-cl068 Glycine max CDNA clone GENOME SYSTEMS CLONE  
DEFINITION ID: Gm-cl068-2465 5', mRNA sequence.  
ACCESSION B1786794  
VERSION B1786794.1 GI:15814519  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine

REFERENCE  
AUTHORS Shoenmaker, R., Kelm, P., Vocklin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
TITLE Public Soybean EST Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Shoenmaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: eest@wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: [info@biogeneticservices.com](mailto:info@biogeneticservices.com))  
Seq primer: -40RP from Gibco  
High quality sequence stop: 428.  
Location/Qualifiers  
1. .525  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Williams 82"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl068-2465"  
/tissue\_type="leaf, drought stressed, 1 month old plants, greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl068"  
/note="Vector: pBlueScript II SK+, Site\_1: EcoRI, Site\_2: XhoI; The CDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended CDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBlueScript vector. The

FEATURES  
source

ligated CDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoenmaker."

## ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 525;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19  
|||||  
Db 439 GACCCACACTACT 426

RESULT 65  
CF350940 534 bp mRNA linear EST 20-AUG-2003  
LOCUS r165d01.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
DEFINITION CDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ;, mRNA sequence.  
ACCESSION CF350940  
VERSION CF350940.1 GI:33953484  
KEYWORDS EST.  
SOURCE Meloidogyne javanica (root-knot nematode)  
ORGANISM Meloidogyne javanica

REFERENCE  
AUTHORS Eukaryote; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 534)  
McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, V., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Peterson, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
TITLE The Washington Univ. Nematode EST Project, 1999  
JOURNAL Unpublished (1999)  
COMMENT Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: eest@wustl.edu

Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See [www.nematode.net](http://www.nematode.net) for additional project information.  
Seq primer: Sp6  
High quality sequence stop: 534.  
Location/Qualifiers  
1. .534  
/organism="Meloidogyne javanica"  
/mol\_type="mRNA"  
/db\_xref="taxon:6303"  
/tissue\_type="whole organism"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Meloidogyne javanica J2 SMART pGEM"  
/note="Vector: pGEM11zf(+) plasmid (ampicillin resistant); Site\_1: XhoI; Site\_2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor'

FEATURES  
source

primed with oligo(dT) with XhoI site and 5'SMART 'anchor'

added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractioned on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See [www.nemacode.net](http://www.nemacode.net) for additional project information."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 534;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGCGACCAACA 14  
71 TTCGCGACCAACA 84

## RESULT 66

AL913399/c AL913399 539 bp mRNA linear EST 06-JUN-2004  
DEFINITION AL913399 PUR-Z1+Z2 Danio rerio cDNA clone 172-B03-2, mRNA sequence.  
ACCESSION AL913399  
VERSION AL913399.1 GI:23178669  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS Lo, J., Lee, S., Xu, M., Liu, F., Ruan, H., Eun, A., He, Y., Ma, W., Wang, W., Wen, Z. and Peng, J.  
15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during embryogenesis  
JOURNAL Genome Res. 13 (3), 455-466 (2003)  
MEDLINE 22505427  
PUBMED 12618976

## TITLE

JOURNAL Contact: Peng J  
MEDLINE Lab of Functional Genomics  
PUBMED Institute of Molecular and Cell Biology  
COMMENT 30 Medical Drive, Singapore, 117609, Singapore  
Email: pengj@imcb.a-star.edu.sg  
Clone requests: info@openbioystems.com  
Open Bioystems,  
6705 Odysey Drive, Huntville, AL 35806.

## FEATURES

source  
1. 539  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/strain="local\_wildtype"  
/db\_xref="taxon:7955"  
/clone="172-B03-2"  
/tissue\_type="whole embryo or fish"  
/dev\_stage="mixed stages"  
/clone\_1b="PUR-Z1+Z2"

## ORIGIN

Query Match 70.0%; Score 14; DB 1; Length 539;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CGGACCAACTACT 16  
496 CGGACCAACTACT 483

Db 496 CGGACCAACTACT 483

RESULT 67  
CO210460/c

LOCUS CO210460 540 bp mRNA linear EST 22-JUN-2004  
DEFINITION WS00918.B21 E20 IS-B-N-A-10 Picea engelmannii x Picea sitchensis  
cDNA clone WS00918\_E20 3', mRNA sequence.  
ACCESSION CO210460  
VERSION CO210460.1 GI:49022900  
KEYWORDS EST.

SOURCE Picea engelmannii x Picea sitchensis  
Picea engelmannii x Picea sitchensis  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

## SOURCE

## REFERENCE

AUTHORS Ralph, S., Kolosova, N., Cooper, D., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G., Babakrif, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.  
The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries  
Unpublished (2004)  
CONTACT: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS00918 row: E column: 20  
High quality sequence stop: 540  
POLA=yes

## JOURNAL

## COMMENT

## FEATURES

## source

Location/Qualifiers  
1. 540  
/organism="Picea engelmannii x Picea sitchensis"  
/mol\_type="mRNA"  
/cultivar="Fal-1028"  
/db\_xref="taxon:273280"  
/clone="WS00918\_E20"  
/sex="Hermaphrodite"  
/lab\_host="E. coli DH10B cells"  
/note="Organ: Bark (with phloem and cambium attached) from one year old clonal trees grown under greenhouse conditions in standard potting soil mixture. Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Bark was wounded using razor blades along the entire length of the tree at 5 mm intervals on opposite sides of the trunk. The same trees were also sprayed with a 0.01% (v/v) methyl jasmonate solution resuspended in 0.1% (v/v) tween 20 (50mls per tree). Bark tissue with phloem attached was harvested 3 hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8 days after initiating the treatment. Untreated control bark was also harvested at time 0 hours. mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldi M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 540;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCAACTACT 19



Db 413 GACCCACACTACT 400

# RESULT 68 CA225879/c

LOCUS 541 bp mRNA linear EST 25-SEP-2003  
DEFINITION SCRLFL3004E02.b Saccharum officinarum FL3 Saccharum officinarum  
CDNA clone SCRLFL3004E02 3', mRNA sequence.

ACCESSION CA225879  
VERSION CA225879.1 GI:35284679  
KEYWORDS EST.  
SOURCE Saccharum officinarum  
ORGANISM Saccharum officinarum

REFERENCE 1 (bases 1 to 541)  
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
TITLE The libraries that made SUCEST  
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
COMMENT Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parida@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 004 row: E column: 02  
Seq primer: SP6 Promoter primer.

FEATURES  
source  
1..541  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCRLFL3004E02"  
/lab\_host="DH10B"  
/clone\_1lb="Saccharum officinarum FL3"  
/note="Organ: Base of developing inflorescence (5cm-long);  
Vector: pSport1, Site 1: SalI, Site 2: NotI. An  
unidirectional cDNA library generated from (Base of  
developing inflorescence (5cm-long)). cDNA was prepared  
from polyA+ mRNA using Superscript Plasmid System Kit  
(Invitrogen). The double-strand cDNAs were fractionated  
in a sepharose CL-2B 40cm-columns and fragments sizing  
between 0.8 and 1.5 Kb were directionally cloned into the  
vector. Details of each source of RNA and library  
construction can be obtained at  
http://sucest.iad.ic.unicamp.br/public"

ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 541;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 481 GACCCACACTACT 468

RESULT 69  
BG593673/c  
LOCUS 556 bp mRNA linear EST 07-MAR-2003  
DEFINITION BG593673 cSTS Solanum tuberosum cDNA clone cSTS515 5' sequence,  
mRNA sequence.  
ACCESSION BG593673  
VERSION BG593673.1 GI:13611813  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)

## ORGANISM

Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Solanum.

# REFERENCE AUTHORS

1 (bases 1 to 556)  
Van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemiango,A.,  
Bongri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.  
Generations of ESTs from sprouting potato eyes  
Unpublished (2000)  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
This clone can be obtained from the University of Arizona Genomics  
Institute. Orders can be made through URL:  
http://genome.arizona.edu/orders/  
Seq primer: M13P-R.

## FEATURES source

1..556  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="cSTS515"  
/issue\_type="sprouting eyes from tubers"  
/dev\_stage="12-14 weeks post harvest"  
/lab\_host="SOLR"  
/clone\_1lb="cSTS"  
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were  
taken from tubers. The tubers were incubated at 26C in the  
dark for 2-3 weeks prior to sprouting. The eyes were  
frozen in liquid nitrogen immediately upon removal from  
tubers."

## ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 556;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 514 GACCCACACTACT 501

RESULT 70  
BM307732/c  
LOCUS 564 bp mRNA linear EST 06-JUL-2004  
DEFINITION BG331a10.y1 Gm-cl075 Glycine max cDNA clone SOYBEAN CLOVE ID:  
Gm-cl075-4651 5' similar to TR:Q9XHS Q9XHS MICROTUBULE-ASSOCIATED  
PROTEIN. (1) ;, mRNA sequence.

ACCESSION BM307732  
VERSION BM307732.1 GI:18039438  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max (soybean)

## REFERENCE AUTHORS

1 (bases 1 to 564)  
Shoemaker,R., Keim,P., Vodkin,L., Eipelidg,J., Coryell,V.,  
Knappa,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,  
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,  
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N.,  
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 605 423 4163; email: info@biogeneticservices.com)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 421.  
 Location/Qualifiers  
 1..564  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Jack"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl075-4651"  
 /tissue\_type="differentiating somatic embryos cultured on MSM6AC"  
 /lab\_host="DH10B"  
 /clone\_id="Gm-cl075"

/note="vector: pBluescript II SK+, Site\_1: EcoRI, Site\_2: XhoI; The cDNA library was constructed from mRNA isolated from differentiating somatic embryos cultured on MSM6AC. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Tissue culture and library construction were performed by Françoise Thibaud-Nissen and Anu Khanna (Lila Vodkin lab, University of Illinois)."

## ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19  
 |||||  
 Db 212 GACCCACACTACT 199

RESULT 71  
 CE261393/c 566 bp DNA linear GSS 26-SEP-2003  
 LOCUS tigr-gss-dog-17000346569937 Dog Library Canis familiaris genomic,  
 DEFINITION genomic survey sequence.  
 ACCESSION CE261393  
 VERSION CE261393.1 GI:35973606  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedata; Canidae; Canis.  
 1 (bases 1 to 566)  
 Kirksess,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 JOURNAL MEDLINE  
 PUBMED 14512627  
 COMMENT Contact: Kirksess EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirksess@tigr.org

Class: shotgun.  
 Location/Qualifiers  
 1..566  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_id="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 566;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCAACACTACTC 20  
 |||||  
 Db 184 ACCCAACACTACTC 171

RESULT 72  
 CK435227/c 572 bp mRNA linear EST 08-JAN-2004  
 LOCUS glauca cDNA clone GQ0063\_P07 3', mRNA sequence.  
 DEFINITION  
 ACCESSION CK435227  
 VERSION CK435227  
 KEYWORDS EST.  
 SOURCE Picea glauca (white spruce)  
 ORGANISM Picea glauca  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
 1 (bases 1 to 572)  
 Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,  
 Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stett,J.,  
 Siddiqui,A., Holt,R., Mair,M. and Mackay,V.  
 Arborea EST sequencing in Picea glauca (white spruce)  
 Unpublished (2004)  
 CONTACT: John Mackay  
 Centre de Recherche en Biologie Forestiere  
 Universite Laval  
 Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4  
 Fax: 418 656 7493  
 Email: jmackay@rsvs.ulaval.ca  
 Center for Computational Genomics and Bioinformatics (CCGB),  
 University of Minnesota, MN id identifier: MNS169674 Clone ID:  
 GQ0063\_P07 Clones available through: John Mackay, Ph. D. Professeur  
 adjoint -Assistant professeur EMAIL: jmackay@rsvs.ulaval.ca Centre  
 de Recherche en Biologie Forestiere (Forest Biology Research  
 Center) Universite Laval Quebec, Quebec CANADA G1K 7P4  
 Plate: 3 row: 07 column: P  
 Seq primer: PolyTplus Primer.

## FEATURES

1..572  
 /organism="Picea glauca"  
 /mol\_type="mRNA"  
 /strain="Two trees of provenance 5333 and one from 5208"  
 /db\_xref="taxon:3330"  
 /clone="GQ0063\_P07"  
 /sex="Hermaphrodite"  
 /tissue\_type="Cambium and phloem region from normal  
 vertical trees"  
 /dev\_stage="Cambium and phloem tissue scraped from inside  
 of bark from trees harvested 2.5 hours, 6 hours and 11  
 hours after day break were pooled"  
 /lab\_host="E. coli DH10B cells"  
 /clone\_id="GQ0063\_P07"  
 /note="Organ: Stem from ground to lower part of live  
 crown, on 33 year old tree; Vector: pBluescript II SK (+)  
 XR; Site\_1: Eco-RI; Site\_2: Xho-I; Tissue was harvested in  
 mid-June, during formation of early wood. cDNA was  
 prepared from 5 mg of poly A+ selected RNA and was

directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitro) for propagation"

Query Match 70.0%; Score 14; DB 7; Length 572;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCAACTACT 19

Db 477 GACCCAACTACT 464

RESULT 73  
LOCUS CO207163 575 bp mRNA linear EST 21-JUN-2004  
DEFINITION WS00913.B21 F10 IS-B-N-A-10 Picea engelmannii x Picea sitchensis  
CNA clone WS00913\_F10 3', mRNA sequence.

ACCESSION CO207163  
VERSION CO207163.1 GI:49018338

KEYWORDS EST.  
SOURCE Picea engelmannii x Picea sitchensis  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

REFERENCE 1 (bases 1 to 575)  
AUTHORS Ralph,S., Kolesova,N., Cooper,D., Butterfield,Y., Kirkpatrick,R.,  
Liu,J., Palmquist,D., Scott,J., Barber,S., Yang,G., Babakoff,R.,  
Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M.,  
Moran,J., Olson,T., Wong,D., Friedmann,M.F., Rittland,C.E.,  
Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C.,  
Rittland,K. and Bohlmann,J.

TITLE The spruce transcriptome: Analysis of expressed sequence tags from  
multiple cDNA libraries  
JOURNAL Unpublished (2004)  
COMMENT Contact: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,  
Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS00913 row: F column: 10  
High quality sequence stop: 575  
POLYA=yes.

FEATURES Location/Qualifiers

source

1. 575  
/organism="Picea engelmannii x Picea sitchensis"  
/mol\_type="mRNA"  
/cultiivar="Fal-1028"  
/db\_xref="taxon:273280"  
/clone="WS00913\_F10"  
/sex="Hermaphrodite"  
/lab\_host="E. coli DH10B cells"  
/clone\_lib="IS-B-N-A-10"  
/note="Organ: Bark (with phloem and cambium attached) from  
one year old clonal trees grown under greenhouse  
conditions in standard potting soil mixture; Vector:  
pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA);  
Site 2: XhoI (3' end of cDNA); Bark was wounded using  
razor blades along the entire length of the tree at 5 mm  
intervals on opposite sides of the trunk. The same trees  
were also sprayed with a 0.01% (v/v) methyl jasmonate  
solution resuspended in 0.1% (v/v) tween 20 (-50mls per  
tree). Bark tissue with phloem attached was harvested 3  
hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8  
days after initiating the treatment. Untreated control  
bark was also harvested at time 0 hours. mRNA was isolated  
from each tissue source independently and equal quantities  
of mRNA from each tissue were then pooled. cDNA was  
prepared from 5 micrograms of mRNA and directionally

ligated into the pBluescript II SK (+) XR vector using the  
pBluescript II XR cDNA Library Construction Kit according  
to manufacturer's instructions with modifications  
(Stratagene). Plasmid DNA was then transformed by  
electroporation into DH10B cells (Invitrogen) for  
propagation. Normalization was applied according to  
published methods (Bonaldi M.F. et al. (1996) Genome  
Research 6(9):791) in order to reduce the abundance of  
highly expressed transcripts."

Query Match 70.0%; Score 14; DB 7; Length 575;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCAACTACT 19

Db 378 GACCCAACTACT 365

RESULT 74  
LOCUS CF351038 579 bp mRNA linear EST 20-AUG-2003  
DEFINITION CF351038  
cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ;, mRNA  
sequence.

ACCESSION CF351038  
VERSION CF351038.1 GI:33953680

KEYWORDS EST.  
SOURCE Meloidogyne javanica (root-knot nematode)  
ORGANISM Meloidogyne javanica

REFERENCE 1 (bases 1 to 579)  
AUTHORS Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Harwood,K., Steptoe,M., Allen,M., Peterson,B., Swaller,T.,  
Haverd,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.

TITLE The Washington Univ. Nematode EST Project, 1999  
JOURNAL Unpublished (1999)  
COMMENT Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu

Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified  
using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
First strand cDNA was created using MMV RT (PowerScript, Clontech)  
and primed with oligo(dT) with xhoi site and 5'SMART 'anchor' added  
using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
strand and primers specific to SMART oligo and 3' end. Double  
stranded cDNA was digested using XhoI/NotI, fractionated on  
Chroma-spin 400 columns (Clontech) and ligated to digested  
pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
host cells. Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff Rousch. See  
www.nematode.net for additional project information.  
Seq primer: Sp6.

FEATURES Location/Qualifiers

source

1. 579  
/organism="Meloidogyne javanica"  
/mol\_type="mRNA"  
/db\_xref="taxon:6303"  
/tissue\_type="whole organism"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Meloidogyne javanica J2 SMART PGEM"  
/note="Vector: plasmid (ampicillin resistant); Site\_1:

XhoI, Site 2: NotI; Cloned unidirectionally. Poly(A)<sup>+</sup> RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See [www.nemacode.net](http://www.nemacode.net) for additional project information.

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 579;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
118 TTCCGACCCACACA 131

Db

## RESULT 75

CLJ233606/c 579 bp DNA linear GSS 19-AUG-2004  
LOCUS RPT14\_458D12.f RPT1-44 Sus scrofa genomic clone RPT14\_458D12,  
DEFINITION genomic survey sequence.  
ACCESSION CLJ233606  
VERSION CLJ233606.1 GI:51375577  
KEYWORDS GSS.

SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 579)

AUTHORS Rogatcheva, M.B., Meyers, S., He, W., Larkin, D.M., Marron, B.M., Piggy-BACing the Human Genome: Constructing a Porcine Physical Map

TITLE Through Comparative Genomics  
JOURNAL Unpublished (2004)  
COMMENT Other GSSs: RPT14\_458D12.r

Contact: Lawrence B. Schook  
Department of Animal Sciences  
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Tel: 217 265 5326  
Fax: 217 244 5617  
Email: [schook@uiuc.edu](mailto:schook@uiuc.edu)

Clones are derived from the porcine BAC library RPT1-44 (<http://www.bacpac.chori.org/mporcine44.htm>). For BAC library availability, please contact Pieter de Jong ([pdj@chori.org](mailto:pdj@chori.org)). Clones may be purchased from BACPAC Resources (<http://BACPACResources.chori.org>). This work was undertaken as part of the International Swine Genome Sequencing Consortium by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG2002-34480-11828 from USDA-CSREES and AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing Initiative)  
Plate: 458 row: D column: 12  
Seq primer: T7

Class: BAC ends.

FEATURES  
source Location/Qualifiers

1..579  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/strain="four pigs (bred: 37.5% Yorks Landrace and 25% Meishan)"  
/db\_xref="taxon:9823"  
/clone="RPT14\_458D12"

/sex="male"  
/cell\_type="blood"  
/clone\_lib="RPT1-44"  
/note="Vector: pTARBAC2; Site 1: EcoRI; Site 2: EcoRI; porcine male BAC library produced by Pieter de Jong"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 579;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACT 19  
280 GACCCAACTACT 267

Db

## RESULT 76

CG810144 586 bp DNA linear GSS 13-NOV-2003  
LOCUS FSAJB1R LargeInsertGenomicLibrary Fusarium virguliforme genomic  
DEFINITION clone KMFV1M18, genomic survey sequence.  
ACCESSION CG810144  
VERSION CG810144.1 GI:38263618  
KEYWORDS GSS.

SOURCE Fusarium virguliforme  
ORGANISM Fusarium virguliforme

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria. 1 (bases 1 to 586)

AUTHORS Meksem, K., Ishihara, H., Koo, H., Shultz, J., Ali, S., Iqbal, J., Lightfoot, D.A. and Town, C.D.  
TITLE End sequencing of BACs from a fingerprint physical map of the causative agent of soybean sudden death syndrome, *Fusarium virguliforme*

JOURNAL Unpublished (2003)  
COMMENT Other GSSs: FSAJB1R  
Contact: Chris Town and K. Meksem  
The Center of Excellence in Soybean Research, Teaching and Outreach, Southern Illinois University at Carbondale and Plant Genomics, The Institute for Genomic Research  
Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415, USA and 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 618 453 3103 and 301-838-3523  
Fax: 618 453-7457 and 301-838-0208  
Email: [meksem@siu.edu](mailto:meksem@siu.edu); [cdtown@tigr.org](mailto:cdtown@tigr.org) (URL: <http://Fusariumvirguliforme.siu.edu>)  
Seq primer: CAGGAAACGCTATGACC  
Class: BAC ends.

FEATURES  
source Location/Qualifiers

1..586  
/organism="Fusarium virguliforme"  
/mol\_type="genomic DNA"  
/cultivar="Monticello"  
/db\_xref="taxon:232082"  
/clone="KMFV1M18"  
/clone\_lib="LargeInsertGenomicLibrary"  
/note="Organ: Hyphae; Vector: pINDIGOBAC5; A single spore derived culture was used. Hyphae were grown in an incubator for four days. Nuclei were isolated and embedded in agarose, restriction digested with Hind III. Large size DNA fragments were ligated in vector pINDIGOBAC5 and electro-transformed into DH10B cells."

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 586;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACTACT 18  
242 CGACCAACTACT 255

Db

RESULT 77  
LOCUS CO209937 593 bp mRNA linear EST 21-JUN-2004  
DEFINITION WS00916.B21.1\_J14 IS-B-N-A-10 Picea engelmannii x Picea sitchensis  
CDNA clone WS00916\_J14 3', mRNA sequence.  
ACCESSION CO209937  
VERSION CO209937.1 GI:49022251  
KEYWORDS EST.  
SOURCE Picea engelmannii x Picea sitchensis  
ORGANISM Picea engelmannii x Picea sitchensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
REFERENCE 1 (bases 1 to 593)  
AUTHORS Ralph,S., Kolosova,N., Cooper,D., Butterfield,Y., Kirkpatrick,R.,  
Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakait,R.,  
Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M.,  
Moran,J., Olson,T., Wong,D., Friedmann,M.F., Ritzland,C.E.,  
Siddiqui,A., Holt,R., Jones,S., Marrs,M., Ellis,B.E., Douglas,C.,  
Ritzland,K. and Bohlmann,J.  
The spruce transcriptome: Analysis of expressed sequence tags from  
multiple cDNA libraries  
multisite cDNA libraries  
Unpublished (2004)  
COMMENT Contact: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,  
Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS00916 row: J column: 14  
High quality sequence stop: 593.  
Location/Qualifiers  
1..593  
/organism="Picea engelmannii x Picea sitchensis"  
/mol\_type="mRNA"  
/culivar="Pal-1028"  
/db\_xref="taxon:273280"  
/clone="WS00916\_J14"  
/sex="Hermaphrodite"  
/lab\_host="E. coli DH10B cells"  
/clone\_lib="IS-B-N-A-10"  
/note="Organ: Bark (with phloem and cambium attached) from  
one year old clonal trees grown under greenhouse  
conditions in standard potting soil mixture; Vector:  
pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA);  
Site 2: XhoI (3' end of cDNA); Bark was wounded using  
razor blades along the entire length of the tree at 5 mm  
intervals on opposite sides of the trunk. The same trees  
were also sprayed with a 0.01% (v/v) methyl jasmonate  
solution resuspended in 0.1% (v/v) tween 20 (-50mls per  
tree). Bark tissue with phloem attached was harvested 3  
hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8  
days after initiating the treatment. Untreated control  
bark was also harvested at time 0 hours. mRNA was isolated  
from each tissue source independently and equal quantities  
of mRNA from each tissue were then pooled. cDNA was  
prepared from 5 micrograms of mRNA and directionally  
ligated into the pBluescript II SK (+) XR vector using the  
pBluescript II XR cDNA Library Construction Kit according  
to manufacturer's instructions with modifications  
(Stratagene). Plasmid DNA was then transformed by  
electroporation into DH10B cells (Invitrogen) for  
propagation. Normalization was applied according to  
published methods [Bonaldo M.F. et al. (1996) Genome  
Research 6(9):791] in order to reduce the abundance of  
highly expressed transcripts."

ORIGIN  
Query Match 70.0%; Score 14; DB 7; Length 593;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCAACTACT 19  
|||||  
Db 382 GACCCAACTACT 395  
|||||

RESULT 78  
LOCUS FR0049660 597 bp DNA linear GSS 05-SEP-2001  
DEFINITION Fugu rubripes GSS sequence, clone B29C07eE1, genomic survey  
sequence.  
ACCESSION AL605469  
VERSION AL605469.1 GI:15487270  
KEYWORDS GSS: genome survey sequence.  
SOURCE Takifugu rubripes (Fugu rubripes)  
ORGANISM Takifugu rubripes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Takifugu.  
REFERENCE 1 (bases 1 to 597)  
AUTHORS Clark,M.S.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2001) MRC Human Genome Mapping Project Resource  
Centre Hinxton, Cambridge, CB10 1SB, UK Email:  
biohelp@hmp.mrc.ac.uk  
Vector: pBluescript II KS  
V\_type: phagemid  
PRIMER: KS  
DESCR: One pass dye-terminator sequencing of BAC (pBelobAC11) cloned  
genomic sequence  
The BACs can be obtained from <http://www.incyte.com>.  
Location/Qualifiers  
1..597  
/organism="Takifugu rubripes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31033"  
/clone="B29C07eE1"  
/clone\_lib="BAC B29C07"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 597;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GACCCAACTACT 18  
|||||  
Db 216 GACCCAACTACT 229  
|||||

RESULT 79  
LOCUS CF629503 599 bp mRNA linear EST 02-OCT-2003  
DEFINITION zmrw48 OA20-002-b10.63 zmrw48 Zea mays cDNA 3', mRNA sequence.  
ACCESSION CF629503  
VERSION CF629503.1 GI:37384806  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 599)  
AUTHORS Bohnerl,H., Sharp,R.E., Springer,G.K., Poroyko,V., Fredicksen,M.,  
Bohnerl,H., Spollen,W.G., Ries,J., Guillen,A., Khambati,A.,  
Topinka,C., Davis,G.E., Schachtman,D., Wu,Y. and Nguyen,H.T.  
NSF Grant DBI-0211842; Functional Genomics of Root Growth and Root  
Signaling Under Drought  
Unpublished (2003)  
JOURNAL Contact: Hans Bohnerl  
University of Illinois, Urbana-Champaign  
1201 West Gregory Drive, Urbana, IL 61801, USA  
Tel: 217-265-5475

FEATURES  
source

1. 599  
/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="taxon:4577"  
/clone\_lib="zmrw848"  
/note="Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high (-0.03 MPa) or low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrw805 and zmrw848) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohnert (University of Illinois-UC). Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RNA using the Oligotex Direct RNA kit (Qiagen). Poly(A)+mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (Root segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of 80 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adapted with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E. coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw805: 3.37 x 10<sup>6</sup>; zmrw848: 4.87 x 10<sup>6</sup>; zmrw00: 3 x 10<sup>6</sup>. The background of empty clones was less than 1%. Inserts ranged from -0.5 kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw805: 2.0x10<sup>7</sup>; zmrw848: 4.2x10<sup>7</sup>; zmrw00: 1.1x10<sup>7</sup>. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5 kb to 2.5 kb. (1) Sharp R E; Silk W K; Hsieh T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W G; Lenoble M E; Samuels T D; Bernstein N; Sharp

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 599;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

2 TCCTGACCCACAC 15  
|||||  
583 TCCTGACCCACAC 596

## RESULT 80

## AZ808200/c

LOCUS 600 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0071E18R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION AZ808200  
clone UGCG2M0071E18 R, genomic survey sequence.

VERSION AZ808200.1 GI:12973498  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 600)  
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss  
University of Utah Genome Center

UNIVERSITY OF UTAH  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA

TEL: 801 585 5606  
FAX: 801 585 7177  
Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0071 row: E column: 18

Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 600.

location/Qualifiers

1. 600

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCG2M0071E18"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: pMD229; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrolytically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD22 (GI4732114|GB|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 600;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19  
|||||  
Db 555 GACCCACACTACT 542

RESULT 81 602 bp mRNA linear EST 31-AUG-2004  
LOCUS BMS81700 Yutaka Satou unpublished cDNA library (csefl) ciona  
DEFINITION BMS81700 Yutaka Satou unpublished cDNA library (csefl) ciona  
SAVIGNYI CDNA clone csef015j23 3', mRNA sequence.  
ACCESSION BMS81700  
VERSION BMS81700.1 GI:51762375  
KEYWORDS EST.  
SOURCE Ciona savignyi  
ORGANISM Ciona savignyi  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.  
REFERENCE 1 (bases 1 to 602)  
Yamada, L., Satoh, N. and Satou, Y.  
Unpublished genes in Ciona savignyi (Yamada, Satoh, Satou)  
JOURNAL Contact: Yutaka Satou  
COMMENT Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4095  
Fax: 81-75-705-1113  
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers

FEATURES  
source 1..602  
/organism="Ciona savignyi"  
/mol\_type="mRNA"  
/db\_xref="taxon:51511"  
/clone="csef015j23"  
/dev\_stage="egg"  
/clone\_lib="Yutaka Satou unpublished cDNA library (csefl)"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 602;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACA 14  
|||||  
Db 477 TTGCGACCCACACA 464

RESULT 82 604 bp DNA linear GSS 18-MAR-2003  
LOCUS BZ878744 CH240\_293M13.TJ CHORI-240 Bos taurus genomic clone CH240\_293M13,  
DEFINITION genomic survey sequence.  
ACCESSION BZ878744  
VERSION BZ878744.1 GI:29106146  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 604)

## AUTHORS

Zhao, S., Shetty, J., Shatsman, S., Tsengaye, G., Geer, K.,  
Shvartsbeyn, A., Gebregorjais, E., Chen, D., Riggs, F., de Jong, P.,  
Crawford, A.M. and McEwan, J.C.  
Bovine BAC End Sequences from Library CHORI-240  
Unpublished (2003)  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

## COMMENT

Clones are derived from the bovine BAC library CHORI-240  
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library  
availability, please contact Pieter de Jong ([pdjong@mail.cno.org](mailto:pdjong@mail.cno.org)).  
Clones may be purchased from BACPAC Resources  
(<http://www.chori.org/bacpac/ordering/information.htm>). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBBMC) by AgResearch Ltd., New Zealand and The  
Institute of Genomic Research (TIGR), USA.  
Plate: 293 row: M column: 13  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source 1..604  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_293M13"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTRABAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
Library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 604;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCAACACTACTC 20  
|||||  
Db 456 ACCCAACACTACTC 443

RESULT 83 605 bp mRNA linear EST 11-JUL-2003  
LOCUS CD856253 DH0AF262D052M1 Hadev87 Helianthus annuus cDNA clone Hadev8726D05,  
DEFINITION mRNA sequence.  
ACCESSION CD856253  
VERSION CD856253.1 GI:32540069  
KEYWORDS EST.  
SOURCE Helianthus annuus (common sunflower)  
ORGANISM Helianthus annuus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.  
REFERENCE 1 (bases 1 to 605)  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

```

FEATURES
  source
    Location/Qualifiers
      1..605
        /organism="Helianthus annuus"
        /mol_type="mRNA"
        /cultiivar="psc8"
        /db_xref="taxon:4232"
        /clone="Hadevr726D05"
        /tissue_type="ovary"
        /clone_lib="Hadevr7"

ORIGIN
  Query Match      70.0%; Score 14; DB 6; Length 605;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCGACCCCACTACT 17
    |||||
    224 GCGACCCCACTACT 237

RESULT 84
LOCUS CO233457/c 620 bp mRNA linear EST 22-JUN-2004
DEFINITION WS0055.B21.1.016 WS-PP-A-6 Picea glauca cDNA clone WS0055_016 3',
ACCESSION CO233457
VERSION CO233457
KEYWORDS mRNA sequence.
SOURCE EST.
ORGANISM Picea glauca (white spruce)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 620)
Ralph,S., Kolosova,N., Cooper,D., Butterfield,Y., Kirkpatrick,R.,
Liu,J., Palmquist,D., Scott,J., Barber,S., Yang,G., Babakaiti,R.,
Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M.,
Moran,J., Olson,T., Wong,D., Friedmann,M.F., Ritland,C.E.,
Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C.,
Ritland,K. and Bohlmann,J.
The spruce transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-6097
Email: bohlmann@interchange.ubc.ca
Plate: WS0055 row: 0 column: 16
High quality sequence stop: 620
POLYA=yes.

FEATURES
  source
    Location/Qualifiers
      1..620
        /organism="Picea glauca"
        /mol_type="mRNA"
        /cultiivar="Pg-29"
        /db_xref="taxon:3330"
        /clone="WS0055_016"
        /sex="Hermaphrodite"
        /tissue_type="Early season phloem harvested June 15th, mid
season phloem harvested July 10th and late season phloem
harvested August 17th"
        /lab_host="E. coli DH10B cells"
        /clone_lib="WS-PP-A-6"
        /note="Organ: Phloem from 25 year old trees harvested at
Kalamalka Research Station in Vernon, British Columbia in
2001; Vector: pBluescript II SK (+) XR, Site 1: EcoRI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); mRNA was
isolated from each tissue source independently and equal
quantities of mRNA from each tissue were then pooled; cDNA
was prepared from 5 micrograms of mRNA and directionally

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ligated into the pBluescript II SK (+) XR vector using the
pBluescript II XR cDNA library Construction kit according
to manufacturer's instructions with modifications
(Stratagene). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation."

ORIGIN
  Query Match      70.0%; Score 14; DB 7; Length 620;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCCACTACT 19
    |||||
    398 GACCCCACTACT 385

RESULT 85
LOCUS CE064314/c 621 bp DNA linear GSS 24-SEP-2003
DEFINITION tigr-gss-dog-17000322608251 Dog Library Canis familiaris genomic,
ACCESSION CE064314
VERSION CE064314
KEYWORDS genomic survey sequence.
SOURCE GSS.
ORGANISM Canis familiaris (dog)
Canis familiaris
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 621)
Kirkness,E.F., Batra,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
PUBMED 14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.

FEATURES
  source
    Location/Qualifiers
      1..621
        /organism="Canis familiaris"
        /mol_type="genomic DNA"
        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /note="Site 1: BclXI; Libraries were prepared from
peripheral blood"

ORIGIN
  Query Match      70.0%; Score 14; DB 9; Length 621;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCACTACTC 20
    |||||
    285 ACCCACTACTC 272

RESULT 86
LOCUS BQ412273 623 bp mRNA linear EST 22-MAY-2002
DEFINITION GA_BQ0056A10r Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_BQ0056A10r, mRNA sequence.
ACCESSION BQ412273
VERSION BQ412273.1 GI:21099960
KEYWORDS EST.

```



SOURCE  
ORGANISM Gossypium arboreum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

REFERENCE  
AUTHORS 1 (bases 1 to 623)  
Wing, R.A., Friesch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution of the cotton fiber

JOURNAL  
COMMENT Unpublished (2000)  
Clemson University  
Contact: Wing RA  
Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total High Quality bases = 534  
Seq primer: TAATACGACTCACTATAGG  
High quality sequence start: 3  
High quality sequence stop: 615.  
Location/Qualifiers

FEATURES  
Source 1..623  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ed0056A10r"  
/issue\_type="Fibers isolated from bolls harvested 7-10 dpa"  
/lab\_host="E. coli"  
/clone\_idb="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
Query Match 70.0%; Score 14; DB 5; Length 623;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19  
|||||  
Db 88 GACCCACACTACT 101

RESULT 87  
CK970699 624 bp mRNA linear EST 16-MAR-2004  
LOCUS 4086553 BARC 9BOV Bos taurus cDNA clone 9BOV31\_P02 5', mRNA  
DEFINITION sequence.  
ACCESSION CK970699  
VERSION CK970699.1 GI:45488673  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus (cow)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 624)  
Somstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gaabare, L.C.  
Production of EST from cDNA libraries derived from immunologically activated bovine gut

JOURNAL  
COMMENT Unpublished (2004)  
Contact: Tad S. Somstegard  
Bovine Functional Genomics Laboratory  
Animal and Natural Resources Institute  
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA  
Tel: 3015048416  
Fax: 3015048414  
Email: tads@anri.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim alt - -trim fasta. Vector identified by cross\_match using options -mismatch 12 -minscore 12  
Plate: 31 row: C Column: 02  
Seq primer: CCCAGTCACGACGTGTGTAACG  
High quality sequence stop: 624.  
Location/Qualifiers

FEATURES  
Source 1..624  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Holstein"  
/db\_xref="taxon:9913"  
/clone="9BOV31\_P02"  
/sex="Male"  
/issue\_type="Pooled"  
/dev\_stage="Multiple"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_idb="BARC 9BOV"  
/note="Organ: Abomasum; Vector: pAGEN-1; Site 1: EcoRV; Site 2: NotI; Equimolar amounts of 18 and 21 week old steers, fundic and pyloric abomasums of 18 and 21 week old steers. Exposure to Osteragia osteragi was initiated at 15 weeks of age, fundic and pyloric abomasum"

ORIGIN  
Query Match 70.0%; Score 14; DB 7; Length 624;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCACACA 14  
|||||  
Db 515 TTCCGACCCACACA 528

RESULT 88  
BQ412405 627 bp mRNA linear EST 22-MAY-2002  
LOCUS BQ412405  
DEFINITION GA\_Ed0057F04r Gossypium arboreum 7-10 dpa fiber library Gossypium  
arboreum cDNA clone GA\_Ed0057F04r, mRNA sequence.  
ACCESSION BQ412405  
VERSION BQ412405.1 GI:21100092  
KEYWORDS EST.  
SOURCE Gossypium arboreum  
ORGANISM Gossypium arboreum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

REFERENCE  
AUTHORS 1 (bases 1 to 627)  
Wing, R.A., Friesch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution of the cotton fiber

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Wing RA  
Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total High Quality bases = 546  
Seq primer: TAATACGACTCACTATAGG  
High quality sequence start: 3  
High quality sequence stop: 616.  
Location/Qualifiers

FEATURES  
Source 1..627  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ed0057F04r"  
/issue\_type="Fibers isolated from bolls harvested 7-10 dpa"

/lab host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

Query Match 70.0%; Score 14; DB 5; Length 627;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
|||||  
88 GACCCACACTACT 101

## RESULT 89

CD878517/c CD878517 627 bp mRNA linear EST 11-JUL-2003  
LOCUS AZ04.102024R011126 AZ04 Triticum aestivum cDNA clone AZ04102024,  
DEFINITION mRNA sequence.

ACCESSION CD878517 GI:32562333  
VERSION CD878517  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 627)

REFERENCE Genoplane, a major partnership french program in plant genomics  
AUTHORS Genoplane.  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplane  
Genoplane  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplane' (<http://www.genoplane.com>  
and <http://genoplane-info.infobiogen.fr>).  
Location/Qualifiers

## FEATURES

source  
1..627  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="rectal"  
/db\_xref="taxon:4565"  
/clone="AZ04102024"  
/tissue\_type="root"  
/clone\_lib="AZ04"

## ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 627;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CCGGACCCACACT 16  
|||||  
Db 183 CCGGACCCACACT 170

## RESULT 90

LOCUS B0410722 631 bp mRNA linear EST 22-MAY-2002  
DEFINITION GA\_Ed0033F04r Gossypium arboreum 7-10 dpa fiber library Gossypium  
arboreum cDNA clone GA\_Ed0033F04r, mRNA sequence.

ACCESSION B0410722  
VERSION B0410722  
KEYWORDS EST.  
SOURCE Gossypium arboreum  
ORGANISM Gossypium arboreum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosids; eustosida II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 631)

## REFERENCE

AUTHORS Wing, R.A., Fritsch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
TITLE An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
JOURNAL Unpublished (2000)  
COMMENT Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total High Quality bases = 133  
Seq primer: TATACGACTACTATAGGG  
High quality sequence start: 2  
High quality sequence stop: 570.  
Location/Qualifiers

## FEATURES

source  
1..631  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ed0033F04r"  
/tissue\_type="Fibers isolated from bolls harvested 7-10  
dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 631;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
|||||  
Db 88 GACCCACACTACT 101

## RESULT 91

CC383900 637 bp DNA linear GSS 19-MAY-2003  
LOCUS PUH0D51TD ZM 0.6.1.0\_KB Zea mays genomic clone ZM0BTA495006,  
DEFINITION genomic survey sequence.

ACCESSION CC383900  
VERSION CC383900.1 GI:30863439  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 637)  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Benner, J.  
Maize Genomics Consortium  
Unpublished (2003)  
Other\_GSSs: PUH0D51TB  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TF  
Class: sheared ends.  
Location/Qualifiers

TITLE  
JOURNAL  
COMMENT

## FEATURES

source  
1..637  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"



```

source
1..642
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ed0102F05r"
/tissue_type="fibers isolated from bolls harvested 7-10 dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match          70.0%; Score 14; DB 5; Length 642;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches   14; Conservative    0; Mismatches    0; Indels      0; Gaps      0

QY       6  GACCCAACTACT 19
         |||||||||
Db        92  GACCCAACTACT 105

RESULT 95
BO915382
LOCUS     QHB14G20.Y9.ab1_QH ABCDI sunflower RHA801 Helianthus annuus cDNA
DEFINITION
ACCESSION BO915382
VERSION    BO915382
KEYWORDS   BI:22314163
SOURCE     EST.
ORGANISM   Helianthus annuus (common sunflower)
            Helianthus annuus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Astroideae;
            Heliantheae; Helianthus.
            1 (bases 1 to 649)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,U.,
Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/unpublished(2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Assandson Hall, UCD, Davis, CA 95616, USA
Tel.: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_Ca_Content4100, see http://cgpdb.ucdavis.edu/
for details.
Plate: QHB14 row: G column: 20.

FEATURES
source
Location/Qualifiers
1..649
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="RHA801"
/db_xref="taxon:4232"
/clone="QHBI4G20"
/lab_host="E. coli"
/clone_lib="QH ABCDI sunflower RHA801"
/note="vector: pBRCNDSflab; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
```

```

ORIGIN
TAG TISSUE=chemical induction
TAG LIB=OH ABCDI sunflower RHA801
TAG_SEQ=TTGTAGCCGGG"

Query Match          70.0%; Score 14; DB 5; Length 649;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GGCACCAACTA 17
      |||||
Db      558 GGCACCAACTA 571

RESULT 96
AG167124
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-035B14.TJ, genomic survey
sequence.
ACCESSION
AG167124
VERSION
AG167124.1 GI:16696802
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Tokoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library RPCI-43
2 (bases 1 to 654)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Tokoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chibbes@gsc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/,
Tel.: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pACE3.6
R.Site 1 : ECORI
R.Site 2 : ECORI
Location/Qualifiers
1. 654
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9596"
/clone="RP43-035B14.TJ"
/sex="male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match          70.0%; Score 14; DB 9; Length 654;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCCAACTACTC 20
      |||||
Db      367 ACCCAACTACTC 380

RESULT 97
BX202031
LOCUS
DEFINITION
Danio rerio genomic clone DKRY-218C15, genomic survey sequence.
558 bp DNA linear GSS 29-JAN-2002

```

```

ACCESSION      BX202031
VERSION        BX202031.1   GI:28033917
KEYWORDS
SOURCE         Danio rerio (zebrafish)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                Cypriniformes; Cyprinidae; Danio.
REFERENCE      1 (bases 1 to 658)
AUTHORS        Humphrey,S.J., Hucklale,E. and Durham,J.L.
TITLE          Direct Submission
JOURNAL        Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
                Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                humphrey@sanger.ac.uk Unpublished
COMMENT        This sequence was generated from the T7 end of BAC 218C15. 218C15
                is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                Keygene. Further details:
                http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES             location/Qualifiers
     source           1..658
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-218C15"
                     /tissue_type="testis"
                     /note="vector pindigoBAC-536"

ORIGIN
Query Match      70.0%; Score 14; DB 9; Length 658;
Best Local Similarity 100.0%; Pred.No. 4,4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0,

QY              3 CGCGACCCAACT 16
                  |||||
                  |||||
Db              584 CGCGACCCAACT 597

RESULT 98
LOCUS          BQ407083               660 bp      mRNA      linear      EST 22-MAY-2002
DEFINITION    GA_Ed0102F05f Gosyepilum arboreum 7-10 dpa fiber library Gosyepilum
ACCESSION     BQ407083
VERSION       BQ407083.1   GI:21094770
KEYWORDS      EST.
SOURCE        Gosyepilum arboreum
ORGANISM      Gosyepilum arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gosyepilum.
1 (bases 1 to 660)
Wing,R.A., Friesch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel.: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 478
Seq primer: TAATGAGCTCACTTAGGG
High quality sequence start: 16
High quality sequence stop: 616.
Location/Qualifiers
1..660
/organism="Gosyepilum arboreum"
/mol_type="mRNA"
/strains="AKA"
/cultivar="8400"

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/db_xref="taxon:29729"
/clone="GA_B0102PF05f"
/issue_type="Fibers isolated from bolls harvested 7-10 dpa"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match      70.0%; Score 14; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 GACCCACACACTACT 19
        |||||||
Db      539 GACCCACACACTACT 526

RESULT 99
CF351082 LOCUS
DEFINITION CF351082 662 bp mRNA linear EST 20-AUG-2003
            r167b12.y1 Meloidogyne javanica J2 SMART cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA
            sequence.
            CF351082
            CF351082.1 GI:33953769
            EST.
            Meloidogyne javanica (root-knot nematode)
            Meloidogyne javanica
            Eukaryote; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchida;
            Tylenchoidea; Heterodidae; Meloidogyninae; Meloidogyne.
            1 (bases 1 to 662)
            McCarter,J., Clifton,S., Chippelli,B., Pape,D., Martin,J.,
            Wyllie,T., Dante,M., Maiza,M., Hillier,L., Kucaba,T., Theising,B.,
            Bowers,Y., Gibbons,M., Riltter,E., Bennett,J., Franklin,C.,
            Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
            Underwood,K., Steptoe,M., Allen,M., Peterson,B., Swaller,T.,
            Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCanan,R., Waterston,R. and Wilson,R.
            The Washington Univ. Nematode EST Project, 1999
            Unpublished (1999)
            Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified
            using Dynabeads (Dynal) and mRNA eluted for first strand synthesis.
            First strand cDNA was created using MMV RT (Powerscript, Clontech)
            and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added
            using chimeric DNA-RNA oligo. 12 PCR cycles were done using first
            strand and primers specific to SMART oligo and 3' end. Double
            stranded cDNA was digested using XhoI/NotI, fractioned on
            Chroma-spin 400 columns (Clontech) and ligated to digested
            pGEM-11ze(+) plasmid. Chemically competent DH10B cells were used as
            host cells. Library materials provided by Dr. David Bird of North
            Carolina State University. Library construction by Jeff Rousch. See
            www.nematode.net for additional project information.
            Seq primer: Sp6.
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            /note="Vector: plasmid (ampicillin resistant); Site_1:
            XhoI; Site_2: NotI; Cloned unidirectionally. Poly(A)+ RNA
            was concentrated and purified using Dynabeads (Dynal) and

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mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART anchor. added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 662;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACA 14  
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Db 118 TTCCGACCCCAACA 131

RESULT 100  
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LOCUS r168907.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
DEFINITION cDNA 5' similar to IR:09VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
sequence.

ACCESSION CF351206 GI:33954015  
VERSION CF351206  
KEYWORDS  
SOURCE  
ORGANISM Meloidogyne javanica (root-knot nematode)

REFERENCE  
AUTHORS Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchima;  
Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 662).

REFERENCE  
AUTHORS McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J.,  
Wyle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Trasarellavilli, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Trasarellavilli, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterson, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter, J.P.  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu

Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART anchor. added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.

## FEATURES

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1. .662  
Location/Qualifiers  
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/db\_xref="taxon:6303"  
/issue\_type="whole organism"

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 662;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACA 14  
|||||  
Db 103 TTCCGACCCCAACA 116

## RESULT 101

LOCUS BQ412020 663 bp mRNA linear EST 22-MAY-2002  
DEFINITION GA\_Ed0053A10r Gossypium arboreum 7-10 dpa fiber library Gossypium  
ARBOREUM cDNA clone GA\_Ed0053A10r, mRNA sequence.

ACCESSION BQ412020  
VERSION BQ412020  
KEYWORDS  
SOURCE  
ORGANISM Gossypium arboreum

REFERENCE  
AUTHORS Gossypium arboreum  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eustrods II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 663)

REFERENCE  
AUTHORS Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
Unpublished (2000)  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu

Total High Quality bases = 457  
Seq primer: TAAATGACTCATATAGCG  
High quality sequence start: 3  
High quality sequence stop: 601.  
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## FEATURES

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ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 663;  
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
 |||||  
 94 GACCCACACTACT 107

RESULT 102  
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 LOCUS r166b12.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
 sequence.  
 CF351008 CF351008.1 GI:33953619

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Meloidogyne javanica (root-knot nematode)  
 Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
 1 (bases 1 to 665)

REFERENCE  
 AUTHORS  
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Ritzer,E., Bennett,J., Franklin,C.,  
 Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Stepcoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCam,R., Waterston,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

TITLE  
 JOURNAL  
 COMMENT  
 Email: east@watson.wustl.edu  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified  
 using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
 First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
 and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added  
 using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
 strand and primers specific to SMART oligo and 3' end. Double  
 stranded cDNA was digested using XhoI/NotI, fractionated on  
 Chroma-spin 400 columns (Clontech) and ligated to digested  
 pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
 host cells. Library materials provided by Dr. David Bird of North  
 Carolina State University. Library construction by Jeff Rousch. See  
 www.nematode.net for additional project information.  
 Seq primer: SP6.

FEATURES  
 source  
 Location/Qualifiers  
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 /note="Vector: plasmid (ampicillin resistant); Site 1:  
 XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA  
 was concentrated and purified using Dynabeads (Dyna) and  
 mRNA eluted for first strand synthesis. Clontech) and  
 primed with oligo(dT) with XhoI site and 5'SMART 'anchor'  
 added using chimeric DNA-RNA oligo. 12 PCR cycles were  
 done using first strand and primers specific to SMART  
 oligo and 3' end. Double stranded cDNA was digested using  
 XhoI/NotI, fractionated on Chroma-spin 400 columns

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 665;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCACACA 14  
 |||||  
 118 TTCCGACCCACACA 131

RESULT 103  
 CF350992 667 bp mRNA linear EST 20-AUG-2003  
 LOCUS cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
 DEFINITION  
 CF350992 CF350992.1 GI:33953587

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Meloidogyne javanica (root-knot nematode)  
 Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
 1 (bases 1 to 667)

REFERENCE  
 AUTHORS  
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Ritzer,E., Bennett,J., Franklin,C.,  
 Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Stepcoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCam,R., Waterston,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

TITLE  
 JOURNAL  
 COMMENT  
 Email: east@watson.wustl.edu  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified  
 using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
 First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
 and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added  
 using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
 strand and primers specific to SMART oligo and 3' end. Double  
 stranded cDNA was digested using XhoI/NotI, fractionated on  
 Chroma-spin 400 columns (Clontech) and ligated to digested  
 pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
 host cells. Library materials provided by Dr. David Bird of North  
 Carolina State University. Library construction by Jeff Rousch. See  
 www.nematode.net for additional project information.  
 Seq primer: SP6.

FEATURES  
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 XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA  
 was concentrated and purified using Dynabeads (Dyna) and  
 mRNA eluted for first strand synthesis. First strand cDNA

was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 667;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACA 14  
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Db 100 TTGCGACCCACACA 113

RESULT 104  
CF351019  
LOCUS  
DEFINITION  
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r166d01.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CF351019  
CF351019.1 GI:33953641  
EST.

Meloidogyne javanica (root-knot nematode)  
Meloidogyne javanica  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heterodidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 668)

REFERENCE  
AUTHORS  
McCartter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steploe,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCamn,R., Waterson,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT  
Contact: McCartter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Cloned unidirectionally. Poly(A) + RNA was concentrated and purified  
using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added  
using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
strand and primers specific to SMART oligo and 3' end. Double  
stranded cDNA was digested using XhoI/NotI, fractionated on  
Chroma-spin 400 columns (Clontech) and ligated to digested  
pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
host cells. Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff Rousch. See  
www.nematode.net for additional project information.  
Seq primer: Sp6.

## FEATURES

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/mol\_type="mRNA"  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACA 14  
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Db 94 TTGCGACCCACACA 107

RESULT 105  
CF351064  
LOCUS  
DEFINITION  
CF351064 668 bp mRNA linear EST 20-AUG-2003  
r166h11.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CF351064  
CF351064.1 GI:33953734  
EST.  
Meloidogyne javanica (root-knot nematode)  
Meloidogyne javanica  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heterodidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 668)

REFERENCE  
AUTHORS  
McCartter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steploe,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCamn,R., Waterson,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT  
Contact: McCartter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Cloned unidirectionally. Poly(A) + RNA was concentrated and purified  
using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added  
using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
strand and primers specific to SMART oligo and 3' end. Double  
stranded cDNA was digested using XhoI/NotI, fractionated on  
Chroma-spin 400 columns (Clontech) and ligated to digested  
pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
host cells. Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff Rousch. See  
www.nematode.net for additional project information.  
Seq primer: Sp6.

## FEATURES

Location/Qualifiers



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/lab\_host="DH10B"  
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/note="Vector: plasmid (ampicillin resistant); Site\_1: XhoI; Site\_2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna1) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractioned on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

Query Match 70.0%; Score 14; DB 7; Length 668;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACA 14  
118 TTGGGACCCACACA 131

Db

RESULT 106  
CL715790 671 bp DNA linear GSS 26-JUL-2004  
LOCUS  
DEFINITION OR\_BB8041P09.r OR\_BB8041P09 genomic clone OR\_BB8041P09  
ACCESSION CL715790  
VERSION CL715790.1 GI:50602828  
KEYWORDS GSS.  
SOURCE Oryza rufipogon  
ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 671)  
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.  
ONAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161 Std Error: 0.00  
Plate: 0041 row: P column: 09  
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Class: BAC ends.

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/tissue\_type="young leaves"  
/lab\_host="DH10B-Ti phage resistant"  
/clone\_id="OR\_BB8041P09"  
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ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 671;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGGGACCCACAC 15  
468 TTGGGACCCACAC 481

Db

RESULT 107  
CV006612/c  
LOCUS  
DEFINITION CS\_gil\_12D06\_M1Reverse Blue crab gill, normalized Callinectes sapidus cDNA clone CS\_gil\_12D06 5' similar to ref|NP\_652222.1| CG14310-P8 - Drosophila melanogaster. Score = 33.5 bits (75), Expect = 3.9, mRNA sequence.  
ACCESSION CV006612  
VERSION CV006612.1 GI:51365835  
KEYWORDS EST.  
SOURCE Callinectes sapidus (blue crab)  
ORGANISM Callinectes sapidus  
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidae; Portunidae; Callinectes.  
1 (bases 1 to 675)  
Shafer,T.H., Coblenz,P.E. and Towle,D.W.  
Expressed sequence tags from normalized cDNA libraries prepared from gill and hypodermis tissues of the blue crab, Callinectes sapidus  
Unpublished (2004)  
Contact: Thomas H. Shafer  
Department of Biological Sciences  
University of North Carolina Wilmington  
601 S. College Rd, Wilmington, NC 28403, USA  
Tel: 910-962-7275  
Fax: 910-962-4066  
Email: shafer@uncw.edu  
Plate: 12 row: D column: 06  
Seq primer: M13 Reverse  
High quality sequence stop: 487.

FEATURES  
Source  
1. .675  
/organism="Callinectes sapidus"  
/mol\_type="mRNA"  
/db\_xref="taxon:6763"  
/clone="CS\_gil\_12D06"  
/tissue\_type="Pooled anterior and posterior gills from crabs acclimated to salinities of 35 and 5 parts per thousand"  
/dev\_stage="Adult intermolt"  
/clone\_id="Blue crab gill, normalized"  
/note="Vector: PCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, and then pooled for construction and normalization of a cDNA library by invitrogen. Plasmids were isolated and inserts sequenced from their 5'-ends by the Blue Crab Molecular Genetics Laboratory at the University of North Carolina Wilmington. Traces were trimmed, compared (BLASTx) to NCBI non-redundant protein database as of 19 July 2004, and processed for submission to dbEST by trace2dbEST software (Parkinson, Anthony and Blaxter, unpublished software)."

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 675;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCAACTACT 19  
 Db 532 GACCCAACTACT 519

RESULT 108  
 LOCUS BQ405787/c  
 DEFINITION GA\_Ed0086H02f Gossypium arboreum 7-10 dpa fiber library Gossypium  
 accession BQ405787  
 VERSION BQ405787.1 GI:21093474  
 KEYWORDS EST.  
 SOURCE Gossypium arboreum  
 ORGANISM Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 676)  
 Wing, R.A., Fritsch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
 Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
 An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1..676  
 /organism="Gossypium arboreum"  
 /mol\_type="mRNA"  
 /strain="AKA"  
 /cultivar="8400"  
 /db\_xref="taxon:29729"  
 /clone="GA\_Ed0086H02f"  
 /tissue\_type="Fibers isolated from bolls harvested 7-10  
 dpa"  
 /lab\_host="E. coli"  
 /clone\_1ib="Gossypium arboreum 7-10 dpa fiber library"  
 /note="Vector: PBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
 Query Match 70.0%; Score 14; DB 5; Length 676;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCAACTACT 19  
 Db 649 GACCCAACTACT 636

RESULT 109  
 LOCUS CF351188  
 DEFINITION CF351188 676 bp mRNA linear EST 20-AUG-2003  
 r168e08.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 cDNA 5' similar to TR:Q9VXP5 Q9VXP5 C89595 PROTEIN.; mRNA  
 sequence.  
 accession CF351188  
 VERSION CF351188.1 GI:33953980  
 KEYWORDS EST.  
 SOURCE Meloidogyne javanica (root-knot nematode)  
 ORGANISM Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchima;  
 Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.

REFERENCE  
 AUTHORS  
 1 (bases 1 to 676)  
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
 Wylie, T., Dante, M., Maria, M., Hillier, L., Kucaba, T., Theising, B.,  
 Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
 Tsagaris, H., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
 Underwood, K., Steptoe, M., Allen, M., Peterson, B., Swaller, T.,  
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterson, R. and Wilson, R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1..676  
 /organism="Meloidogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /tissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_1ib="Meloidogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site\_1:  
 XhoI; Site\_2: NotI; Cloned unidirectionally. Poly(A)+ RNA  
 was concentrated and purified using Dynabeads (Dyna) and  
 mRNA eluted for first strand synthesis. First strand cDNA  
 was created using MMLV RT (Powerscript, Clontech) and  
 primed with oligo(dt) with XhoI site and 5'SMART 'anchor'  
 added using chimeric DNA-RNA oligo. 12 PCR cycles were  
 done using first strand and primers specific to SMART  
 oligo and 3' end. Double stranded cDNA was digested using  
 XhoI/NotI, fractionated on Chroma-spin 400 columns  
 (Clontech) and ligated to digested pGEM-11zf(+) plasmid.  
 Chemically competent DH10B cells were used as host cells.  
 Library materials provided by Dr. David Bird of North  
 Carolina State University. Library construction by Jeff  
 Rousch. See www.nematode.net for additional project  
 information. Seq primer: Sp6.

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 676;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACA 14  
 Db 118 TTGGGACCCACA 131

RESULT 110  
 LOCUS CF351106  
 DEFINITION CF351106 677 bp mRNA linear EST 20-AUG-2003  
 r167e08.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 cDNA 5' similar to TR:Q9VXP5 Q9VXP5 C89595 PROTEIN.; mRNA  
 sequence.  
 accession CF351106

VERSION CF351077  
 KEYWORDS EST.  
 SOURCE Meiodogyne javanica (root-knot nematode)  
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodermidae; Meiodogyninae; Meiodogyne.  
 REFERENCE 1 (bases 1 to 677)  
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Rilter,E., Bennett,J., Franklin,C., Tsagarishevili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Stepcoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCam,R., Waterston,R. and Wilson,R.  
 TITLE The Washington Univ. Nematode EST Project, 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information. Seq primer: SP6.

FEATURES  
 source  
 1. 677  
 /organism="Meiodogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /cissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_id="Meiodogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 677;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
 ||||||||||||  
 DB 118 TTCCGACCCACACA 131

RESULT 111

CF351077  
 LOCUS 681 bp mRNA linear EST 20-AUG-2003  
 DEFINITION r167b05.v1 Meiodogyne javanica J2 SMART pGEM Meiodogyne javanica cDNA 5' similar to TR:09VXP5 09VXP5 CG8959 PROTEIN. ; mRNA sequence.  
 ACCESSION CF351077  
 VERSION CF351077  
 KEYWORDS  
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodermidae; Meiodogyninae; Meiodogyne.  
 REFERENCE 1 (bases 1 to 681)  
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Rilter,E., Bennett,J., Franklin,C., Tsagarishevili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Stepcoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCam,R., Waterston,R. and Wilson,R.  
 TITLE The Washington Univ. Nematode EST Project, 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information. Seq primer: SP6.

FEATURES  
 source  
 1. 681  
 /organism="Meiodogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /cissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_id="Meiodogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 681;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
 |||||  
 118 TTCCGACCCACACA 131

RESULT 112  
 LOCUS CF350912  
 DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ; mRNA sequence.

ACCESSION CF350912  
 VERSION CF350912  
 KEYWORDS GI:33953430  
 SOURCE EST.  
 ORGANISM Meloidogyne javanica (root-knot nematode)

REFERENCE  
 AUTHORS Meloidogyne javanica (root-knot nematode); Tylenchida; Tylenchina; Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodridae; Meloidogyninae; Meloidogyne.  
 1 (bases 1 to 683)  
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterson,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)

TITLE JOURNAL  
 COMMENT The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Cloned unidirectionally. Poly(A) + RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.

Seq primer: Sp6.

FEATURES  
 source  
 Location/Qualifiers  
 1..683  
 /organism="Meloidogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /tissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_lib="Meloidogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A) + RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 683;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
 |||||  
 118 TTCCGACCCACACA 131

RESULT 113  
 LOCUS CF350974  
 DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ; mRNA sequence.

ACCESSION CF350974  
 VERSION CF350974  
 KEYWORDS GI:33953551  
 SOURCE EST.  
 ORGANISM Meloidogyne javanica (root-knot nematode)

REFERENCE  
 AUTHORS Meloidogyne javanica (root-knot nematode); Tylenchida; Tylenchina; Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodridae; Meloidogyninae; Meloidogyne.  
 1 (bases 1 to 685)  
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterson,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)

TITLE JOURNAL  
 COMMENT The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Cloned unidirectionally. Poly(A) + RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.

Seq primer: Sp6.

FEATURES  
 source  
 Location/Qualifiers  
 1..685  
 /organism="Meloidogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /tissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_lib="Meloidogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A) + RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns

(Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rouch. See [www.nematode.net](http://www.nematode.net) for additional project information."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 685;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCAACA 14  
|||||  
Db 118 TTCCGACCAACA 131

RESULT 114  
BM026959/c  
LOCUS  
DEFINITION BM026959 689 bp mRNA linear EST 13-OCT-2002  
inestinalis cDNA clone rcibd085d12 3', mRNA sequence.

ACCESSION BM026959  
KEYWORDS  
SOURCE EST.  
ORGANISM  
Ciona intestinalis  
Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 689)  
Sato Y., Satake, M., Azumi, K., Nonaka, M., Shin-i, T., Kohara, Y. and  
Sato, N.

TITLE  
JOURNAL  
COMMENT  
Expressed genes in *Ciona intestinalis* (2002)  
Unpublished (2002)  
Contact: Nori Sato  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: [sato@ascidian.zool.kyoto-u.ac.jp](mailto:sato@ascidian.zool.kyoto-u.ac.jp).

FEATURES  
source  
1..689  
location/Qualifiers  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="rcibd085d12"  
/issue\_type="blood cells"  
/clone\_id="Nori Sato unpublished cDNA library, blood cells"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 689;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCAACA 17  
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Db 494 GCGACCAACA 481

RESULT 115  
CL622579  
LOCUS  
DEFINITION CL622579 689 bp DNA linear GSS 01-JUL-2004  
OR\_BBA0017H11.r OR\_BBA Oryza rufipogon genomic clone OR\_BBA0017H11  
3', genomic survey sequence.

ACCESSION CL622579  
KEYWORDS  
SOURCE GSS.  
ORGANISM  
Oryza rufipogon  
Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 689)  
AUTHORS  
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Miller, C., Hatfield, J., Soderlund, C. and Wing, R.

TITLE  
JOURNAL  
COMMENT  
OMP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: <http://genome.arizona.edu>

PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161 Std Error: 0.00  
Plate: 0017 row: H column: 11  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

FEATURES  
source  
1..689  
location/Qualifiers  
/organism="Oryza rufipogon"  
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/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_id="OR\_BBA"  
/note="Vector: pGIRAC1, Site\_1: HindIII, Site\_2: HindIII"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 689;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TTCCGACCAACAC 15  
|||||  
Db 468 TTCCGACCAACAC 481

RESULT 116  
AI908584/c  
LOCUS  
DEFINITION AI908584 696 bp mRNA linear EST 30-MAR-2000  
CM-B1178-220499-027 B1178 Homo sapiens cDNA, mRNA sequence.

ACCESSION AI908584  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 696)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Macsukuma, A., Bata, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongenel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/seq/gethtml.pl?cl=CM-BT178-027.html  
&t3=220499&t4=1)  
Seq primer: puc 18 forward.  
Location/Qualifiers

FEATURES  
source 1..696

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/sex="female"  
/dev\_stage="Adult"  
/clone\_lib="BT178"

/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (O.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 70.0%; Score 14; DB 1; Length 696;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GACCCCAACTACT 18  
|||||

Db 412 GACCCCAACTACT 399

## RESULT 117

CN852507 704 bp mRNA linear EST 03-JUN-2004  
LOCUS Ha\_mx0\_01F05\_Spe Lobster Multiple Tissues, Normalized Homarus  
DEFINITION americanus cDNA clone Ha\_mx0\_01F05 5', mRNA sequence.  
ACCESSION CN852507  
VERSION CN852507.1 GI:48107332  
KEYWORDS EST.

SOURCE Homarus americanus (American lobster)  
ORGANISM

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
Nephropidae; Nephropidae; Homarus.

REFERENCE 1 (bases 1 to 704)  
Towle D.W. and Smith C.M.  
Expressed sequence tags in a normalized cDNA library prepared from multiple tissues of adult intermolt American lobster, Homarus americanus  
Unpublished (2004)

JOURNAL COMMENT  
Contact: David W. Towle  
Marine DNA Sequencing and Analysis Center  
Mount Desert Island Biological Laboratory  
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA  
Tel: 207-288-9880 x474  
Fax: 207-288-2130  
Email: dtowle@mdibl.org

Plate: 01 row: F column: 05  
Seq primer: SP6  
High quality sequence stop: 522.  
Location/Qualifiers

## FEATURES

source

1..704

/organism="Homarus americanus"  
/mol\_type="mRNA"

/db\_xref="taxon:6706"  
/clone\_lib="mx0\_01F05"

/tissue\_type="Gill, epipodite, branchiostegite, heart,  
ovary, testis, antennal gland, abdominal muscle,  
hepatopancreas, brain"

/dev\_stage="Adult intermolt"

/clone\_lib="Lobster Multiple Tissues, Normalized"  
/note="Vector: PCMV Sport 6.1; Total RNA samples were  
prepared individually from each tissue, checked for  
quality, then pooled for construction and normalization"

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 704;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GACCCCAACTACT 19  
|||||

Db 92 GACCCCAACTACT 105

## RESULT 118

BZ834863/c 706 bp DNA linear GSS 18-MAR-2003  
LOCUS CH240\_287D4\_TV CHORI-240 Bos taurus genomic clone CH240\_287D4,  
DEFINITION genomic survey sequence.  
ACCESSION BZ834863  
VERSION BZ834863.1 GI:29062220  
KEYWORDS GSS.

SOURCE Bos taurus (cow)  
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (bases 1 to 706)  
Zhao S., Shetty, J., Shatsman, S., Tsagaye, G., Geer, K.,  
Shvartsbeyn, A., Gebregorgis, E., Chen, D., Riggs, F., de Jong, P.,  
Crawford, A.M. and McEwan, J.C.  
Bovine BAC End Sequences from Library CHORI-240  
Unpublished (2003)  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@igr.org

(http://www.chori.org/bacpac/bovine240.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBMC) by AgResearch Ltd., New Zealand and The  
Institute of Genomic Research (TIGR), USA.  
Plate: 287 row: D column: 4  
Seq primer: T7  
Class: BAC ends.

## FEATURES

source

1..706

/organism="Bos taurus"  
/mol\_type="genomic DNA"

/strain="bred: Hereford"  
/db\_xref="taxon:9913"

/clone="CH240\_287D4"  
/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 706;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCGACACTACTC 20  
 |||||  
 Db 638 ACCGACACTACTC 625

RESULT 119  
 CD939205 707 bp mRNA linear EST 15-JUL-2003  
 LOCUS OV.112L23P010309 OV Triticum aestivum cDNA clone OV112L23, mRNA  
 DEFINITION  
 BEQUENCE.  
 ACCESSION CD939205  
 VERSION CD939205.1 GI:32786713  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Triticum.  
 1 (bases 1 to 707)  
 Genoplane.  
 Genoplane, a major partnership french program in plant genomics  
 UNPUBLISHED (2003)  
 CONTACT: Genoplane  
 COMMENT  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplane' (http://www.genoplane.com  
 and http://genoplane-info.inbio.gen.fr).  
 Location/Qualifiers  
 1..707  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="recital"  
 /db\_xref="taxon:4565"  
 /clone="OV112L23"  
 /tissue\_type="ovary"  
 /clone\_1ib="OV"

ORIGIN  
 Query Match 70.0%; Score 14; DB 6; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCGACCAACTACT 16  
 |||||  
 Db 631 CGCGACCAACTACT 644

RESULT 120  
 B2780370/c 708 bp DNA linear GSS 14-MAR-2003  
 LOCUS 1139c07.g1 WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor  
 DEFINITION  
 genomic clone 1139c07, genomic survey sequence.  
 ACCESSION B2780370  
 VERSION B2780370.1 GI:28957813  
 KEYWORDS GSS.  
 SOURCE Sorghum bicolor (sorghum)  
 ORGANISM Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 708)  
 Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,  
 Katzenburger, F., King, L., Miller, B., Miller, S., Nascimento, L.,  
 Zuber, T., Palmer, L., McCombie, W.R. and Martienssen, R.A.  
 Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)  
 UNPUBLISHED (2002)  
 CONTACT: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mcombie@cshl.org  
 Plate: 1139 row: c column: 07  
 Seq primer: -21M13UnivRev  
 Class: shotgun  
 High quality sequence atp: 708.  
 Location/Qualifiers  
 1..708  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4558"  
 /clone="1139c07"  
 /lab\_host="DH5a"  
 /clone\_1ib="WGS-SbicolorF (DH5a methyl filtered)"  
 /note="Site 1: Xba I; Site 2: Xba I; The vector was  
 digested with Xba I and one nucleotide was added by fill in  
 in the recessive 3' end. The genomic DNA was nebulized,  
 end repaired, adaptor ligated and size fractionated using  
 sephadex. The resulting fragments were between 0.8 and 3  
 kb and were cloned into the vector (x/y reads in M13mp19,  
 b/g reads in pUC19). The same ligation was transformed  
 into DH5a."

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 708;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACT 19  
 |||||  
 Db 404 GACCCACACTACT 391

RESULT 121  
 BM086868/c 711 bp mRNA linear EST 22-OCT-2002  
 LOCUS BM086868  
 DEFINITION  
 BM086868 Nori Satoh unpublished cDNA library, larva Clona  
 intestinalis cDNA clone rc1lv047d09 3', mRNA sequence.  
 ACCESSION BM086868  
 VERSION BM086868.1 GI:24262148  
 KEYWORDS EST.  
 SOURCE Clona intestinalis  
 ORGANISM Clona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Cloniidae; Clona.  
 1 (bases 1 to 711)  
 Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.  
 Expressed genes in Clona intestinalis (2002c)  
 UNPUBLISHED (2002)  
 CONTACT: Nori Satoh  
 Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: satoh@acidian.zool.kyoto-u.ac.jp.  
 Location/Qualifiers  
 1..711  
 /organism="Clona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="rc1lv047d09"  
 /tissue\_type="whole animal"  
 /dev\_stage="larva"  
 /clone\_1ib="Nori Satoh unpublished cDNA library, larva"

ORIGIN  
 Query Match 70.0%; Score 14; DB 5; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGACCAACTACT 17

Db 495 GCGACCCCACTACT 482

RESULT 122  
LOCUS CF473928  
DEFINITION RTMW2\_19 B10\_g1\_A021 Well-watered loblolly pine roots WM2 Pinus taeda cDNA clone RTMW2\_19\_B10\_A021 5', mRNA sequence.  
ACCESSION CF473928  
VERSION CF473928.1  
KEYWORDS GI:34491300  
SOURCE EST.  
ORGANISM Pinus taeda (loblolly pine)  
Pinus taeda  
Pinus taeda (loblolly pine)  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 712)  
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.  
An EST database from well-watered loblolly pine (Pinus taeda) roots Unpublished (2003)  
Other ESTs: RTMW2\_19\_B10\_b1\_A021  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmprratt@uga.edu  
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement  
Seg primer: JENREV (CAGGAACAGCTATGACC).  
Location/Qualifiers  
1..712  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="CLONES"  
/db\_xref="taxon:3352"  
/clone="RTMW2\_19\_B10\_A021"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Well-watered loblolly pine roots WM2"  
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 712;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCCACTACT 19  
Db 640 GACCCCACTACT 653

RESULT 123  
LOCUS CG197500  
DEFINITION CG197500 713 bp DNA linear GSS 21-AUG-2003  
PUIFF58TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBta0569020, genomic survey sequence.  
ACCESSION CG197500  
VERSION CG197500.1  
KEYWORDS GI:34088575  
GSS.

SOURCE  
ORGANISM Zea mays  
Zea mays  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 713)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Benneken, J.  
Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PUIFF58TB  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seg primer: TP  
Class: sheared ends.  
Location/Qualifiers  
1..713  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZMMBta0569020"  
/clone="ZM 0.6 1.0 KB"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high cot selected genomic DNA library"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 713;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACT 14  
Db 376 TTGCGACCCCACTACT 389

RESULT 124  
LOCUS CC700610/c  
DEFINITION CC700610 716 bp DNA linear GSS 19-JUN-2003  
OGUIM02TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBma0477A03, genomic survey sequence.  
ACCESSION CC700610  
VERSION CC700610.1  
KEYWORDS GI:32105386  
GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 716)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGUIM02TH  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seg primer: TP  
Class: sheared ends.  
Location/Qualifiers  
1..716  
/organism="Zea mays"  
/mol\_type="genomic DNA"

FEATURES  
source



/strain="873"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA0471A03"  
 /clone\_id="ZM\_0.7\_1.5\_KB"  
 /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 716;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCCAACA 14  
 |||||||||  
 Db 634 TTCCGACCCCAACA 621

RESULT 125  
 CE147261 716 bp DNA linear GSS 25-SEP-2003  
 LOCUS tigr-g98-dog-17000371298782 Dog Library Canis familiaris genomic,  
 DEFINITION genomic survey sequence.  
 ACCESSION CE147261  
 VERSION CE147261.1 GI:35263354  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM  
 Canis familiaris (dog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 716)  
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 PUBMED 14512627

## COMMENT

Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.  
 Location/Qualifiers

FEATURES  
 source  
 1..716  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_id="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 716;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ACCCACTACTC 20  
 |||||||||  
 Db 38 ACCCACTACTC 51

RESULT 126  
 CC154782 718 bp DNA linear GSS 25-APR-2003  
 LOCUS CSU-K34-124F11.T7 CSU-K34 Aedes aegypti genomic clone  
 DEFINITION CSU-K34-124F11, genomic survey sequence.  
 CC154782  
 ACCESSION CC154782.1 GI:30108078  
 VERSION GSS.  
 KEYWORDS

SOURCE  
 ORGANISM  
 Aedes aegypti (yellow fever mosquito)  
 Aedes aegypti  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;  
 Stegomyia.  
 1 (bases 1 to 718)

Loftus,B., Shetty,J., Knudson,D. and Severson,D.  
 BAC end sequencing of Aedes aegypti  
 Unpublished (2003)

Other GSSs: CSU-K34.124F11.SP6  
 Contact: Brendan Loftus  
 Department of Eukaryotic Genomics  
 TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-3543  
 Fax: 301-838-0208  
 Email: entae@tigr.org  
 Library was provided by Susan Brown and Dennis Knudson at Colorado  
 State University.  
 Seq primer: T7  
 Class: BAC ends.  
 Location/Qualifiers

FEATURES  
 source  
 1..718  
 /organism="Aedes aegypti"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7159"  
 /clone="CSU-K34-124F11"  
 /clone\_id="CSU-K34"  
 /note="Vector: pBAC3.6; Site 1: EcoRI; Source DNA: Aedes  
 aegypti; strain unknown (derived from freshly hatched  
 larvae at the Virus Research Centre, Poona, India.  
 Reference: SINGH, K. R. P., 1967 Cell cultures derived  
 from larvae of Aedes albopictus (Skuse) and Aedes aegypti  
 (L.). Current Science 36: 506-508; ATC-10 cell line ATCC  
 CCL-125"

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 718;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCCAACA 14  
 |||||||||  
 Db 184 TTCCGACCCCAACA 197

RESULT 127  
 BQ971958 721 bp mRNA linear EST 21-AUG-2002  
 LOCUS QHB9D19.yg.ab1 QH ABCDI sunflower RH801 Helianthus annuus cDNA  
 DEFINITION clone QHB9D19, mRNA sequence.  
 ACCESSION BQ971958  
 VERSION BQ971958.1 GI:22389479  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM  
 Helianthus annuus (common sunflower)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;  
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
 Heliantheae; Helianthus.  
 1 (bases 1 to 721)

Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,  
 Lin,H., Van Damme,W., Lavelle,D., Chevalier,P., Ziegler,J.,  
 Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,  
 Lai,Z., Church,S., Jackson,L. and Bradford,K.  
 Lettuce and Sunflower ESTs from the Compositae Genome Project  
 http://compogenetics.ucdavis.edu/  
 Unpublished (2002)

CONTACT: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Amundson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659  
 Email: akozaki@atgc.org [michelmore@vegmail.ucdavis.edu]  
 belongs to contig OH\_Ca\_Contig4100, see <http://cspdb.ucdavis.edu/>  
 for details.  
 Plate: QHB9 row: D column: 19.  
 Location/Qualifiers  
 1..721  
 /organism="Helianthus annuus"  
 /mol\_type="mRNA"  
 /cultivar="RHA801"  
 /db\_xref="taxon:4232"  
 /clone="QHB9D19"  
 /lab\_host="E.coli"  
 /clone\_lib="OH ABCDI sunflower RHA801"  
 /note="Vector: pBRCDNA5fiAB: The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cspdb.ucdavis.edu/>  
 TAG\_LIB=OH ABCDI sunflower RHA801  
 TAG\_SEQ=TTGACCGCGG"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 721;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCGACCCACACTA 17  
 |||||  
 Db 556 GCGACCCACACTA 569

RESULT 128 728 bp DNA linear GSS 03-JUN-2004  
 AG407958  
 LOCUS  
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-267C14.T7, genomic survey  
 sequence.

ACCESSION AG407958 GI:48050644  
 VERSION AG407958.1  
 KEYWORDS Mus musculus molossinus  
 SOURCE Mus musculus molossinus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 BAC end Sequences of Library MSMg01  
 Unpublished  
 2 (bases 1 to 728)  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 Direct Submision  
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel:81-45-503-9111, Fax:81-45-503-9170  
 (E-mail:hattori@gsc.riken.jp, URL:<http://hgp.gsc.riken.go.jp/>,  
 Clones are derived from the mouse BAC library MSMg01. For BAC  
 library availability, please contact Kunya Abe (abe@rtc.riken.jp).  
 Teukuba Institute, Bio Resource Center.  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyada, Teukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp

## COMMENT

PRIMERS  
 Sequencing : T7  
 LIBRARY  
 Vector : pBAC3.6  
 R.Site 1 : EcoRI

R.Site 2 : EcoRI.  
 Location/Qualifiers  
 1..728  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMg01-267C14.T7"  
 /sex="male"  
 /tissue\_type="mixture of kidney and spleen"  
 /clone\_lib="MSMg01 Mouse Male BAC Library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 728;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCGCACCCACAC 15  
 |||||  
 Db 487 TCGCACCCACAC 500

RESULT 129 730 bp mRNA linear EST 29-SEP-2004  
 CV434255/c  
 LOCUS  
 DEFINITION CS\_hyp\_33b05\_M13Reverse Blue crab hypodermis, normalized  
 Callinectes sapidus cDNA clone CS\_hyp\_33b05.5' similar to  
 ref|NP\_652222.1| CG14310-PB - Drosophila melanogaster. Score = 33.9  
 bits (76), Expect = 3.5, mRNA sequence.

ACCESSION CV434255 GI:52843545  
 VERSION CV434255.1  
 KEYWORDS EST.  
 SOURCE Callinectes sapidus (blue crab)  
 ORGANISM Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 Eubrachyura; Portunodea; Portunidae; Callinectes.

REFERENCE 1 Shafer, T.H., Coblenz, F.E. and Towle, D.W.  
 Expressed sequence tags from normalized cDNA libraries prepared  
 from gill and hypodermis tissues of the blue crab, Callinectes  
 sapidus  
 Unpublished (2004)  
 Contact: Thomas H. Shafer  
 Department of Biological Sciences  
 University of North Carolina Wilmington  
 601 S. College Rd, Wilmington, NC 28403, USA  
 Tel: 910-962-7275  
 Fax: 910-962-4066  
 Email: shafer@uncw.edu

## JOURNAL

COMMENT  
 Plate: 33 row: b column: 05  
 Seg primer: M13 Reverse  
 High quality sequence stop: 494.  
 Location/Qualifiers  
 1..730  
 /organism="Callinectes sapidus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6763"  
 /clone="CS\_hyp\_33b05"  
 /tissue\_type="Pooled hypodermal epithelium from the  
 mid-dorsal region and arthrodial membrane of pre-molt  
 (stage D2) and 3-hour postmolt crabs"  
 /dev\_stage="adult"  
 /clone\_lib="Blue crab hypodermis, normalized"  
 /note="Vector: pCMV Sport 6.1; Total RNA samples were  
 prepared individually from each tissue, checked for  
 quality, and then pooled for construction and  
 normalization of a cDNA library by Invitrogen. Plasmids  
 were isolated and inserts sequenced from their 5'-ends by  
 the Blue Crab Molecular Genetics Laboratory at the  
 University of North Carolina Wilmington. Tissues were  
 trimmed, compared (BLASTx) to NCBI non-redundant protein  
 database as of 19 July 2004, and processed for submission

## FEATURES

source

to dbEST by trace2dbEST software (Parkinson, Anthony and Blaxter, unpublished software)."

Query Match 70.0%; Score 14; DB 7; Length 730;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
|||||  
Db 311 GACCCACACTACT 298

RESULT 130  
LOCUS CF437404 733 bp mRNA linear EST 04-SEP-2003  
DEFINITION EST673749 normalized cDNA library of onion Allium cepa cDNA clone  
ACADT02, mRNA sequence.  
ACCESSION CF437404  
VERSION CF437404.1 GI:34460094  
KEYWORDS EST.  
SOURCE Allium cepa (onion)  
ORGANISM Allium cepa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
Allium.

REFERENCE 1 (bases 1 to 733)  
AUTHORS Haavey,M.J., Cheung,F., Van Aken,S., Uterback,T. and Town,C.D.  
TITLE Expressed Sequence Tags from a normalized library of mixed onion  
tissues (Allium cepa)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Haavey MJ  
Department of Horticulture  
USDA-ARS and University of Wisconsin  
1575 Linden Drive, Madison, WI 53706, USA  
Tel: 608-262-1830  
Fax: 608-262-4743  
Email: mhaavey@facstaff.wisc.edu  
TIGR sequence name ACADT02NR. For more information:  
http://haavey1ab.hort.wisc.edu  
Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES  
source  
Location/Qualifiers  
1..733  
/organism="Allium cepa"  
/mol\_type="mRNA"  
/cultiVar="Red Creole (bulbs), unknown (callus), Ebano &  
Texas Legend (roots)"  
/db\_xref="taxon:4679"  
/clone="ACADT02"  
/issue\_type="Callus, roots, and young bulbs"  
/clone\_lib="normalized cDNA library of onion"  
/note="Vector: pCMVSPORT6.1-ccdb (Invitrogen); Site 1:  
ECORV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA  
from callus, roots, and young bulbs were combined to  
synthesize the library. Normalization to enrich for  
low-copy transcripts was performed by proprietary  
techniques of Invitrogen."

#### ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 733;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCGACACTACTC 20  
|||||  
Db 75 ACCGACACTACTC 86

RESULT 131  
LOCUS CV526561 743 bp mRNA linear EST 07-OCT-2004  
DEFINITION CS GIL\_14A04 SP6 Blue crab gill, normalized Callinectes sapidus  
cDNA clone CG\_14A04 5' similar to ref|NP\_652222.1| CG14310-PB -

Drosophila melanogaster. Score = 33.9 bits (76), Expect = 3.6, mRNA  
sequence.  
ACCESSION CV526561  
VERSION CV526561.1 GI:53910940  
KEYWORDS EST.  
SOURCE Callinectes sapidus (blue crab)  
ORGANISM Callinectes sapidus  
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
Eumalacostraca; Eucarida; Decapoda; Ploceymata; Brachyura;  
Eubrachyura; Portunoidae; Portunidae; Callinectes.  
1 (bases 1 to 743)  
AUTHORS Shafer,T.H., Coblenz,F.E. and Towle,D.W.  
TITLE Expressed sequence tags from normalized cDNA libraries prepared  
from gill and hypodermis tissues of the blue crab, Callinectes  
sapidus  
JOURNAL Unpublished (2004)  
COMMENT Contact: Thomas H. Shafer  
Department of Biological Sciences  
University of North Carolina Wilmington  
601 S. College Rd, Wilmington, NC 28403, USA  
Tel: 910-962-7275  
Fax: 910-962-4066  
Email: shafer@uncw.edu  
Plate: 14 row: A column: 04  
Seq primer: SP6  
High quality sequence stop: 508.

FEATURES  
source  
Location/Qualifiers  
1..743  
/organism="Callinectes sapidus"  
/mol\_type="mRNA"  
/db\_xref="taxon:6763"  
/clone="CS GIL\_14A04"  
/tissue\_type="Pooled anterior and posterior gills from  
crabs acclimated to salinities of 35 and 5 parts per  
thousand"  
/dev stage="Adult intermolt"  
/clone\_lib="Blue crab gill, normalized"  
/note="Vector: pCMV Sport 6.1; Total RNA samples were  
prepared individually from each tissue, checked for  
quality, and then pooled for construction and  
normalization of a cDNA library by Invitrogen. Plasmids  
were isolated and inserts sequenced from their 5'-ends by  
the Blue Crab Molecular Genetics Laboratory at the  
University of North Carolina Wilmington. Traces were  
trimmed, compared (BLASTx) to NCBI non-redundant protein  
database as of 19 July 2004, and processed for submission  
to dbEST by trace2dbEST software (Parkinson, Anthony and  
Blaxter, unpublished software)."

#### ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 743;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
|||||  
Db 410 GACCCACACTACT 397

RESULT 132  
LOCUS CG067495 746 bp DNA linear GSS 19-AUG-2003  
DEFINITION P01AH36TD\_ZM\_0.6\_1.0\_KB Zea mays genomic clone ZM8BTA0537F24,  
genomic survey sequence.  
ACCESSION CG067495  
VERSION CG067495.1 GI:33939675  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 746)

**AUTHORS**  
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and Benneken, J.

**TITLE**  
 Maize Genomics Consortium

**JOURNAL**  
 Unpublished (2003)

**COMMENT**  
 Other GSSs: PUAH36TB  
 Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TP  
 Class: sheared ends.

**FEATURES**  
 Location/Qualifiers  
 1..746  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBTa0537F24"  
 /clone\_id="ZM\_0\_6\_1.0\_KB"  
 /note="Vector: PCR4-TOPD; Site 1: EcoRI; 0.6-1.0 kb high Cor selected genomic DNA library"

**ORIGIN**  
 Query Match 70.0%; Score 14; DB 9; Length 746;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
 4 GCGAGCCACACTA 17  
 |||||  
 642 GCGAGCCACACTA 655

**RESULT 133**  
 BF864639/c

**LOCUS**  
 BF864639 747 bp mRNA linear EST 19-JAN-2001

**DEFINITION**  
 963053B05.y1 C. reinhardtii CC-1690, Stress condition I, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA

**ACCESSION**  
 BF864639

**VERSION**  
 BF864639.1 GI:12254783

**KEYWORDS**  
 EST.

**SOURCE**  
 Chlamydomonas reinhardtii

**ORGANISM**  
 Chlamydomonas reinhardtii  
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

**REFERENCE**  
 1 (bases 1 to 747)  
 Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C., Lefebvre, P., McDermott, J. P., Shrager, J., Sillflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants, Project phase 3 unpublished (2000)

**JOURNAL**  
 Contact: Charles Hauser  
 DCMB Box 91000  
 Durham, NC 27708-1000  
 Tel: 919 613 8159  
 Fax: 919 613 8177  
 Email: chauser@duke.edu.

**COMMENT**  
 Location/Qualifiers  
 1..747  
 /organism="Chlamydomonas reinhardtii"  
 /mol\_type="mRNA"  
 /strain="CC-1690 wild type mt+ 21gr"  
 /db\_xref="taxon:3055"  
 /clone\_id="C. reinhardtii CC-1690, Stress condition I, normalized, Lambda Zap II"  
 /note="Vector: Bluescript II SK-; Site 1: EcoRI, Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to

**AUTHORS**  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

**TITLE**  
 BAC end Sequences of Library MSMg01

**JOURNAL**  
 Unpublished

**REFERENCE**  
 2 (bases 1 to 749)  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. Direct Submision Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shuhiro-chou Tsunagi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

**COMMENT**  
 Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp

**PRIMERS**  
 Sequencing : TV

**LIBRARY**  
 Vector : pBACe3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.

**FEATURES**  
 Location/Qualifiers  
 1..749  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSWg01-499C06.TU"  
 /sex="male"  
 /tissue\_type="mixture of kidney and spleen"  
 /clone\_id="MSWg01 Mouse Male BAC Library"

**ORIGIN**  
 Query Match 70.0%; Score 14; DB 9; Length 749;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
 2 TCGGAGCCACAC 15  
 |||||  
 711 TCGGAGCCACAC 698

**RESULT 134**  
 AG575296

**LOCUS**  
 AG575296 749 bp DNA linear GSS 05-JUN-2004

**DEFINITION**  
 Mus musculus molossinus DNA, clone:MSWg01-499C06.TU, genomic survey sequence.

**ACCESSION**  
 AG575296

**VERSION**  
 AG575296.1 GI:48336126

**KEYWORDS**  
 GSS.

**SOURCE**  
 Mus musculus molossinus

**ORGANISM**  
 Mus musculus molossinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

**REFERENCE**  
 1  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. BAC end Sequences of Library MSMg01

**JOURNAL**  
 Unpublished

**COMMENT**  
 mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min, 1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, 1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. Bluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

Oy 7 ACCGACACTACTC 20  
 Db 519 ACCGACACTACTC 532

RESULT 135  
 CC889635/c  
 LOCUS  
 DEFINITION CC889635 753 bp DNA linear GSS 31-JUL-2003  
 ZMMBRC0504N21f ZMMBRC Zea mays genomic clone ZMMBRC0504N21 5',  
 genomic survey sequence.  
 ACCESSION CC889635  
 VERSION CC889635.1 GI:33367503  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 753)  
 Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
 Ronzard,K., Fuks,G., Yu,Y., Wang,R. and Messing,J.  
 Sequencing of the maize genome at PGIR (2003)  
 Unpublished (2003)  
 CONTACT: Bharti, A.K.  
 Dr. Joachim Messing's lab  
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
 University  
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 Tel: 732 445 3801  
 Fax: 732 445 5735  
 Email: bharti@waksman.rutgers.edu  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence start: 118.  
 Location/Qualifiers  
 1..753  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultiivar="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBRC0504N21"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="ZMMBRC"  
 /note="Vector: pTRABAC1.3; Site\_1: BamHI; Site\_2: BamHI"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCCACACTA 17  
 Db 718 GCGACCCACACTA 705

RESULT 136  
 BW407445/c  
 LOCUS  
 DEFINITION BW407445 Yutaka Satou unpublished cDNA library, embryo whole animal  
 Ciona intestinalis cDNA clone ciem854g11 3', mRNA sequence.  
 ACCESSION BW407445  
 VERSION BW407445.1 GI:47823273  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.  
 1 (bases 1 to 754)  
 Satou,Y., Shin-I,T., Kohara,Y. and Satou,N.  
 Expressed genes in Ciona intestinalis (2004)  
 Unpublished (2004)  
 Contact: Yutaka Satou

Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4095  
 Fax: 81-75-705-1113  
 Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES  
 source  
 1..754  
 /organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="ciem854g11"  
 /issue\_type="whole animal"  
 /dev\_stage="embryo"  
 /clone\_lib="Yutaka Satou unpublished cDNA library, embryo  
 whole animal"

ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 754;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCCACACTA 17  
 Db 496 GCGACCCACACTA 483

RESULT 137  
 BQ968763  
 LOCUS  
 DEFINITION OHB35B10.YG.ab1 OH ABCD1 sunflower RHA801 Helianthus annuus cDNA  
 clone OHB35B10, mRNA sequence.  
 ACCESSION BQ968763  
 VERSION BQ968763.1 GI:22386284  
 KEYWORDS EST.  
 SOURCE Helianthus annuus (common sunflower)  
 ORGANISM Helianthus annuus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
 Heliantheae; Helianthus.  
 1 (bases 1 to 760)  
 Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,  
 Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,  
 Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,  
 Lai,Z., Church,S., Jackson,L. and Bradford,K.  
 lettuce and sunflower ESTs from the Compositae Genome Project  
 http://compgenome.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmudson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
 belongs to contig OH\_Ca\_Config4100, see http://cgdb.ucdavis.edu/  
 for details.  
 Plate: OHB35 row: B column: 10.  
 Location/Qualifiers  
 1..760  
 /organism="Helianthus annuus"  
 /mol\_type="mRNA"  
 /cultiivar="RHA801"  
 /db\_xref="taxon:4232"  
 /clone="OHB35B10"  
 /clone\_lib="OH ABCD1 sunflower RHA801"  
 /lab\_host="E. coli"  
 /note="Vector: pBRCDNASflab; The library was constructed  
 from 11 different sources of RNA from a single genotype.  
 Separate cDNAs were generated using primers that  
 incorporated unique 5' and 3' tags to distinguish each  
 source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at [http://cgpsdb.ucdavis.edu/TAG\\_TISSUE=chemical\\_induction](http://cgpsdb.ucdavis.edu/TAG_TISSUE=chemical_induction)  
TAG LIB=OH ABCDI sunflower RHAB01  
TAG\_SEQ=GTGAGCCGGG

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 760;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GCGACCACTACTC 17  
|||||  
Db 556 GCGACCACTACTC 569

RESULT 138  
BX172443 765 bp DNA linear GSS 28-JAN-2003  
LOCUS BX172443  
DEFINITION Danio rerio genomic clone DKRY-145G10, genomic survey sequence.  
ACCESSION BX172443  
VERSION BX172443.1 GI:28004148  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

REFERENCE  
AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.  
TITLE Submitted (27-JUN-2003) The Sanger Institute, Wellcome Trust Genome  
JOURNAL Direct Submission  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humphray@sanger.ac.uk Unpublished  
This sequence was generated from the SP6 end of BAC 145G10. 145G10  
is part of the Daniokey BAC library created by R. Plasterk and N.V.  
Keygene. Further details:  
[http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/)  
Location/Qualifiers  
1. 765  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKRY-145G10"  
/tissue\_type="Testis"  
/note="vector pindigobAC-536"

## COMMENT

FEATURES  
source

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 765;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACTACTC 20  
|||||  
Db 569 ACCCAACTACTC 582

RESULT 139  
BF631334 768 bp mRNA linear EST 22-OCT-2001  
LOCUS BF631334  
DEFINITION HVSMB0015K06f Hordeum vulgare seedling shoot EST library  
HVCDA0002 (Dehydration stress) Hordeum vulgare subsp. vulgare cDNA  
clone HVSMB0015K06f, mRNA sequence.  
ACCESSION BF631334  
VERSION BF631334.2 GI:13092041  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.

RESULT 140  
CB350437 769 bp mRNA linear EST 17-MAY-2003  
LOCUS CB350437  
DEFINITION P2A06 Cotton fiber subtracted cDNA library Gossypium hirsutum cDNA,  
mRNA sequence.

## REFERENCE

1 (bases 1 to 768)  
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D.,  
Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W.,  
Fenton, R.D., Oates, R. and Main, D.  
Development of a genetically and physically anchored EST resource  
for barley genomics: Morex drought-stressed seedling shoot cDNA  
library  
Unpublished (2001)

## JOURNAL

On Dec 19, 2000 this sequence version replaced gi:11895492.

## COMMENT

Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: [twing@clemson.edu](mailto:twing@clemson.edu)  
Total hg bases = 329  
Seq primer: AATTACCTCTCAAGG  
High quality sequence stop: 431.

## FEATURES

source

1. 768  
/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
/cultivar="Morex"  
/sub\_species="vulgare"  
/db\_xref="taxon:112509"  
/clone="HVSMB0015K06f"  
/tissue\_type="Seedling shoot"  
/lab\_host="TUC121"  
/clone\_lib="Hordeum vulgare seedling shoot EST library  
HVCDA0002 (Dehydration stress)"  
/note="Vector: lambdaZAP, Site 1: EcoRI, Site 2: XhoI,  
Seeds were surface sterilized then germinated under axenic  
conditions in the dark at room temperature on filter paper  
with water, nystatin and cefotaxime in covered  
crystallization dishes. Five-day old seedlings were  
incubated at 90% RH for 24 hr. Shoots were then harvested,  
total RNA was prepared, poly(A) RNA was purified, one  
primary unamplified cDNA library was made, 600000 pfu were  
in vivo excised to give plasmid SK(-) cDNA phagemids.  
These steps were performed in the TU Close laboratory at  
the University of California, Riverside (Choi, Close,  
Fenton). Phagemids were plated and picked at the Clemson  
University Genomics Institute (CUGI) (Begum, Palmer,  
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
sequencing and sequence analysis were performed at CUGI  
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
The sequence has been trimmed to remove vector sequence  
and contains a minimum of 100 bases of phred value 20 or  
above. For more details on library preparation and  
sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
this clone see <http://www.genome.clemson.edu/orders> Also  
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30  
(<http://wheat.pw.usda.gov/99pages/bgn/31/cover.html>)"

## ORIGIN

Query Match 70.0%; Score 14; DB 2; Length 768;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACTACTC 20  
|||||  
Db 757 ACCCAACTACTC 744

RESULT 140  
CB350437 769 bp mRNA linear EST 17-MAY-2003  
LOCUS CB350437  
DEFINITION P2A06 Cotton fiber subtracted cDNA library Gossypium hirsutum cDNA,  
mRNA sequence.

ACCESSION CB350437  
 VERSION CB350437.1 GI:30841117  
 KEYWORDS EST  
 SOURCE Gossypium hirsutum (upland cotton)  
 ORGANISM Gossypium hirsutum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 769)  
 J1.S.J., Lu,Y.C., Feng,J.X., Wei,G., Li,J., Shi,Y.H., Fu,Q., Liu,D., Luo,J.C. and Zhu,Y.X.  
 Isolation and analyses of genes preferentially expressed during early cotton fiber development by subtractive PCR and cDNA array  
 Nucleic Acids Res. 31 (10), 2534-2543 (2003)  
 JOURNAL 25622070  
 MEDLINE 12736302  
 PUBMED  
 COMMENT Contact: Zhu, Y.  
 National Laboratory of Protein Engineering and Plant Genetic Engineering  
 College of Life Sciences, Peking University  
 Beijing 100871, China  
 Tel: 86 10 6275 1193  
 Fax: 86 10 6275 4427  
 Email: zhuyx@water.pku.edu.cn.  
 Location/Qualifiers  
 1..769  
 /organism="Gossypium hirsutum"  
 /mol\_type="mRNA"  
 /cultivar="Xu-142"  
 /db\_xref="taxon:3635"  
 /tissue\_type="fiber"  
 /dev\_stage="10 days post anthesis (dpa)"  
 /clone\_lib="Cotton fiber subtracted cDNA library"  
 /note="The library was constructed using PCR-select cDNA subtraction method with 10 dpa cotton fiber as tester and fiberless mutant as driver"

ORIGIN  
 Query Match 70.0%; Score 14; DB 6; Length 769;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19  
 |||||  
 Db 659 GACCCACACTACT 646

RESULT 141  
 BH422873 771 bp DNA linear GSS 12-DEC-2001  
 LOCUS BOHFW02TF BOHF Brassica oleracea genomic clone BOHFW02, genomic survey sequence.  
 ACCESSION BH422873  
 VERSION BH422873.1 GI:17608601  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 771)  
 Town,C.D., Van Aken,S., Utechtack,T., Koo,H. and Fraser,C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other GSSs: BOHFW02TR  
 COMMENT Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF

Class: sheared ends.  
 Location/Qualifiers  
 1..771  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="T01000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOHFW02"  
 /clone\_lib="BOHF"  
 /note="Vector: pHOS1; Site\_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 771;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCACACA 14  
 |||||  
 Db 258 TTCCGACCCACACA 271

RESULT 142  
 AZ187767 779 bp DNA linear GSS 30-AUG-2000  
 LOCUS SP\_1009\_B2\_H12\_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1009 Col=24 Row=P, genomic survey sequence.  
 ACCESSION AZ187767  
 VERSION AZ187767.1 GI:8370946  
 KEYWORDS GSS.  
 SOURCE Strongylocentrotus purpuratus  
 ORGANISM Strongylocentrotus purpuratus  
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae; Strongylocentrotus.  
 1 (bases 1 to 779)  
 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Iehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.  
 A sea urchin genome project: Sequence scan, virtual map, and additional resources  
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
 JOURNAL 20402566  
 MEDLINE 10920195  
 PUBMED  
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L  
 Division of Biology 156-29  
 California Institute of Technology  
 Pasadena California 91125, USA  
 Tel: (626) 395-8421  
 Fax: (626) 793-3047  
 Email: acameron@caltech.edu  
 Plate: 1009 row: P column: 24  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 779.  
 Location/Qualifiers  
 1..779  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7668"  
 /clone="Plate=1009 Col=24 Row=P"  
 /clone\_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"  
 /note="Organ: sperm, Vector: BACs3.6, BAC Clones in E-Coli DH10B"

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 779;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCACTACTAC 18  
 Db 15 CGACCACTACTAC 28

RESULT 143  
 B2822648  
 LOCUS 779 bp DNA linear GSS 18-MAR-2003  
 DEFINITION PUBB95STD ZM\_0.6\_1.0\_KB Zea mays genomic clone ZMBR317P22,  
 genomic survey sequence.  
 ACCESSION B2822648  
 VERSION B2822648.1 GI:29038307  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 779)  
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennezen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other GSSs: PUBB95STB  
 Contact: Cathy WhiteJaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteJaw@tigr.org  
 Seq primer: TF  
 Class: sheared ends.

FEATURES  
 source  
 1..779  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMBR317P22"  
 /clone\_lib="ZM\_0.6\_1.0\_KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cot selected genomic DNA library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 779;  
 Best Local Similarity 100.0%; Pred.No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCACTACTCTC 20  
 Db 518 ACCCACTACTCTC 531

RESULT 144  
 AG581296  
 LOCUS 783 bp DNA linear GSS 05-JUN-2004  
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-507A20.T7, genomic survey  
 sequence.  
 ACCESSION AG581296  
 VERSION AG581296.1 GI:48342126  
 KEYWORDS GSS.  
 SOURCE Mus musculus molossinus  
 ORGANISM Mus musculus molossinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1  
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 BAC end Sequences of Library MSMg01  
 2 (bases 1 to 783)  
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 Direct Submission

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE

JOURNAL  
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suenho-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 Clones are derived from the mouse BAC library MSMg01. For BAC  
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
 Tsukuba Institute, Bio Resource Center,  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp

COMMENT  
 PRIMERS  
 Sequencing : T7  
 LIBRARY  
 Vector : pBAC3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.

FEATURES  
 source  
 Location/Qualifiers  
 1..783  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMg01-507A20.T7"  
 /sex="male"  
 /issue\_type="mixture of kidney and spleen"  
 /clone\_lib="MSMg01 Mouse Male BAC Library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 783;  
 Best Local Similarity 100.0%; Pred.No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCACTACTCTC 20  
 Db 521 ACCCACTACTCTC 534

RESULT 145  
 B2468932  
 LOCUS 785 bp DNA linear GSS 13-DEC-2002  
 DEFINITION BONPQ48R BO\_1.6\_2\_KB tot Brassica oleracea genomic clone BONPQ48,  
 genomic survey sequence.  
 ACCESSION B2468932  
 VERSION B2468932.1 GI:26764413  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 785)  
 Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Frazer,C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other GSSs: BONPQ48TF  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 Location/Qualifiers  
 1..785  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BONPQ48"



```

/clone_lib="BO_1.6.2_KB_tot"
/note="Vector: pHOSt1; Site 1: BstXI; 1.6-2 kb shared
total DNA inserted into pHOSt1 using BstXI linkers"

```

Query Match	70.0%	Score 14	DB 8	Length 785
Best Local Similarity	100.0%	Pred. No.	4.3e+02	
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	TTGCGACCCACA	14
Db	302	TTGCGACCCACA	315

RESULT 146	LOCUS	DEFINITION
BZ477400	BZ477400	791 bp DNA linear
	BOND31TR BO.1.6.2 KB tot	GSS 13-DEC-2002
	Brassicica oleracea genomic clone	
	genomic survey sequence.	BOND31,

ACCESSION	B2477400
VERSION	B2477400.1
KEYWORDS	GI:26779798
SOURCE	GSS.
ORGANISM	Brassica oleracea
	Brassica oleracea

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 791)	Town, C.D., Van Aken, S., Utecherack, T., Koo, H. and Fraser, C.M.	Whole genome shotgun sequencing of <i>Brassica oleracea</i>	Unpublished (2001)	
Other_GSSs: BOND311P				

9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel.: 301-638-3523  
Fax: 301-838-0208  
Email: [cdrown@isgr.org](mailto:cdrown@isgr.org)  
DNA is from a doubled haploid provided by Tom Osborn  
Seq primer: TR  
Class: sheared ends

FEATURES	Location/Qualifiers
source	1. .791

```

/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BONDR31"
/clone_1b="BO_1.6_2_KB tot"
/note="Vector: pHD01; Site 1:
total DNA inserted into pHD01
BstXI; 1.6-2 kb sheared
using BstXI linkers"

```

QY 1 TTGCGGACCCACACA 14  
 |||||  
 b 445 TTGCGGACCCACACA 458  
 |||||

Query Match 70.0%; Score 14; DB 8; Length 791;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT	147
BUS852379	
LOCUS	BUS852379
DEFINITION	793 bp mRNA linear EST 16-OCT-2002
	AGENCOURT_10402281 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6617916
	5' mRNA sequence.

ORGANISM	VERSION	KEYWORDS
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	BU852379.1	GI:24037342
Homo sapiens (human)	EST.	
Homo sapiens		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 793)	NIH-MGC	<a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.			

Email: [CGAP05-rcw@mail.nih.gov](mailto:CGAP05-rcw@mail.nih.gov)  
Tissue Procurement: CLONTECH  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
plate: LLCM2863 row: p column: 12  
High quality sequence stop: 659.

**FEATURES**  
**SOURCE**

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/_clone="IMAGE:6617916"
/_lab_host="DH10B (T1 phage-resistant)"
/_clone_lib="NIH MGC 82"
/_note="Organ: testis; Vector: pDNR-LIB (Clontech); Site.1:
5'fl1 (ggccgcctcgcgc); Site.2: 5'fl1 (ggccattatggc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGCGC-3' and 3' adaptor sequence:
5'-ATTTAGAGCGCCGAGCGCGCCGACATC-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 clones contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
```

```

ORIGIN
Query Match      70.0%; Score 14; DB 5; Length 793;
Best Local Similarity 100.0%; Pred. No. 4,3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCCAACACTACTC 20
        |||||
db       312 ACCCAACACTACTC 325

```

RESULT 148	
CF449870	
LOCUS	793 bp mRNA
DEFINITION	linear
ACACCT90, mRNA sequence.	EST 04-SEP-2003
CF449870	onion Allium cepa cDNA clone
ACCESSION	

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
CE449870.1	GI:34472572	EST	<i>Allium cepa</i> (onion)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta	
			<i>Allium cepa</i>	Streptophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.	
			1 (bases 1 to 793)		
			Havey, M.J., Cheung, F., Van Aken, S., Utecher, T. and Town, C.D.		

TITLE	Expressed Sequence Tags from a normalized library of mixed onion tissues ( <i>Allium cepa</i> )
JOURNAL	Unpublished (2003)
COMMENT	Contact: Havery MJ Department of Horticulture USDA-ARS and University of Wisconsin 1575 Linden Drive, Madison, WI 53706, USA

Tel: 608-262-1830  
Fax: 608-262-4743  
Email: [mjhavey@facstaff.wisc.edu](mailto:mjhavey@facstaff.wisc.edu)  
TIGR sequence name ACACt910T. For more information  
<http://haveylab.hort.wisc.edu>  
Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES  
source

Location/Qualifiers  
1. 793  
/organism="Allium cepa"  
/mol\_type="mRNA"  
/cultivar="Red Creole(bulbs), unknown(callus), Ebano & Texas Legend(roots)"  
/db\_xref="taxon:4679"  
/clone="ACACT90"  
/tissue\_type="Callus, roots, and young bulbs"  
/clone\_lib="normalized cDNA library of onion"  
/note="Vector: pCMVSPORT6.1-ccdb (Invitrogen); Site 1: EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA from callus, roots, and young bulbs were combined to synthesize the library. Normalization to enrich for low-copy transcripts was performed by proprietary techniques of Invitrogen."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 793;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 ACCCAACACTACTC 20  
|||||  
Db 97 ACCCAACACTACTC 110  
|||||

## RESULT 149

LOCUS CC860424 800 bp DNA linear GSS 24-JUN-2003  
DEFINITION NDL.118M17.77 Notre Dame Liverpool Aedes aegypti genomic clone  
ACCESSION CC860424  
VERSION CC860424.1 GI:33220434  
KEYWORDS GSS.  
SOURCE Aedes aegypti (yellow fever mosquito)  
ORGANISM Aedes aegypti  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes; Stegomyia.

REFERENCE 1 (bases 1 to 800)  
AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.  
TITLE BAC end sequencing of Aedes aegypti  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: NDL.118M17.SP6  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: enta@tigr.org  
Library was provided by David Severson  
Seq primer: T7  
Class: BAC ends.

FEATURES  
source

Location/Qualifiers  
1. 800  
/organism="Aedes aegypti"  
/mol\_type="genomic DNA"  
/strain="Liverpool"  
/db\_xref="taxon:7159"  
/clone="Notre Dame Liverpool-118M17"  
/clone\_lib="Notre Dame Liverpool"  
/note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 800;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
|||||  
Db 140 ACCCAACACTACTC 153  
|||||

## RESULT 150

LOCUS CK860367/c 801 bp mRNA linear EST 09-MAR-2004  
DEFINITION 31304 in vitro Root Solanum tuberosum cDNA, mRNA sequence.  
ACCESSION CK860367  
VERSION CK860367.1 GI:45290024  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

## REFERENCE

AUTHORS Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De Koeijer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.  
TITLE Generation of ESTs from in vitro root tissues of potato  
JOURNAL Unpublished (2004)  
COMMENT Contact: Barry Flinn  
The Canadian Potato Genome Project - BioAtlantech  
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
Email: bflinn@biocatlantech.nb.ca  
Seq primer: T3.

FEATURES  
source

Location/Qualifiers  
1. 801  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Shepody"  
/db\_xref="taxon:4113"  
/tissue\_type="Root"  
/lab\_host="XLI0-Gold"  
/clone\_lib="In vitro Root"  
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI; Site 2: XhoI; supplier: Developmental series. Sterile stem sections from pathogen-free Solanum tuberosum var. Shepody, clone 1756, nuclear stock were cultured in Magenta boxes containing 1/10 strength MS medium, solidified with 0.8% (w/v) Phytagar. Roots of all sizes, originating from the stem bottoms were collected from these cultures, washed to remove residual Phytagar, and used in RNA isolations and library construction."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 801;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GACCCAACTACT 19  
|||||  
Db 727 GACCCAACTACT 714  
|||||

## RESULT 151

LOCUS CC631959 802 bp DNA linear GSS 19-JUN-2003  
DEFINITION OGD089TH ZM 0.7.1.5 KB Zea mays genomic clone ZMMBMA0423009, genomic survey sequence.  
ACCESSION CC631959  
VERSION CC631959.1 GI:32006725  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

## REFERENCE

AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uutterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

TITLE	CONSORTIUM for Maize Genomics
JOURNAL	Unpublished (2002)
COMMENT	Other_GSSs: OGUQG89TV

**ORIGIN**

Query Match	70.0%;	Score 14;	DB 9;	Length 802;
Best Local Similarity	100.0%;	Pred. No. 4.3e+02;		
Matches 14; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      5 CGACCCCAACTAC 18
         |||||
Db      99 CGACCCCAACTAC 112

```

RESULT	152
CG155334	
LOCUS	
DEFINITION	806 bp DNA linear GSS 21-ANG-2001
	PUKRS97B ZM_0.6.1.0_KB Zea mays genomic clone ZMmBTA0605122,
	genomic survey sequence.

**ORIGIN**

Query Match 70.0%; Score 14; DB 9; Length 806;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 7 ACCCAACTACTC 20  
|||||||  
Db 195 ACCCAACTACTC 208

RESULT	153
LOCUS	BF696995/c
DEFINITION	BF696995 809 bp mRNA linear EST 22-DEC-2000 602130174P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286922 5', mRNA sequence.
ACCESSION	BF696995
VERSION	BF696995
KEYWORDS	EST. GI:11982403
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

FEATURES	Location/Qualifiers
source	1. .809

**ORIGIN**

Query Match	70.0%;	Score 14;	DB 2;	Length 809;
Best Local Similarity	100.0%;	Pred. No. 4.3e+02;		
Matches 14; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	7	ACCCACACTACTC	20
Db	435	ACCCACACTACTC	422

RESULT	154
BF666387/c	
LOCUS	811 bp mRNA linear EST 21-DEC-2000
DEFINITION	60212373791f NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280812 5 ,
ACCESSION	mRNA sequence.
VERSION	BF666387
	BF666387.1 GI:11940282

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 811)  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov  
Plate: LCM108 row: e column: 05  
High quality sequence stop: 625.  
Location/Qualifiers  
1. 811  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4280812"  
/tissue\_type="primitive neuroectoderm"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site: 1; SfiI (ggccatcgcc); Site 2: SfiI (ggccatcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTTCGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACG-3' (30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN  
Query Match 70.0%; Score 14; DB 2; Length 811;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTCTC 20  
|||||  
db 431 ACCCAACTACTCTC 418

RESULT 155  
CNS0100/c 811 bp DNA linear GSS 14-JUN-2001  
LOCUS Anopheles gambiae GSS SP6 end of clone 26113 of NotreDame1 library  
DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.  
ACCESSION AL153606  
VERSION AL153606.1 GI:7014525  
KEYWORDS GSS.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.  
1 (bases 1 to 811)  
Genoscope.  
Direct Submission  
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
REFERENCE 2 (bases 1 to 811)  
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

TITLE Direct Submission  
JOURNAL Submitted (16-FEB-2000) BMJ, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France  
COMMENT This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.  
Location/Qualifiers  
1. 811  
/organism="Anopheles gambiae"  
/mol\_type="genomic DNA"  
/strain="PEST"  
/db\_xref="taxon:7165"  
/clone\_lib="26113"  
/clone\_lib="NotreDame1"  
/note="end : SP6"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 811;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACT 19  
|||||  
db 704 GACCCAACTACT 691

RESULT 156  
BX143045 812 bp DNA linear GSS 28-JAN-2003  
LOCUS Danio rerio genomic clone DKEX-108C18, genomic survey sequence.  
DEFINITION BX143045  
ACCESSION BX143045  
VERSION BX143045.1 GI:27974382  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 812)  
Humphray,S.J., Huckle,E. and Durham,J.L.  
Direct Submission  
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished  
This sequence was generated from the T7 end of BAC 108C18. 108C18 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D\_rerio/  
Location/Qualifiers  
1. 812  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone\_lib="DKEX-108C18"  
/tissue\_type="testis"  
/note="Vector pIndigobac-536"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 812;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTCTC 20  
|||||  
db 668 ACCCAACTACTCTC 655

RESULT 157  
BZ822645 815 bp DNA linear GSS 18-MAR-2003  
LOCUS PUFH957B ZM.0.6.1.0 KB Zee may's genomic clone ZMBRta317P22, genomic survey sequence.

ACCESSION B2822645  
VERSION B2822645.1 GI:29038301  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 815)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennerzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: PUFH95TD  
Contact: Cathy WhiteLaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1. 815  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBTA317P2"  
/clone\_1lb="ZM 0.6 1.0 KB"  
/note="Vector: pCR4-TORO; Site\_1: EcoRI; 0.6-1.0 kb high  
COT selected genomic DNA library"

ORIGIN  
Query Match 70.0%; Score 14; DB 8; Length 815;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTC 20  
|||||  
664 ACCCAACTACTC 651

Db

RESULT 158  
LOCUS CG459141  
DEFINITION CG459141 827 bp DNA linear GSS 17-SEP-2003  
genomic survey sequence.  
ACCESSION CG459141  
VERSION CG459141.1 GI:3484141  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 827)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennerzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Contact: Cathy WhiteLaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1. 827

FEATURES  
SOURCE

/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBTA0600M21"  
/clone\_1lb="ZM 0.6 1.0 KB"  
/note="Vector: pCR4-TORO; Site\_1: EcoRI; 0.6-1.0 kb high  
COT selected genomic DNA library"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 827;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACTAC 18  
|||||  
Db 183 CGACCAACTAC 196

RESULT 159  
LOCUS CG112064  
DEFINITION PUFN188TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA0689P07,  
genomic survey sequence.  
ACCESSION CG112064  
VERSION CG112064.1 GI:33995501  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 829)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennerzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: PUFN188TB  
Contact: Cathy WhiteLaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1. 829  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBTA0689P07"  
/clone\_1lb="ZM 0.6 1.0 KB"  
/note="Vector: pCR4-TORO; Site\_1: EcoRI; 0.6-1.0 kb high  
COT selected genomic DNA library"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 829;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACTAC 18  
|||||  
Db 174 CGACCAACTAC 187

RESULT 160  
LOCUS CG086099/c  
DEFINITION PUFKL69TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTA0670L18,  
genomic survey sequence.  
846 bp DNA linear GSS 20-AUG-2003  
Location/Qualifiers  
1. 827

ACCESSION CG086099 GI:33968393  
 VERSION GSS.  
 KEYWORDS Zea mays  
 SOURCE Zea mays  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 846)  
 WhiteLw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Benneker,J.  
 TITLE Maize Genomics Consortium  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: PUFRL69TB  
 Contact: Cathy WhiteLw  
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLw@tigr.org  
 Seq primer: TP  
 Class: sheared ends.

FEATURES  
 source  
 1..846  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="873"  
 /db\_xref="taxon:4577"  
 /clone="ZMBR06701.8"  
 /clone\_1b="2M 0.6-1.0 KB"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high Cor selected genomic DNA library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 846;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAGCCACACTACT 19  
 |||||  
 Db 518 GAGCCACACTACT 505

RESULT 161  
 CO368423 856 bp mRNA linear EST 23-JUN-2004  
 LOCUS RTK1\_40\_C05\_g1\_A029 Roots minus potassium Pinus taeda cDNA clone  
 DEFINITION  
 CO368423  
 CO368423  
 CO368423.1 GI:49449740  
 EST.  
 SOURCE Pinus taeda (loblolly pine)  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 856)  
 Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Zimmermann,C. and Dean,J.F.D.  
 TITLE An EST database from potassium-deficient loblolly pine (Pinus taeda) roots  
 JOURNAL Unpublished (2004)  
 COMMENT Other ESTs: RTK1\_40\_C05\_b1\_A029  
 Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmp@uga.edu  
 RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia)

Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
 Seq primer: JENREV (GAGGAACGCTATACC).  
 Location/Qualifiers  
 1..856  
 /organism="Pinus taeda"  
 /mol\_type="mRNA"  
 /strain="3 CLONES"  
 /db\_xref="taxon:3352"  
 /clone="RTK1\_40\_C05\_A029"  
 /lab\_host="DH10B-T1 phage-resistant E. coli"  
 /clone\_1b="Roots minus potassium"  
 /note="Organ: Root; Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. The rooted cuttings were maintained for 117 days (July 2003 harvest) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. For twenty-eight days (28 d) prior to harvesting roots for mRNA preparation, the trees received Hoagland's solution lacking potassium (K) to induce a potassium-deficiency. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGGACCCACTACTA 17  
 |||||  
 Db 38 GGGACCCACTACTA 51

RESULT 162  
 CM007611/c 861 bp DNA linear GSS 23-SEP-2004  
 LOCUS ZMMLA0009F06.f ZMBL04 Zea mays genomic clone ZMMLA0009F06 5',  
 DEFINITION  
 CM007611  
 CM007611  
 CM007611.1 GI:52588449  
 GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 861)  
 Wing,R., Luo,M., Soderlund,C. and Haller,K.  
 TITLE ZMML sequences  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu  
 Plate: 0009 row: F column: 06  
 Class: BAC ends.

FEATURES  
 source  
 1..861  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"

```

ORIGIN
Query Match      70.0%; Score 14; DB 9; Length 861;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTGCGGACCCACA 14
Db 427 TTGCGGACCCACA 414

RESULT 163
BF680379/c 865 bp mRNA linear EST 21-DEC-2000
LOCUS 602154164F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295295 5'
DEFINITION mRNA sequence.
ACCESSION BF680379
VERSION BF680379.1 GI:11954274
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L16M145 row: p column: 16
High quality sequence stop: 689.
Location/Qualifiers
1. 865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4295295"
/lab_host="DH10B (TI phage-resistant)"
/clone_1lb="NIH_MGC_83"
/notes="Organ: prostate; Vector: PDNR-LIB (Clontech);
Site 1: SfiI (ggccgctcgcc); Site 2: SfiI
(ggcccattagcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGCGGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
```

```

RESULT 164
CL504784 877 bp DNA linear GSS 01-APR-2004
LOCUS SAIL_742_G03.v1 SAIL Collection Arabidopsis thaliana genomic clone
DEFINITION SAIL_742_G03.v1, genomic survey sequence.
ACCESSION CL504784
VERSION CL504784.1 GI:46002104
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D.,
AUTHORS Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D.,
Bullis, D., Snell, J., Miguel, T., Hutcheson, D., Kimmey, B.,
Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A.
A high-throughput Arabidopsis reverse genetics system
J Plant Cell 14 (12), 2985-2994 (2002)
JOURNAL MEDLINE
PUBMED 22356987
COMMENT Contact: Sessions A
Applied Trait Genetics
Syringia Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syringenta.com
ABRC Stock Number CS833179; T-DNA left border flanking sequences of
Syringia Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers
1. 877
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_742_G03.v1"
/clone_1lb="SAIL_Collection"
/notes="T-DNA left border sequences were isolated using a
modified Tail-PCR strategy"
```

```

FEATURES
source
1. 865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4295295"
/lab_host="DH10B (TI phage-resistant)"
/clone_1lb="NIH_MGC_83"
/notes="Organ: prostate; Vector: PDNR-LIB (Clontech);
Site 1: SfiI (ggccgctcgcc); Site 2: SfiI
(ggcccattagcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGCGGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
```

```

ORIGIN
Query Match      70.0%; Score 14; DB 9; Length 877;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 GCGACCCACACTA 17
Db 84 GCGACCCACACTA 97

RESULT 165
CG226100 883 bp DNA linear GSS 22-AUG-2003
LOCUS CG5D880TC ZM 0.7.1.5 Zea mays genomic clone ZMMBMA0838N15,
DEFINITION genomic survey sequence.
ACCESSION CG226100
VERSION CG226100.1 GI:34125988
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE White, A., Quackenbush, J., Van Aken, S., Uterback, T.,
AUTHORS Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
```

TITLE Consortium for Maize Genomics  
JOURNAL Unpublished (2002)  
COMMENT Contact: Cathy WhiteLew

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLew@tigr.org  
Seq primer: TP  
Class: sheared ends.

FEATURES  
source  
1. .883  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1ib="ZMMBMA0838N15"  
/clone\_1ib="ZM 0.7.1.5 KB"  
/note="Vector: pBESK-; Site\_1: HindIII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 883;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCACACTAC 18  
|||||  
93 CGACCCACACTAC 106

RESULT 166  
CG956406 888 bp DNA linear GSS 15-DEC-2003  
LOCUS MBIR68TF\_mch2 Medicago truncatula genomic clone 64K16, genomic  
DEFINITION survey sequence.

ACCESSION CG956406  
VERSION CG956406.1 GI:39872964  
KEYWORDS GSS:  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

REFERENCE 1 (bases 1 to 888)  
AUTHORS Town,C.D., Shetty,J., Koo,H. and Feldblum,T.F.  
TITLE Sequencing of BAC ends from Medicago truncatula  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: MBIR68TR  
Contact: Chris Town

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
Seq primer: TGTAAACGACGGCCACT  
Class: BAC ends.

FEATURES  
source  
1. .888  
/organism="Medicago truncatula"  
/mol\_type="genomic DNA"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone\_1ib="64K16"  
/clone\_1ib="mch2"  
/note="Vector: pBelBAC11; Site\_1: HindIII; Site\_2:  
HindIII; Cook, D.R. and Kim, D.U, unpublished"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 888;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACT 19  
|||||  
Db 642 GACCCACACTACT 655

RESULT 167  
B2817219 893 bp DNA linear GSS 18-MAR-2003  
LOCUS PUFDS06TB\_ZM\_0.6.1.0\_KB\_Zea mays genomic clone ZMMBTA296A11,  
DEFINITION genomic survey sequence.  
ACCESSION B2817219  
VERSION B2817219.1 GI:29032041  
KEYWORDS GSS:  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 893)  
WhiteLew,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennetzen,J.

REFERENCE  
AUTHORS Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: PUFDS06TD  
Contact: Cathy WhiteLew

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLew@tigr.org  
Seq primer: TR  
Class: sheared ends.

FEATURES  
source  
1. .893  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1ib="ZMMBTA296A11"  
/clone\_1ib="ZM 0.6.1.0 KB"  
/note="Vector: pCR4-toPO; Site\_1: EcoRI; 0.6-1.0 kb high  
cot selected genomic DNA library"

ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 893;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCACACTAC 18  
|||||  
Db 164 CGACCCACACTAC 177

RESULT 168  
CO921238 906 bp mRNA linear EST 16-AUG-2004  
LOCUS AGENCOURT\_30432439 NIH\_ZGC\_14 Danio rerio cDNA clone IMAGE:7408909  
DEFINITION 5', mRNA sequence.  
ACCESSION CO921238  
VERSION CO921238.1 GI:51271451  
KEYWORDS EST:  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 906)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.



Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: John Ngai, Nancy Freeman, NIDCD  
CDNA Library Preparation: Dr. Sumio Sugano  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLML15612 row: j column: 11  
High quality sequence start: 9  
High quality sequence stop: 695.

## FEATURES

Source

Location/Qualifiers  
1..906  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:7408909"  
/rissue\_type="olfactory epithelium"  
/lab\_host="DH10B Tona"  
/clone\_1lb="NTL ZGC\_14"  
/note="Organ: Olfactory epithelium; Vector: PME18S-FL3;  
Site 1: DraIII; Site 2: DraIII; 1st strand cDNA was primed  
with an oligo(dT) primer  
[GGCGTGAAGACGCGCTATGCGCTTTTCTTTTCTTTT];  
double-stranded cDNA was ligated to a DraIII adaptor  
[GGCCUACUGG], digested and directionally cloned into  
distinct DraIII sites of the PME18S-FL3 library was size  
selected for 1.0 kb, with a average insert size of ~1.2kb.  
Library constructed by Yutaka Suzuki (University of Tokyo  
Institute of Medical Science). Custom primers recommended  
for sequencing: 5' end primer 5'-GGATGTCCTTACTCTCA-3'  
and 3' end primer 5'-CGACCTGACCTCGACGCA-3'. Note: This  
is a Zebrafish Gene Collection (ZGC) library"

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 906;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TCGGACCCACAC 15  
Db 876 TCGGACCCACAC 889

RESULT 169  
CG126612/c 916 bp DNA linear GSS 20-AUG-2003  
LOCUS  
DEFINITION  
genomic survey sequence.  
CG126612  
CG126612.1 GI:34010049  
GSS.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 916)  
WhiteLaw.C.A., Quackenbush.J., Van Aken.S., Uterback.T.,  
Reanick.A., Frazer.C.M., Yuan.Y., San Miguel.P., Ma.J. and  
Bennetzen.J.

## REFERENCE

AUTHORS  
TITLE  
JOURNAL  
COMMENT

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PUF5N84TB  
Contact: Cathy WhiteLaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org

Seq primer: TF  
Class: sheared ends.  
Location/Qualifiers  
1..916  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZM587a0723M24"  
/clone\_1lb="ZM\_0.6\_1.0 KB"  
/note="Vector: PCR4-TOP0; Site 1: EcoRI; 0.6-1.0 kb high  
COR selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 916;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ACCCACTACTCTC 20  
Db 785 ACCCACTACTCTC 772

RESULT 170  
CG388749/c 929 bp DNA linear GSS 27-AUG-2003  
LOCUS  
DEFINITION  
genomic survey sequence.  
CG388749  
CG388749.1 GI:34307901  
GSS.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 929)  
Bharti.A.K., Young.S., Kavchok.S., Keiser.G., Bronzino.A.C.,  
Rouzaud.K., Fuks.G., Yu.Y., Wing.R. and Messing.J.  
Sequencing of the maize genome at PGR (2003b)  
Unpublished (2003)  
Contact: Bharti.A.K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 51.  
Location/Qualifiers  
1..929  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZM587a0569P17"  
/lab\_host="E. coli DH10B"  
/clone\_1lb="ZM587a0569P17"  
/note="Vector: PTARBAC1.3; Site\_1: BamHI; Site\_2: BamHI"

## REFERENCE

AUTHORS  
TITLE  
JOURNAL  
COMMENT

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PUF5N84TB  
Contact: Cathy WhiteLaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org

## FEATURES

Source

Location/Qualifiers  
1..929  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZM587a0569P17"  
/lab\_host="E. coli DH10B"  
/clone\_1lb="ZM587a0569P17"  
/note="Vector: PTARBAC1.3; Site\_1: BamHI; Site\_2: BamHI"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 929;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCCACACTA 17  
Db 824 GCGACCCACACTA 811

```

RESULT 171
BU961968      930 bp      mRNA      linear      EST 21-OCT-2002
LOCUS          AGENCOURT 10617415 NIH MGC 169 Mus musculus cDNA clone
DEFINITION     IMAGE:6742628 5', mRNA sequence.
ACCESSION      BU961968
VERSION         BU961968.1 GI:24191540
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 930)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LICM3080 row: P column: 19
High quality sequence, stop: 134.
Location/Qualifiers
1..930
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6742628"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH_MGC_169"
/note="Organ: Testicles; Vector: pDNR-LIB; Site 1: SfiI
(ggcatatggcc); Site 2: SfiI (ggcgcgcgcgcgc); cDNA made
by oligo-dt priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCATGCGTATACCCAGATGCGGCATTCAGCGCGG-3' and
5'-ATTCTAGAGGCCGAGCGCGGCAGCATG-dt(30)NM-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN
Query Match      70.0%; Score 14; DB 5; Length 930;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
7 ACCCAACACTAC 20
|||||
826 ACCCAACACTAC 839

RESULT 172
BZ817225      937 bp      DNA      linear      GSS 18-MAR-2003
LOCUS          PUFDS06TD_ZM_0.6_1.0_KB Zea mays genomic clone ZMBETA296A11,
DEFINITION     genomic survey sequence.
ACCESSION      BZ817225
VERSION         BZ817225.1 GI:29032047
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 937)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uteback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.

FEATURES
SOURCE
1..944
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"

```

```

TITLE          Maize Genomics Consortium
JOURNAL        Unpublished (2003)
COMMENT        Other GSSs: PUFDS06TB
Contact: Cathy Whitelaw
TRIGR          9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@trigr.org
Seq primer: TP
Class: shared ends.
Location/Qualifiers
1..937
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBETA296A11"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN
Query Match      70.0%; Score 14; DB 8; Length 937;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
5 CGACCACACTAC 18
|||||
886 CGACCACACTAC 873

RESULT 173
AG602080      944 bp      DNA      linear      GSS 05-JUN-2004
LOCUS          AG602080/c
DEFINITION     Mus musculus molossinus DNA, clone:MSMG01-534G02.TJ, genomic survey
sequence.
ACCESSION      AG602080
VERSION         AG602080.1 GI:48362910
KEYWORDS       GSS.
SOURCE         Mus musculus molossinus
ORGANISM       Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMG01
Unpublished
2 (bases 1 to 944)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Maabira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMG01. For BAC
library availability, please contact Kuniya Aoe (aoe@tc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyada, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
E-mail: aoe@tc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : PBACe3.6
R Site 1 : EcoRI
R Site 2 : EcoRI.
Location/Qualifiers
1..944
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"

```

```

/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMG01-534G02.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMG01 Mouse Male BAC Library"

ORIGIN
Query Match      70.0%; Score 14; DB 9; Length 944;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      7 ACCCAACTACTC 20
      |||||
      669 ACCCAACTACTC 656

RESULT 174
CG056404      948 bp      DNA      linear      GSS 19-AUG-2003
LOCUS      PUFV68TD ZM_0.6.1.0_KB Zea mays genomic clone ZMMB7a0742L16,
DEFINITION      genomic survey sequence.
ACCESSION      CG056404
VERSION      CG056404.1 GI:33928584
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 948)
Renick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Benneken,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFV68TB
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Classes: sheared ends.
FEATURES
Source      Location/Qualifiers
1..948
/mol_type="genomic DNA"
/db_xref="taxon:573"
/db_xref="taxon:4577"
/clone_lib="ZMMB7a0742L16"
/clone_id="ZM_0.6.1.0_KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN
Query Match      70.0%; Score 14; DB 9; Length 948;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      7 ACCCAACTACTC 20
      |||||
      911 ACCCAACTACTC 924

RESULT 175
BE957748      952 bp      mRNA      linear      EST 14-DEC-2000
LOCUS      BE957748
DEFINITION      601655861R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838934 3',
      mRNA sequence.
ACCESSION      BE957748
VERSION      BE957748.2 GI:11774319

```

```

KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 952)
REFERENCE      NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      On Oct 3, 2000 this sequence version replaced gi:10568453.
      Contact: Robert Strauberg, Ph.D.
      Email: cgabs-remail.nih.gov
      Tissue Procurement: ATCC
      CDNA Library Preparation: CLONTECH laboratories, Inc.
      CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      http://image.llnl.gov
      plate: LICMS26 row: 1 column: 15
      High quality sequence stop: 4.
      Location/Qualifiers
1..952
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3838934"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
      Site 1: SfiI (ggccgctggcc); Site 2: SfiI
      (ggccatcggcc); Double-stranded cDNA was prepared from
      cell line RNA. 5' and 3' adaptors were used in cloning as
      follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and
      3' adaptor sequence:
      5'-ATTAGAGCGCGCGCGGCAGATG-dT(30)BN-3' (where B = A,
      C, or G and N = A, C, G, or T) Average insert size
      1.65 kb (range 0.9-4.0 kb). 14/15 clones contained
      inserts by PCR. This library was enriched for full-length
      clones and was constructed by Clontech Laboratories (Palo
      Alto, CA)."

ORIGIN
Query Match      70.0%; Score 14; DB 2; Length 952;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGCGGACCGACA 14
      |||||
      918 TTGCGGACCGACA 931

RESULT 176
CG218509      955 bp      DNA      linear      GSS 22-AUG-2003
LOCUS      OGMKR46TV ZM_0.7.1.5_KB Zea mays genomic clone ZMMBwa0610G20,
DEFINITION      genomic survey sequence.
ACCESSION      CG218509
VERSION      CG218509.1 GI:34118397
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 955)
Renick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGMKR46TH

```

Contract: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1..955  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1b="ZM 0.7\_1.5\_KB"  
/note="Vector: pBSCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 955;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
|||||  
Db 253 ACCCAACACTACTC 240

RESULT 177  
CG126611 965 bp DNA linear GSS 20-AUG-2003  
LOCUS PUF5N84TB ZM 0.6\_1.0\_KB Zea mays genomic clone ZMBR1a0723M24,  
DEFINITION genomic survey sequence.  
ACCESSION CG126611  
VERSION CG126611.1 GI:34010048  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
1 (bases 1 to 965)  
Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennetzen,J.  
Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PUF5N84TD  
Contact: Cathy Whitelaw  
TIGR

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1..965  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1b="ZM 0.6\_1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
COT selected genomic DNA library"

FEATURES  
source

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 965;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
|||||  
Db 471 ACCCAACACTACTC 484

RESULT 178  
BZ463975/c 974 bp DNA linear GSS 13-DEC-2002  
LOCUS BONGK66TR BO 1.6\_2\_KB lot Brassica oleracea genomic clone BONGK66,  
DEFINITION genomic survey sequence.  
ACCESSION BZ463975  
VERSION BZ463975.1 GI:26750364  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 974)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished (2001)  
Other GSSs: BONGK66TF  
Contact: Chris Town

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1..974  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone\_1b="BO\_1.6\_2\_KB lot"  
/note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared  
total DNA inserted into pHOS1 using BstXI linkers"

FEATURES  
source

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 974;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGCGACCCACCA 14  
|||||  
Db 479 TTCGCGACCCACCA 466

RESULT 179  
BY17843 975 bp mRNA linear EST 17-DEC-2002  
LOCUS BY17843/c  
DEFINITION BY17843 RIKEN full-length enriched, adult male thymus Mus musculus  
CDNA clone 5830427D03 5, mRNA sequence.  
ACCESSION BY17843  
VERSION BY17843.1 GI:27130960  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 975)  
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,  
Nikaido,I., Otsu,N., Saito,R., Suzuki,H., Yamanka,I.,  
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,  
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,  
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,  
Batulov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,  
Chochia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giasi, C., Godzik, A., Gough, J., Grimmond, S., Gusticich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Matsuda, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavan, W.J., Perera, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyrshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Zingales, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Waki, J., Aizawa, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shindawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

COMMENT

CONTACT: Yoshihide Hayashizaki  
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The Institute of Physical and Chemical Research (RIKEN)  
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Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

# FEATURES

## source

1. 975

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="5830427D03"

/sex="male"

/tissue\_type="thymus"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="RIKEN full-length enriched, adult male thymus"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia"

# FEATURES

## source

1. 976

Location/Qualifiers

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="POAD580"

/tissue\_type="POAD580"

/lab\_host="DH10B-Tona"

/clone\_lib="potato abiotic stress treated leaf and root tissue"

/supplier="Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d. Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after

# ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 975;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCGACACTACTC 20  
Db 863 ACCGACACTACTC 850

# RESULT 180

CK272536 976 bp mRNA linear EST 03-AUG-2004  
LOCUS CK272536/C  
DEFINITION EST718614 potato abiotic stress cDNA library Solanum tuberosum cDNA  
clone POAD580 5' end, mRNA sequence.

ACCESSION CK272536  
VERSION CK272536.1 GI:39829514  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 976)  
Buell, C.R., Hart, A., Zismann, V., Karaycheva, S.A. and Baker, B.

REFERENCE Buell, C.R., Hart, A., Zismann, V., Karaycheva, S.A. and Baker, B.  
AUTHORS Generation of ESTs from abiotic stressed potato tissue  
TITLE Unpublished (2003)  
JOURNAL Other ESTs: EST118615

COMMENT The Institute for Genomic Research  
Contact: Robin Buell  
7912 Medical Center Dr. Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/  
Seq primer: ATT TAG GTG ACA CTA TAG.

cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 976;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACT 19  
|||||  
Db 68 GACCCAACTACT 55

## RESULT 181

CG086097 976 bp DNA linear GSS 20-AUG-2003  
LOCUS PUFKL697B.ZM.0.6.1.0\_KB\_Zea\_mays\_genomic\_clone\_ZM0670L18,  
DEFINITION genomic survey sequence.

ACCESSION CG086097  
VERSION CG086097.1 GI:33968391  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD 1 (bases 1 to 976)

## AUTHORS

WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennettzen,J.

TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUFKL697D  
Contact: Cathy Whitelaw

## TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR

Class: sheared ends.  
Location/Qualifiers

FEATURES  
source 1..976  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1ib="ZM.0.6.1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cot selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 976;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACT 19  
|||||  
Db 811 GACCCAACTACT 824

## RESULT 182

CK406129 980 bp mRNA linear EST 05-JAN-2004  
LOCUS CK406129  
DEFINITION AUF Ifsbn 236 g1l Ictalurus furcatus spleen cDNA library Ictalurus furcatus cDNA 5', mRNA sequence.

ACCESSION CK406129  
VERSION CK406129.1 GI:40565632  
KEYWORDS EST.  
SOURCE Ictalurus furcatus  
ORGANISM Ictalurus furcatus

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.  
1 (bases 1 to 980)

AUTHORS Liu,Z., Li,P., Liu,L., He,C., Kucuktas,H., Feng,J., Chen,L., Peatman,E., Baoprasertkul,P., Simmons,M., Muir,W., Grizzle,J., Dunham,R. and Brady,Y.  
30,000 new catfish ESTs: new resources for functional analysis of genes involved in aquaculture performance traits

Unpublished (2004)  
Contact: Liu ZD

The Fish Molecular Genetics and Biotechnology Laboratory, Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences

Auburn University  
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA  
Tel: 334 844 4054  
Fax: 334 844 9208  
Email: zliu@acesag.auburn.edu  
Seq primer: T7.

FEATURES  
source 1..980  
Location/Qualifiers

/organism="Ictalurus furcatus"  
/mol\_type="mRNA"  
/db\_xref="taxon:66913"  
/clone\_1ib="Ictalurus furcatus spleen cDNA library"  
/note="Organ: Spleen; Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 980;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACT 19  
|||||  
Db 258 GACCCAACTACT 271

## RESULT 183

CL986792 998 bp DNA linear GSS 23-SEP-2004  
LOCUS ZM0670L18.ZM.0.6.1.0\_KB\_Zea\_mays\_genomic\_clone\_ZM0670L18,  
DEFINITION genomic survey sequence.

ACCESSION CL986792  
VERSION CL986792.1 GI:52554870  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD 1 (bases 1 to 998)

AUTHORS Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and Bennettzen,J.

TITLE ZM0670L18 sequences  
JOURNAL Unpublished (2004)  
COMMENT Contact: Jeff Bennettzen  
Bennetzen Lab  
The University of Georgia  
Department of Genetics, C426a Life Sciences Building, Athens, GA

30602, USA  
Tel: 706-542-3698  
Fax: 706-583-0972

Email: maize@uga.edu  
Plate: 0003 row: d column: 24  
Class: BAC ends.

FEATURES  
Source

1. .998  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBHe0003d24"  
/issue\_type="Immature ear"  
/dev\_stage="6-8 weeks"  
/lab\_host="DH10B"  
/clone\_lib="ZMMBHe"  
/note="Vector: TOPOpcr4; Site\_1: EcoRI; Site\_2: EcoRI"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 998;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACA 14  
Db 88 TTCCGACCCACACA 75

RESULT 184  
BG116258 1020 bp mRNA linear EST 30-JAN-2001  
LOCUS 602318508P1 NIH\_MGC\_88 Homo sapiens cDNA IMAGE:4418929 5',  
DEFINITION mRNA sequence.

ACCESSION BG116258  
VERSION BG116258.1 GI:12609764  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1020)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Plate: LLM10153 row: p column: 02  
High quality sequence start: 22

High quality sequence stop: 257.  
Location/Qualifiers

FEATURES

Source

1. .1020  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4418929"  
/issue\_type="duodenal adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_88"  
/note="Organ: small intestine; Vector: PCMV-SPORT6;  
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;  
oligo-dt primed. Average insert size 1.767 kb. Library  
enriched for full-length clones and constructed by Life  
Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 1020;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCACACTAC 18  
Db 677 CGACCCACACTAC 690

RESULT 185  
BQ119721 1024 bp mRNA linear EST 16-JUL-2002  
LOCUS AGENCOURT\_8304560 Lupski\_sym pathetic\_trunk Homo sapiens cDNA clone  
DEFINITION IMAGE:6193778 5', mRNA sequence.  
ACCESSION BQ119721  
VERSION BQ119721.1 GI:21858618  
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1024)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski  
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Plate: LLM13597 row: p column: 03  
High quality sequence stop: 386.  
Location/Qualifiers

FEATURES

Source

1. .1024  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6193778"  
/sex="male"  
/issue\_type="sympathetic trunk"  
/dev\_stage="adult, 16 yr"  
/lab\_host="DH10B"  
/clone\_lib="Lupski\_sym pathetic\_trunk"  
/note="Vector: PCMV-SPORT6 (Life Technologies); Site\_1:  
NotI; Site 2: SalI; cDNA made by oligo-dt priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCCGCGTCG-3' and  
5'-GACTAGTTCAGATCGGACGCGCCCT(15)-3'. Size selected >  
1 kb for average insert length 1.9 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine); available through Life  
Technologies."

ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 1024;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCACACTAC 18  
Db 978 CGACCCACACTAC 991

RESULT 186  
BZ603974/c

LOCUS BZ603974 1029 bp DNA linear GSS 08-JUN-2003  
DEFINITION WHAD96tr Human MCF7 breast cancer cell line library (MCF7\_1) Homo  
sapiens genomic clone MCF7\_1-23023, genomic survey sequence.

ACCESSION BZ603974  
VERSION BZ603974.1 GI:31512436  
KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS 1 (bases 1 to 1029)  
Volik, S., Zhao, S., Chin, K., Brebner, J. H., Herndon, D. R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Xu, W.-L., Magrane, G., de Jong, P., Gray, J. W. and Collins, C.

TITLE End-sequence profiling: Sequence-based analysis of aberrant genomes

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)

PMID 12788976

COMMENT Contact: Volik SV  
Collin Collins, lab  
UCSF Comprehensive Cancer Center  
UCSF Box 0808, San Francisco, CA 94143-0808, USA  
Tel: 415 502 7066  
Fax: 415 502 5665  
Email: svolik@cc.ucsf.edu  
This clone is available from Amplicon Express  
http://www.genomex.com  
Class: BAC ends.

FEATURES  
Location/Qualifiers  
1..1029  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="MCF7\_1-23023"  
/sex="female"  
/clone\_1id="Human MCF7 breast cancer cell line library (MCF7\_1)"  
/note="Vector: pECBAC1, Site 1: HindIII. This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 1029;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCACTACTCTC 20  
|||||  
520 ACCCACTACTCTC 507

Db

RESULT 187  
CL992091 1032 bp DNA linear GSS 23-SEP-2004  
ZMMBHf0003f23.f ZMMBHf Zea mays genomic clone ZMMBHf0003f23 5',  
genomic survey sequence.

DEFINITION CL992091  
CL992091  
CL992091.1 GI:52560169  
GSS.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Ze mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 1032)  
Ma, J., Sanmiquel, P., Liu, R., Haller, K., Soderlund, C. and Bennett, J.  
ZMMBH sequences  
Unpublished (2004)  
Contact: Jeff Bennett  
Bennettzen lab  
The University of Georgia  
Department of Genetics, C426a Life Sciences Building, Athens, GA 30602, USA  
Tel: 706-542-3698  
Fax: 706-583-0972  
Email: maize@uga.edu  
Plate: 0003 row: f column: 23

Class: BAC ends.

FEATURES  
Location/Qualifiers  
1..1032  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBHf0003f23"  
/tissue\_type="immature ear"  
/dev\_stage="6-8 weeks"  
/lab\_host="DH10B"  
/clone\_1id="ZMMBHf"  
/note="Vector: TOPOpcr4, Site\_1: EcoRI, Site\_2: EcoRI"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 1032;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACACA 14  
|||||  
88 TTGGGACCCACACA 75

Db

RESULT 188  
BG177123 1047 bp mRNA linear EST 06-FEB-2001  
LOCUS 602313372F1 NIH\_MGC\_85 Homo sapiens CDNA clone IMAGE:4419329 5',  
DEFINITION mRNA sequence.  
BG177123  
ACCESSION BG177123.1 GI:12683826  
VERSION  
KEYWORDS  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1047)  
NIH-MGC http://mgc.nhl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Louis Staudt, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM10154 row: p column: 18  
High quality sequence start: 4  
High quality sequence stop: 326.  
Location/Qualifiers  
1..1047  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4419329"  
/tissue\_type="lymphoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1id="NIH MGC 85"  
/note="Organ: lymph. Vector: PCMV-SPORT6, Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC library."

ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 1047;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCGGACCCACAC 15



Db 994 TCGCGACCCAC 1007

RESULT 189  
CM509808/c  
LOCUS  
DEFINITION CM509808 1049 bp DNA linear GSS 06-OCT-2004  
ZMMBHC0001124.r ZMMBHC Zea mays genomic clone ZMMBHC0001124.3',  
genomic survey sequence.

ACCESSION CM509808  
VERSION CM509808.1 GI:53839314  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1049)  
AUTHORS Ma,J., Sam Miguel,P., Liu,R., Haller,K., Soderlund,C. and  
Bennetzen,J.  
TITLE ZMMBHC sequences  
JOURNAL Unpublished (2004)  
COMMENT Contact: Jeff Bennetzen  
Bennetzen Lab  
The University of Georgia  
Department of Genetics, C426a Life Sciences Building, Athens, GA  
30602, USA  
Tel: 706-542-3698  
Fax: 706-583-0972  
Email: maize@uga.edu  
Plate: 0001 row: 1 column: 24  
Class: BAC ends

FEATURES  
Source Location/Qualifiers  
1..1049  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/culivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBHC0001124"  
/tissue\_type="immature ear"  
/dev\_stage="6-8 weeks"  
/lab\_host="DH10B"  
/clone\_lib="ZMMBHC"  
/note="Vector: TOPopcr4, Site\_1: EcoRI, Site\_2: EcoRI"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 1049;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACA 14  
|||||  
88 TTGCGACCCACACA 75

Db 88 TTGCGACCCACACA 75

RESULT 190  
BE791977/c  
LOCUS  
DEFINITION BE791977 1072 bp mRNA linear EST 20-SEP-2000  
601585886F1 NIH\_MGC\_7 Homo sapiens cDNA IMAGE:3940364 5',  
mRNA sequence.

ACCESSION BE791977  
VERSION BE791977.1 GI:10213175  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1072)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE NIH-MGC Unpublished (1999)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov

Tissue Procurement: DCTD/DPF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov  
Plate: LICM790 row: k column: 21  
High quality sequence stop: 737.

FEATURES  
Source Location/Qualifiers  
1..1072  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3940364"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOT87; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN  
Query Match 70.0%; Score 14; DB 2; Length 1072;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCGACACTACTC 20  
|||||  
Db 1065 ACCGACACTACTC 1052

RESULT 191  
AG071244/c  
LOCUS  
DEFINITION AG071244 1102 bp DNA linear GSS 03-NOV-2001  
Pan troglodytes DNA, clone: PTB-062G02.R, genomic survey sequence.

ACCESSION AG071244  
VERSION AG071244.1 GI:16623046  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE 1  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE BAC end sequences of library PTB  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1102)  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Aao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Sueni-ro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

COMMENT PRIMERS  
Sequencing: M13rev  
LIBRARY  
Vector : pKS145  
R.site 1 : SacI  
R.site 2 : SacI.  
Location/Qualifiers  
1..1102

```

/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-062G02.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          70.0%; Score 14; DB 9; Length 1102;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20
    |||
Db 513 ACCCAACACTACTC 500

RESULT 192
LOCUS B08792 1115 bp DNA linear GSS 14-MAY-1997
DEFINITION FB6-T7 IGF Arabidopsis thaliana genomic clone FB6, genomic survey
sequence.
ACCESSION B08792
VERSION B08792.1 GI:2089911
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1115)
Peng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
Ecker, J.
BAC End Sequences at ATGC
Unpublished (1997)
Other GSSs: FB6-5p6
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenom.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 78
High quality sequence stop: 973.
Location/Qualifiers
1. 1115
/mol_type="genomic DNA"
/organism="Arabidopsis thaliana"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="FB6"
/sex="hermaphrodite"
/clone_lib="IGF"
/note="Vector: BelbacII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"

ORIGIN
Query Match          70.0%; Score 14; DB 8; Length 1115;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20
    |||
Db 547 ACCCAACACTACTC 560

RESULT 193
LOCUS CL494700 1125 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL_599_G08.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_599_G08.v1, genomic survey sequence.
ACCESSION CL494700
VERSION CL494700.1 GI:45984532
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1125)
Sessions, A., Burke, E., Presting, G., Aux, G., McEliver, J., Paton, D.,
Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J. D., Cotton, D.,
Bullis, D., Snell, J., Miguel, T., Hutchinson, D., Kimerly, B.,
Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S. A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
2356987
MEDLINE
PUBMED
12468722
TITLE A high-throughput Arabidopsis reverse genetics system
AUTHORS Sessions, A., Burke, E., Presting, G., Aux, G., McEliver, J., Paton, D.,
Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J. D., Cotton, D.,
Bullis, D., Snell, J., Miguel, T., Hutchinson, D., Kimerly, B.,
Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S. A.
CONTACT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number C8825573; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers
1. 1125
/mol_type="genomic DNA"
/organism="Arabidopsis thaliana"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_599_G08.v1"
/clone_lib="SAIL_Collection"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
Query Match          70.0%; Score 14; DB 9; Length 1125;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACT 19
    |||
Db 819 GACCCACACTACT 806

RESULT 194
LOCUS BU504326 1126 bp mRNA linear EST 12-SEP-2002
DEFINITION AGENCOURT 8968993 NIH_MGC_94 Mus musculus cDNA IMAGE:6492135
5', mRNA sequence.
ACCESSION BU504326
VERSION BU504326.1 GI:22810559
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1126)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

```

DNA Sequencing by: Agencourt Bioscience Corporation  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov

Plate: LLM14044 row: k column: 16  
High quality sequence start: 106  
High quality sequence stop: 216.

## FEATURES

## SOURCE

Location/Qualifiers

1. 1126

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGR:6492135"

/tissue\_type="retina"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_94"

/note="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 1126;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## CY

2 TCGGACCCCAAC 15  
|||||  
408 TCGGACCCCAAC 421

## RESULT 195

AG078906 1132 bp DNA linear GSS 03-NOV-2001  
LOCUS Pan troglodytes DNA, clone: PTB-074F17.R, genomic survey sequence.  
ACCESSION AG078906  
VERSION AG078906.1 GI:16630708  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of library PTB  
Unpublished  
2 (bases 1 to 1132)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-ANG-2001) Ageo Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Shuho-chou, Tsukuba, Ibaraki, Japan 305-8565, Japan  
(E-mail: shuho@ipc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone cracking errors.

## PRIMERS

Sequencing: M13Rev

## LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. 1132

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-074F17.R"

/sex="male"

## FEATURES

## SOURCE

/cell\_type="Tymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

Query Match 70.0%; Score 14; DB 9; Length 1132;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## CY

2 TCGGACCCCAAC 15  
|||||  
873 TCGGACCCCAAC 886

## RESULT 196

BU466931 1161 bp mRNA linear EST 30-NOV-2002  
LOCUS 603372833F1 CSEORBN20 Gallus gallus cdna clone CHEST282a10 5', mRNA  
DEFINITION sequence.  
ACCESSION BU466931  
VERSION BU466931.1 GI:25960508  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 1161)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken CDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
PUBMED 12445392  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1OD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers

## FEATURES

## SOURCE

1. 1161

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Layer and broiler"

/db\_xref="taxon:9031"

/clone="CHEST282a10"

/sex="Male and female"

/tissue\_type="Chondrocytes isolated from growth plate  
cartilage"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="CSEORBN20"

/note="Vector: pBluescript II KS(+); Site 1: EcoRI;  
Site 2: NotI. This normalized library was constructed from  
1 million independent clones. cDNA synthesis was initiated  
using an oligo(dT) primer, using methylated C in the first  
strand synthesis reaction. Following this first strand  
reaction, double-stranded cDNA was blunt-ended, ligated to  
NotI adapters, digested with EcoRI, size-selected, and  
cloned into the NotI and EcoRI compatible sites of a  
custom modified MCS of the pBluescript (KS+) vector. The  
library was normalized in 2 rounds using conditions  
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and  
Bonaldo et al., Genome Research 6 (1996): 791, except that  
a significantly longer reannealing hybridization was  
used."

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 1161;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGACCCAACTAC 18  
 Db 497 CGACCCAACTAC 510

RESULT 197  
 B2573835 1187 bp DNA linear GSS 17-DEC-2002  
 LOCUS B2573835  
 DEFINITION msh2\_3383.x1 msh Pseudomonas aeruginosa genomic clone msh2\_3383,  
 genomic survey sequence.

ACCESSION B2573835  
 VERSION B2573835.1 GI:27208896  
 KEYWORDS GSS.  
 SOURCE Pseudomonas aeruginosa  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 1187)  
 Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,  
 Burns,J.L., Kaul,R. and Olsen,M.V.  
 Whole-Genome-Sequence variation among multiple isolates of  
 Pseudomonas aeruginosa library  
 J. Bacteriol. (2002) in press  
 CONTACT: Chris K. Raymond  
 Genome Center  
 University of Washington  
 Box 352145, Seattle, WA 98105-2145, USA  
 Tel: 2062216954  
 Fax: 2066857244  
 Email: craymond@u.washington.edu  
 Class: shotgun.

FEATURES  
 source  
 1..1187  
 /organism="Pseudomonas aeruginosa"  
 /mol\_type="genomic DNA"  
 /strain="M5H"  
 /db\_xref="taxon:287"  
 /clone="msh2\_3383"  
 /clone\_1ib="msh"  
 /note="Environmental isolate. Whole genomic shotgun  
 library."

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 1187;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGACCCAACTAC 18  
 Db 1062 CGACCCAACTAC 1075

RESULT 198  
 B2571441 1260 bp mRNA linear EST 12-MAR-2002  
 LOCUS B2571441  
 DEFINITION AGENCOURT 6626371 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5752888  
 5', mRNA sequence.

ACCESSION B2571441  
 VERSION B2571441.1 GI:19371820  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1260)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: L1AM12787 row: m column: 17  
 High quality sequence start: 378  
 High quality sequence stop: 545.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5752888"  
 /lab\_host="DH10B"  
 /clone\_1ib="NIH\_MGC\_115"  
 /note="Organ: pooled brain, lung, testis; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 1260;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TCGCCGCCAACAC 15  
 Db 842 TCGCCGCCAACAC 855

RESULT 199  
 CC210351 1262 bp DNA linear GSS 12-MAY-2003  
 LOCUS CC210351  
 DEFINITION CH261-18512\_RML.1 CH261 Gallus gallus genomic clone CH261-18512,  
 genomic survey sequence.

ACCESSION CC210351  
 VERSION CC210351.1 GI:30529019  
 KEYWORDS GSS.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 1262)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 Kremetzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,  
 Warren,W., Graves,T., Mardis,E. and Wilson,R.  
 Gallus gallus BAC End Reads  
 Unpublished (2003)  
 CONTACT: Richard K. Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@watson.wustl.edu  
 Insert Length: 182000 Std Error: 0.00  
 Seq primer: RML TACGACTCCTATAGGAGGA  
 Class: BAC ends  
 High quality sequence start: 165  
 High quality sequence stop: 504.  
 Location/Qualifiers  
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 /organism="Gallus gallus"  
 /mol\_type="genomic DNA"  
 /strain="Red Jungle Fowl"  
 /db\_xref="taxon:9031"  
 /clone="CH261-18512"  
 /sex="female"  
 /cell\_line="UCD001, inbred 256"

## FEATURES

source

/clone.lib="CH261"  
 /note="Vector: PTRRBA2.1; Site 1: EcoRI, Site 2: EcoRI;  
 CH261 Female Chicken Library - For library and clone  
 ordering information: http://www.chori.org/bacpac"

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 1262;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGACCCACACTA 17  
 |||||  
 Db 998 GCGACCCACACTA 1011

## RESULT 200

CL106095 1277 bp DNA linear GSS 05-JAN-2004  
 LOCUS ISB1-46D17\_Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-46D17,  
 DEFINITION genomic survey sequence.

ACCESSION CL106095  
 VERSION CL106095.1 GI:40599730  
 KEYWORDS GSS.

SOURCE Xenopus tropicalis (western clawed frog)  
 ORGANISM Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 1277)  
 Kremetzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
 Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome  
 Unpublished (2003)

CONTACT: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 75000 Std Error: 0.00

Seq primer: Sp6 ATTAGGTGACACTATAG

Class: BAC ends

High quality sequence start: 77

High quality sequence stop: 427.

Location/Qualifiers

1..1277  
 /organism="Xenopus tropicalis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:8364"  
 /clone="ISB1-46D17"  
 /clone.lib="ISB1"  
 /note="Vector: pBelOBAC11; ISB-1 Xenopus tropicalis BAC  
 Library Segment: 1"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 1277;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTC 20  
 |||||  
 Db 1135 ACCCAACTACTC 1148

Search completed: April 25, 2005, 14:49:26  
 Job time : 1995.68 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 25, 2005, 13:09:45 ; Search time 76.3158 Seconds  
(without alignments)  
428.817 Million cell updates/sec

Title: US-08-887-505B-28

Perfect score: 20

Sequence: 1 TTCCGGACCCCACTACTC 20

Scoring table: OLIGO\_NUC

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/PCRTUS\_COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	25 4 US-09-493-353-13	Sequence 13, Appl
2	20	100.0	27 4 US-08-648-272-21	Sequence 21, Appl
3	20	100.0	27 4 US-09-494-332A-12	Sequence 12, Appl
4	20	100.0	27 4 US-09-493-353-12	Sequence 12, Appl
5	20	100.0	33 1 US-08-438-639-50	Sequence 50, Appl
6	20	100.0	33 1 US-07-813-338A-50	Sequence 50, Appl
7	20	100.0	33 2 US-08-470-124-60	Sequence 60, Appl
8	20	100.0	33 3 US-08-441-971-126	Sequence 126, App
9	20	100.0	33 3 US-08-221-653-126	Sequence 126, App
10	20	100.0	33 3 US-08-442-144A-126	Sequence 126, App
11	20	100.0	33 3 US-08-441-970-126	Sequence 126, App
12	20	100.0	40 3 US-09-358-972-181	Sequence 181, App
13	20	100.0	40 3 US-09-406-147-43	Sequence 43, Appl
14	20	100.0	40 4 US-09-790-417-181	Sequence 181, App
15	20	100.0	46 1 US-08-429-181-10	Sequence 10, Appl
16	20	100.0	46 1 US-08-164-388-10	Sequence 10, Appl
17	20	100.0	108 1 US-09-798-641-31	Sequence 31, Appl
18	20	100.0	108 2 US-08-690-495-31	Sequence 31, Appl
19	20	100.0	108 4 US-08-690-494-31	Sequence 31, Appl
20	20	100.0	108 4 US-09-299-217-31	Sequence 31, Appl
21	20	100.0	108 4 US-09-728-265-31	Sequence 31, Appl
22	20	100.0	108 5 PCR-US95-07671-31	Sequence 31, Appl
23	20	100.0	194 1 US-08-244-116B-12	Sequence 12, Appl
24	20	100.0	232 3 US-09-034-205-37	Sequence 37, Appl
25	20	100.0	232 3 US-08-934-097A-37	Sequence 37, Appl
26	20	100.0	232 3 US-08-851-588-37	Sequence 37, Appl
27	20	100.0	232 3 US-09-677-218B-37	Sequence 37, Appl

28	20	100.0	232 3 US-09-677-192-37	Sequence 37, Appl
29	20	100.0	232 4 US-09-402-618B-37	Sequence 37, Appl
30	20	100.0	232 4 US-09-825-574-37	Sequence 37, Appl
31	20	100.0	232 4 US-09-676-768-37	Sequence 37, Appl
32	20	100.0	239 3 US-09-034-205-32	Sequence 32, Appl
33	20	100.0	239 3 US-09-034-205-36	Sequence 36, Appl
34	20	100.0	239 3 US-08-934-097A-32	Sequence 32, Appl
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38	20	100.0	239 3 US-09-677-218B-32	Sequence 32, Appl
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49	20	100.0	240 3 US-09-034-205-38	Sequence 38, Appl
50	20	100.0	240 3 US-09-034-205-35	Sequence 35, Appl
51	20	100.0	240 3 US-08-934-097A-35	Sequence 35, Appl
52	20	100.0	240 3 US-08-934-097A-38	Sequence 38, Appl
53	20	100.0	240 3 US-08-851-588-35	Sequence 35, Appl
54	20	100.0	240 3 US-08-851-588-38	Sequence 38, Appl
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58	20	100.0	240 3 US-09-677-218B-35	Sequence 35, Appl
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61	20	100.0	240 3 US-09-677-192-35	Sequence 35, Appl
62	20	100.0	240 3 US-09-677-192-38	Sequence 38, Appl
63	20	100.0	240 4 US-09-402-618B-33	Sequence 33, Appl
64	20	100.0	240 4 US-09-402-618B-35	Sequence 35, Appl
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69	20	100.0	240 4 US-09-676-768-33	Sequence 33, Appl
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73	20	100.0	244 3 US-09-034-205-27	Sequence 27, Appl
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93	20	100.0	244 4 US-09-402-618B-27	Sequence 27, Appl
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95	20	100.0	244 4 US-09-402-618B-31	Sequence 31, Appl
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98	20	100.0	244 4 US-09-402-618B-127	Sequence 127, App
99	20	100.0	244 4 US-09-402-618B-128	Sequence 128, App
100	20	100.0	244 4 US-09-825-574-26	Sequence 26, Appl

C 101	20	100.0	244	4	US-09-825-574-27	Sequence 27, Appl	C 174	20	100.0	256	2	US-07-965-286-25	Sequence 25, Appl
C 102	20	100.0	244	4	US-09-825-574-29	Sequence 29, Appl	C 175	20	100.0	256	2	US-07-965-286-26	Sequence 26, Appl
C 103	20	100.0	244	4	US-09-825-574-31	Sequence 31, Appl	C 176	20	100.0	256	2	US-08-487-231-1	Sequence 1, Appl
C 104	20	100.0	244	4	US-09-676-768-26	Sequence 26, Appl	C 177	20	100.0	256	2	US-08-487-231-24	Sequence 24, Appl
C 105	20	100.0	244	4	US-09-676-768-27	Sequence 27, Appl	C 178	20	100.0	256	2	US-08-487-231-25	Sequence 25, Appl
C 106	20	100.0	244	4	US-09-676-768-29	Sequence 29, Appl	C 179	20	100.0	256	2	US-08-487-231-26	Sequence 26, Appl
C 107	20	100.0	244	4	US-09-676-768-31	Sequence 31, Appl	C 180	20	100.0	256	3	US-09-401-912-1	Sequence 1, Appl
C 108	20	100.0	252	3	US-08-441-971-33	Sequence 33, Appl	C 181	20	100.0	256	3	US-09-401-912-24	Sequence 24, Appl
C 109	20	100.0	252	3	US-08-441-971-34	Sequence 34, Appl	C 182	20	100.0	256	3	US-09-401-912-25	Sequence 25, Appl
C 110	20	100.0	252	3	US-08-441-971-35	Sequence 35, Appl	C 183	20	100.0	256	3	US-09-401-912-26	Sequence 26, Appl
C 111	20	100.0	252	3	US-08-441-971-37	Sequence 37, Appl	C 184	20	100.0	281	2	US-08-757-653-121	Sequence 121, Appl
C 112	20	100.0	252	3	US-08-441-971-36	Sequence 36, Appl	C 185	20	100.0	281	2	US-08-757-653-123	Sequence 123, Appl
C 113	20	100.0	252	3	US-08-441-971-38	Sequence 38, Appl	C 186	20	100.0	281	2	US-08-757-653-126	Sequence 126, Appl
C 114	20	100.0	252	3	US-08-441-971-39	Sequence 39, Appl	C 187	20	100.0	281	2	US-08-757-653-127	Sequence 127, Appl
C 115	20	100.0	252	3	US-08-441-971-41	Sequence 41, Appl	C 188	20	100.0	281	2	US-08-757-653-128	Sequence 128, Appl
C 116	20	100.0	252	3	US-08-441-971-41	Sequence 42, Appl	C 189	20	100.0	281	2	US-08-757-653-129	Sequence 129, Appl
C 117	20	100.0	252	3	US-08-441-971-42	Sequence 43, Appl	C 190	20	100.0	281	2	US-08-757-653-132	Sequence 132, Appl
C 118	20	100.0	252	3	US-08-441-971-43	Sequence 44, Appl	C 191	20	100.0	281	3	US-08-520-946-121	Sequence 121, Appl
C 119	20	100.0	252	3	US-08-441-971-44	Sequence 45, Appl	C 192	20	100.0	281	3	US-08-520-946-123	Sequence 123, Appl
C 120	20	100.0	252	3	US-08-441-971-45	Sequence 46, Appl	C 193	20	100.0	281	3	US-08-520-946-126	Sequence 126, Appl
C 121	20	100.0	252	3	US-08-441-971-48	Sequence 48, Appl	C 194	20	100.0	281	3	US-08-520-946-127	Sequence 127, Appl
C 122	20	100.0	252	3	US-08-441-971-49	Sequence 49, Appl	C 195	20	100.0	281	3	US-08-520-946-128	Sequence 128, Appl
C 123	20	100.0	252	3	US-08-221-653-33	Sequence 33, Appl	C 196	20	100.0	281	3	US-08-520-946-129	Sequence 129, Appl
C 124	20	100.0	252	3	US-08-221-653-34	Sequence 34, Appl	C 197	20	100.0	281	3	US-08-520-946-132	Sequence 132, Appl
C 125	20	100.0	252	3	US-08-221-653-35	Sequence 35, Appl	C 198	20	100.0	281	4	US-09-655-378A-121	Sequence 121, Appl
C 126	20	100.0	252	3	US-08-221-653-36	Sequence 36, Appl	C 199	20	100.0	281	4	US-09-655-378A-123	Sequence 123, Appl
C 127	20	100.0	252	3	US-08-221-653-37	Sequence 37, Appl	C 200	20	100.0	281	4	US-09-655-378A-126	Sequence 126, Appl
C 128	20	100.0	252	3	US-08-221-653-38	Sequence 38, Appl	C 201	20	100.0	281	4	US-09	





C 393	19	95.0	177	3	US-09-038-369B-70	Sequence 70, Appl	466	17	85.0	20	1	US-08-471-966A-1	Sequence 1, Appl
C 394	19	95.0	177	3	US-09-038-369B-72	Sequence 72, Appl	467	17	85.0	20	3	US-08-829-637A-122	Sequence 122, App
C 395	19	95.0	177	3	US-09-038-369B-73	Sequence 73, Appl	468	17	85.0	20	3	US-08-650-093C-107	Sequence 107, App
C 396	19	95.0	177	3	US-09-038-369B-74	Sequence 74, Appl	469	17	85.0	20	5	PCT-US96-08757A-1	Sequence 1, Appl
C 397	19	95.0	177	3	US-09-038-369B-75	Sequence 75, Appl	470	17	85.0	177	1	US-08-244-116B-18	Sequence 18, Appl
C 398	19	95.0	177	3	US-09-038-369B-76	Sequence 76, Appl	471	16	80.0	20	1	US-08-468-447-2	Sequence 2, Appl
C 399	19	95.0	177	3	US-09-038-369B-77	Sequence 77, Appl	472	16	80.0	20	1	US-08-468-851A-2	Sequence 2, Appl
C 400	19	95.0	177	3	US-09-038-369B-78	Sequence 78, Appl	473	16	80.0	20	1	US-08-467-597A-2	Sequence 2, Appl
C 401	19	95.0	177	3	US-09-038-369B-79	Sequence 79, Appl	474	16	80.0	20	1	US-08-468-569A-2	Sequence 2, Appl
C 402	19	95.0	177	3	US-09-038-369B-80	Sequence 80, Appl	475	16	80.0	20	1	US-08-466-692A-2	Sequence 2, Appl
C 403	19	95.0	177	4	US-09-378-900A-57	Sequence 58, Appl	476	16	80.0	20	1	US-08-471-966A-2	Sequence 2, Appl
C 404	19	95.0	177	4	US-09-378-900A-58	Sequence 58, Appl	477	16	80.0	20	3	US-08-397-220B-62	Sequence 62, Appl
C 405	19	95.0	177	4	US-09-378-900A-61	Sequence 61, Appl	478	16	80.0	20	3	US-08-629-637A-123	Sequence 123, App
C 406	19	95.0	177	4	US-09-378-900A-62	Sequence 62, Appl	479	16	80.0	20	3	US-08-650-093C-62	Sequence 62, Appl
C 407	19	95.0	177	4	US-09-378-900A-65	Sequence 65, Appl	480	16	80.0	20	4	US-09-519-859A-4	Sequence 4, Appl
C 408	19	95.0	177	4	US-09-378-900A-66	Sequence 66, Appl	481	16	80.0	20	4	US-09-546-956A-13	Sequence 13, Appl
C 409	19	95.0	177	4	US-09-378-900A-67	Sequence 67, Appl	482	16	80.0	20	4	US-08-117-363A-13	Sequence 13, Appl
C 410	19	95.0	177	4	US-09-378-900A-68	Sequence 68, Appl	483	16	80.0	20	5	PCT-US96-08757A-2	Sequence 2, Appl
C 411	19	95.0	177	4	US-09-378-900A-69	Sequence 69, Appl	484	16	80.0	26	1	US-08-240-547-17	Sequence 17, Appl
C 412	19	95.0	177	4	US-09-378-900A-70	Sequence 70, Appl	485	15	75.0	15	1	US-08-182-968A-11	Sequence 11, Appl
C 413	19	95.0	177	4	US-09-378-900A-72	Sequence 72, Appl	486	15	75.0	15	2	US-08-774-306A-11	Sequence 11, Appl
C 414	19	95.0	177	4	US-09-378-900A-73	Sequence 73, Appl	487	15	75.0	15	3	US-09-064-156A-11	Sequence 11, Appl
C 415	19	95.0	177	4	US-09-378-900A-74	Sequence 74, Appl	488	15	75.0	16	4	US-09-474-432B-14	Sequence 14, Appl
C 416	19	95.0	177	4	US-09-378-900A-75	Sequence 75, Appl	489	15	75.0	16	4	US-09-476-387-14	Sequence 14, Appl
C 417	19	95.0	177	4	US-09-378-900A-76	Sequence 76, Appl	490	15	75.0	28	3	US-08-474-700B-10	Sequence 10, Appl
C 418	19	95.0	177	4	US-09-378-900A-77	Sequence 77, Appl	491	15	75.0	28	5	PCT-US95-05812-10	Sequence 10, Appl
C 419	19	95.0	177	4	US-09-378-900A-78	Sequence 78, Appl	492	15	75.0	45	1	US-09-798-641-23	Sequence 23, Appl
C 420	19	95.0	177	4	US-09-378-900A-79	Sequence 79, Appl	493	15	75.0	45	2	US-08-690-955-23	Sequence 23, Appl
C 421	19	95.0	177	4	US-09-378-900A-80	Sequence 80, Appl	494	15	75.0	45	2	US-08-690-954-23	Sequence 23, Appl
C 422	19	95.0	177	4	US-09-899-044-57	Sequence 57, Appl	495	15	75.0	45	4	US-09-299-217-23	Sequence 23, Appl
C 423	19	95.0	177	4	US-09-899-044-58	Sequence 58, Appl	496	15	75.0	45	4	US-09-728-265-23	Sequence 23, Appl
C 424	19	95.0	177	4	US-09-899-044-61	Sequence 61, Appl	497	15	75.0	45	5	PCT-US95-076617-23	Sequence 23, Appl
C 425	19	95.0	177	4	US-09-899-044-62	Sequence 62, Appl	498	14	70.0	16	4	US-08-474-432B-13	Sequence 13, Appl
C 426	19	95.0	177	4	US-09-899-044-65	Sequence 65, Appl	499	14	70.0	16	4	US-09-476-387-15	Sequence 15, Appl
C 427	19	95.0	177	4	US-09-899-044-66	Sequence 66, Appl	500	14	70.0	18	4	US-09-576-537-1	Sequence 1, Appl
C 428	19	95.0	177	4	US-09-899-044-67	Sequence 67, Appl	501	14	70.0	20	1	US-08-157-235-7	Sequence 7, Appl
C 429	19	95.0	177	4	US-09-899-044-68	Sequence 68, Appl	502	14	70.0	20	1	US-08-157-235-18	Sequence 18, Appl
C 430	19	95.0	177	4	US-09-899-044-69	Sequence 69, Appl	503	14	70.0	20	3	US-08-397-220B-61	Sequence 61, Appl
C 431	19	95.0	177	4	US-09-899-044-70	Sequence 70, Appl	504	14	70.0	20	3	US-08-650-093C-61	Sequence 61, Appl
C 432	19	95.0	177	4	US-09-899-044-72	Sequence 72, Appl	505	14	70.0	23	1	US-08-356-287-28	Sequence 28, Appl
C 433	19	95.0	177	4	US-09-899-044-73	Sequence 73, Appl	506	14	70.0	23	5	PCT-US93-04863-28	Sequence 28, Appl
C 434	19	95.0	177	4	US-09-899-044-74	Sequence 74, Appl	507	14	70.0	33	1	US-08-356-287-26	Sequence 26, Appl
C 435	19	95.0	177	4	US-09-899-044-75	Sequence 75, Appl	508	14	70.0	33	5	PCT-US93-04863-26	Sequence 26, Appl
C 436	19	95.0	177	4	US-09-899-044-76	Sequence 76, Appl	509	14	70.0	53	1	US-08-429-181-48	Sequence 48, Appl
C 437	19	95.0	177	4	US-09-899-044-77	Sequence 77, Appl	510	14	70.0	53	1	US-08-164-288-48	Sequence 48, Appl
C 438	19	95.0	177	4	US-09-899-044-78	Sequence 78, Appl	511	14	70.0	57	1	US-08-356-287-36	Sequence 36, Appl
C 439	19	95.0	177	4	US-09-899-044-79	Sequence 79, Appl	512	14	70.0	57	5	PCT-US93-04863-36	Sequence 36, Appl
C 440	19	95.0	177	4	US-09-899-044-80	Sequence 80, Appl	513	14	70.0	64	1	US-08-429-181-30	Sequence 30, Appl
C 441	19	95.0	178	2	US-08-256-568B-59	Sequence 59, Appl	514	14	70.0	64	1	US-08-164-388-30	Sequence 30, Appl
C 442	19	95.0	178	2	US-08-256-568B-60	Sequence 60, Appl	515	14	70.0	180	3	US-08-441-971-50	Sequence 50, Appl
C 443	19	95.0	178	2	US-08-256-568B-71	Sequence 71, Appl	516	14	70.0	180	3	US-08-441-971-51	Sequence 51, Appl
C 444	19	95.0	178	2	US-08-256-568B-81	Sequence 81, Appl	517	14	70.0	180	3	US-08-221-653-50	Sequence 50, Appl
C 445	19	95.0	178	3	US-09-038-369B-59	Sequence 59, Appl	518	14	70.0	180	3	US-08-221-653-51	Sequence 51, Appl
C 446	19	95.0	178	3	US-09-038-369B-60	Sequence 60, Appl	519	14	70.0	180	3	US-08-442-144A-50	Sequence 50, Appl
C 447	19	95.0	178	3	US-09-038-369B-61	Sequence 61, Appl	520	14	70.0	180	3	US-08-442-144A-51	Sequence 51, Appl
C 448	19	95.0	178	3	US-09-038-369B-81	Sequence 81, Appl	521	14	70.0	180	3	US-08-441-970-50	Sequence 50, Appl
C 449	19	95.0	178	4	US-09-378-900A-59	Sequence 59, Appl	522	14	70.0	180	3	US-08-441-970-51	Sequence 51, Appl
C 450	19	95.0	178	4	US-09-378-900A-60	Sequence 60, Appl	523	14	70.0	97	7	US-09-710-279-1771	Sequence 1771, Ap
C 451	19	95.0	178	4	US-09-378-900A-71	Sequence 71, Appl	524	14	70.0	97	3	US-09-134-001C-202	Sequence 202, App
C 452	19	95.0	178	4	US-09-378-900A-81	Sequence 81, Appl	525	14	70.0	148	2	US-09-252-991A-11453	Sequence 11453, A
C 453	19	95.0	178	4	US-09-899-044-59	Sequence 59, Appl	526	14	70.0	235	2	US-09-051-239A-14	Sequence 14, Appl
C 454	19	95.0	178	4	US-09-899-044-60	Sequence 60, Appl	527	14	70.0	235	2	US-10-151-668-14	Sequence 14, Appl
C 455	19	95.0	178	4	US-09-899-044-71	Sequence 71, Appl	528	14	70.0	406	9	US-09-710-279-3976	Sequence 3976, Ap
C 456	19	95.0	178	4	US-09-899-044-81	Sequence 81, Appl	529	13	65.0	15	1	US-08-182-968A-12	Sequence 12, Appl
C 457	18	90.0	21	3	US-08-650-093C-16	Sequence 16, Appl	530	13	65.0	15	2	US-08-774-306A-11	Sequence 12, Appl
C 458	18	90.0	21	3	US-08-823-895A-16	Sequence 16, Appl	531	13	65.0	15	3	US-09-064-156A-12	Sequence 12, Appl
C 459	18	90.0	21	3	US-09-292-563-9	Sequence 9, Appl	532	13	65.0	16	3	US-08-954-210-18	Sequence 18, Appl
C 460	18	90.0	39	3	US-08-468-447-1	Sequence 1, Appl	533	13	65.0	18	3	US-09-431-419A-18	Sequence 18, Appl
C 461	17	85.0	20	1	US-08-468-851A-1	Sequence 1, Appl	534	13	65.0	18	2	US-08-097-853-1	Sequence 1, Appl
C 462	17	85.0	20	1	US-08-468-851A-1	Sequence 1, Appl	535	13	65.0	18	2	US-08-438-435-1	Sequence 1, Appl
C 463	17	85.0	20	1	US-08-467-597A-1	Sequence 1, Appl	536	13	65.0	18	4	US-09-792-361-4	Sequence 4, Appl
C 464	17	85.0	20	1	US-08-466-692A-1	Sequence 1, Appl	537	13	65.0	19	3	US-09-311-260-75	Sequence 75, Appl
C 465	17	85.0	20	1	US-08-466-692A-1	Sequence 1, Appl	538	13	65.0	21	4	US-09-875-945-13	Sequence 13, Appl



C 685	12	60.0	4115	1	US-09-912-161-7	Sequence 7, Appl1	C 758	12	60.0	254964	4	US-09-949-016-12583	Sequence 12583, A
C 686	12	60.0	4516	1	US-08-832-883-49	Sequence 49, Appl1	C 759	12	60.0	254964	4	US-09-949-016-17392	Sequence 17392, A
C 687	12	60.0	4576	2	US-08-832-883-49	Sequence 49, Appl1	C 760	12	60.0	265036	4	US-09-949-016-15779	Sequence 15779, A
C 688	12	60.0	4700	3	US-09-150-460B-9	Sequence 9, Appl1	C 761	12	60.0	321022	4	US-09-949-016-11852	Sequence 11852, A
C 689	12	60.0	4898	4	US-09-636-499-17	Sequence 17, Appl1	C 762	12	60.0	321022	4	US-09-949-016-11852	Sequence 11852, A
C 690	12	60.0	5438	3	US-08-456-200B-5	Sequence 5, Appl1	C 763	12	60.0	340380	4	US-09-949-016-14176	Sequence 14176, A
C 691	12	60.0	5531	4	US-08-956-171E-408	Sequence 408, App	C 764	12	60.0	403355	4	US-09-949-016-15473	Sequence 15473, A
C 692	12	60.0	5531	4	US-08-956-171E-408	Sequence 408, App	C 765	12	60.0	462589	4	US-09-949-016-161290	Sequence 161290, A
C 693	12	60.0	5531	4	US-08-956-171E-408	Sequence 408, App	C 766	12	60.0	462589	4	US-09-949-016-161290	Sequence 161290, A
C 694	12	60.0	11947	4	US-09-949-016-15369	Sequence 15369, A	C 767	12	60.0	476044	4	US-09-949-016-12412	Sequence 12412, A
C 695	12	60.0	12847	4	US-09-949-016-13866	Sequence 13866, A	C 768	12	60.0	536165	4	US-09-214-808-1	Sequence 1, Appl1
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C 697	12	60.0	13970	6	US-09-949-016-16690	Sequence 16690, A	C 770	12	60.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
C 698	12	60.0	20951	4	US-09-805-455-3	Sequence 3, Appl1	C 771	12	60.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
C 699	12	60.0	22547	4	US-09-849-016-13879	Sequence 13879, A	C 772	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 700	12	60.0	23218	4	US-09-849-016-13879	Sequence 13879, A	C 773	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 701	12	60.0	23218	4	US-09-849-016-13879	Sequence 13879, A	C 774	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 702	12	60.0	23319	4	US-09-949-016-13396	Sequence 13396, A	C 775	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 703	12	60.0	23319	4	US-09-949-016-13396	Sequence 13396, A	C 776	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 704	12	60.0	23417	4	US-09-902-540-1207	Sequence 1207, Ap	C 777	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 705	12	60.0	24221	4	US-09-949-016-14964	Sequence 14964, A	C 778	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 706	12	60.0	24979	2	US-08-147-777-3	Sequence 3, Appl1	C 779	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 707	12	60.0	24979	3	US-08-452-872-3	Sequence 3, Appl1	C 780	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 708	12	60.0	24979	5	PCT-US83-03985-3	Sequence 3, Appl1	C 781	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 709	12	60.0	26502	4	US-09-949-016-15855	Sequence 15855, A	C 782	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 710	12	60.0	28030	4	US-09-949-016-12305	Sequence 12305, A	C 783	12	60.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 711	12	60.0	32068	4	US-09-949-016-15948	Sequence							



C 977 11 55.0 601 4 US-09-949-016-142848 Sequence 142848,  
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C 979 11 55.0 601 4 US-09-949-016-146894 Sequence 146894,  
C 980 11 55.0 601 4 US-09-949-016-148707 Sequence 148707,  
C 981 11 55.0 601 4 US-09-949-016-150286 Sequence 150286,  
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C 990 11 55.0 601 4 US-09-949-016-156862 Sequence 156862,  
C 991 11 55.0 601 4 US-09-949-016-167050 Sequence 167050,  
C 992 11 55.0 601 4 US-09-949-016-169379 Sequence 169379,  
C 993 11 55.0 601 4 US-09-949-016-169380 Sequence 169380,  
C 994 11 55.0 601 4 US-09-949-016-176033 Sequence 176033,  
C 995 11 55.0 601 4 US-09-949-016-176565 Sequence 176565,  
C 996 11 55.0 601 4 US-09-949-016-179675 Sequence 179675,  
C 997 11 55.0 601 4 US-09-949-016-179676 Sequence 179676,  
C 998 11 55.0 601 4 US-09-949-016-180761 Sequence 180761,  
C 999 11 55.0 601 4 US-09-949-016-180762 Sequence 180762,  
C1000 11 55.0 601 4 US-09-949-001-812 Sequence 812, App

## ALIGNMENTS

RESULT 1  
US-09-493-353-13

Sequence 13, Application US/09493353  
Patent No. 6638714  
GENERAL INFORMATION:  
APPLICANT: Johnson & Johnson  
APPLICANT: Gorman, K.M.  
TITLE OF INVENTION: DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE  
TITLE OF INVENTION: THEROP  
FILE REFERENCE: 2094/1E286-US1  
CURRENT APPLICATION NUMBER: US/09/493,353  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/118,497  
PRIOR FILING DATE: 1999-02-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer  
US-09-493-353-13

Query Match 100.0%; Score 20; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
Db 2 TTGGGACCCCAACTACTC 21

RESULT 2  
US-08-648-272-21/c  
Sequence 21, Application US/08648272  
Patent No. 6107028  
GENERAL INFORMATION:  
APPLICANT: Kay, Mark A.  
APPLICANT: Lieber, Andre  
TITLE OF INVENTION: Ribozymes for Treating Hepatitis C  
NUMBER OF SEQUENCES: 24

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STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/648,272  
FILING DATE: 15-MAY-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/534,220  
FILING DATE: 11-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/476,257  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/357,508  
FILING DATE: 14-DEC-1994  
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-648-272-21

Query Match 100.0%; Score 20; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
Db 24 TTGGGACCCCAACTACTC 5

RESULT 3  
US-09-494-332A-12  
Sequence 12, Application US/09494332A  
Patent No. 6623919  
GENERAL INFORMATION:  
APPLICANT: GORMAN, Kevin  
APPLICANT: PATTERSON, David  
APPLICANT: LINNEN, Jeffrey  
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT MULTIPLEX DETECTION OF HEP  
FILE REFERENCE: 2049/1E285-US1  
CURRENT APPLICATION NUMBER: US/09/494,332A  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/118,498  
PRIOR FILING DATE: 1999-02-03  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Version 3.0  
SEQ ID NO 12  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer

US-09-494-332A-12

Query Match 100.0%; Score 20; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 4 TTGGGACCCCACTACTC 23

RESULT 4

US-09-493-353-12  
Sequence 12, Application US/09493353  
Patent No. 6638714  
GENERAL INFORMATION:  
APPLICANT: Johnson & Johnson  
APPLICANT: Limmen, J.M.  
APPLICANT: Gorman, K.M.  
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT  
DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE  
FILE REFERENCE: 2094/1E286-US1  
CURRENT APPLICATION NUMBER: US/09/493,353  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/118,497  
PRIOR FILING DATE: 1999-02-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer  
US-09-493-353-12

Query Match 100.0%; Score 20; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 4 TTGGGACCCCACTACTC 23

RESULT 5

US-08-438-639-50  
Sequence 50, Application US/08438639  
Patent No. 5712383  
GENERAL INFORMATION:  
APPLICANT: Sheridan, Patrick  
APPLICANT: Chang, Chu-An  
APPLICANT: Running, Joyce  
APPLICANT: Urdea, Michael S.  
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID  
TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION - R440  
STREET: P.O. Box 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,639  
FILING DATE: 10-MAY-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,338  
FILING DATE: 23-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth, M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0232.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-438-639-50

Query Match 100.0%; Score 20; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 10 TTGGGACCCCACTACTC 29

RESULT 6

US-07-813-338A-50  
Sequence 50, Application US/07813338A  
Patent No. 5747244  
GENERAL INFORMATION:  
APPLICANT: Sheridan, Patrick  
APPLICANT: Chang, Chu-An  
APPLICANT: Running, Joyce  
APPLICANT: Urdea, Michael S.  
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID  
TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION - R440  
STREET: P.O. Box 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/813,338A  
FILING DATE: 23-DEC-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth, M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0232.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-813-338A-50

Query Match 100.0%; Score 20; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGAGCCCAACACTACTC 20  
10 TTGCGAGCCCAACACTACTC 29  
Db

## RESULT 7

US-08-470-124-60  
; Sequence 60, Application US/08470124  
; Patent No. 5849481  
; GENERAL INFORMATION:  
; APPLICANT: Urdea, Michael S.  
; APPLICANT: Horn, Thomas  
; APPLICANT: Chang, Chu-An  
; APPLICANT: Warner, Brian  
; APPLICANT: Fultz, Timothy J.  
; TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED  
; TITLE OF INVENTION: POLYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 545 Middlefield Road, Suite 200  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/470.124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/813,588  
; FILING DATE: 23 December 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ciotli, Thomas E.  
; REGISTRATION NUMBER: 21,013  
; REFERENCE/DOCKET NUMBER: 22300-20104.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-327-2951  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 60:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-470-124-60

Query Match 100.0%; Score 20; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGAGCCCAACACTACTC 20  
10 TTGCGAGCCCAACACTACTC 29  
Db

## RESULT 8

US-08-441-971-126  
; Sequence 126, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janluk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-441-971-126

Query Match 100.0%; Score 20; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGAGCCCAACACTACTC 20  
10 TTGCGAGCCCAACACTACTC 29  
Db

## RESULT 9

US-08-221-653-126  
; Sequence 126, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-221-653-126

Query Match 100.0%; Score 20; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
Db 10 TTGCGACCCCAACTACTC 29

RESULT 10  
US-08-442-144A-126  
Sequence 126, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439

TELEX:  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
US-08-442-144A-126

Query Match 100.0%; Score 20; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
Db 10 TTGCGACCCCAACTACTC 29

RESULT 11  
US-08-441-970-126  
Sequence 126, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-441-970-126

Query Match 100.0%; Score 20; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
Db 10 TTGCGACCCCAACTACTC 29

```
RESULT 12
US-09-358-972-181/C
; Sequence 181, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528,972
; CURRENT APPLICATION NUMBER: US/09/358,972
; EARLIER FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 181
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; OTHER INFORMATION: probe for Hepatitis C
US-09-358-972-181

Query Match          100.0%; Score 20; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGGCGACCCCAACTACTC 20
Db      29 TTGGCGACCCCAACTACTC 10

RESULT 13
US-09-406-147-43/C
; Sequence 43, Application US/09406147
; Patent No. 6270974
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K
; APPLICANT: Leippe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A
; APPLICANT: Hartnett, James R
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith V
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: EXOGENOUS NUCLEIC ACID DETECTION
; FILE REFERENCE: EXOGENOUS NUCLEIC ACID DETECTION
; CURRENT APPLICATION NUMBER: US/09/406,147
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 43
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; LENGTH: 40
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-406-147-43

Query Match          100.0%; Score 20; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGGCGACCCCAACTACTC 20
Db      29 TTGGCGACCCCAACTACTC 10

RESULT 14
US-09-790-417-181/C
; Sequence 181, Application US/09790417
; Patent No. 6730479
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790,417
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 181
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; OTHER INFORMATION: probe for Hepatitis C
US-09-790-417-181

Query Match          100.0%; Score 20; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGGCGACCCCAACTACTC 20
Db      29 TTGGCGACCCCAACTACTC 10

RESULT 15
US-08-429-181-10
; Sequence 10, Application US/08429181
; Patent No. 5635352
; GENERAL INFORMATION:
; APPLICANT: URDEA, MICHAEL S.
; APPLICANT: FULTZ, TIMOTHY
; APPLICANT: WARNER, BRIAN D.
; APPLICANT: COLLINS, MARK
; TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
; TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
; ADDRESSER: R440
```

STREET: 4560 HORTON STREET  
CITY: EMERYVILLE  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/429,181  
FILING DATE: 26-APR-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/164,388  
FILING DATE: 08-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: GOLDMAN, KENNETH M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0300.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-429-181-10

Query Match 100.0%; Score 20; DB 1; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 10 TTCCGACCCCACTACTC 29

RESULT 16  
US-08-164-388-10  
Sequence 10, Application US/08164388  
Patent No. 5681697  
GENERAL INFORMATION:  
APPLICANT: URDEA, MICHAEL S.  
APPLICANT: FILITZ, TIMOTHY  
APPLICANT: WARNER, BRIAN D.  
APPLICANT: COLLINS, MARK  
TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH  
TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESS: CHIRON CORPORATION - INTELLECTUAL PROPERTY  
ADDRESS: R440  
STREET: 4560 HORTON STREET  
CITY: EMERYVILLE  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/164,388  
FILING DATE: 08-DEC-1993  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:

NAME: GOLDMAN, KENNETH M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0300.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-164-388-10

Query Match 100.0%; Score 20; DB 1; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 10 TTCCGACCCCACTACTC 29

RESULT 17  
US-09-798-641-31  
Sequence 31, Application US/09798641  
Patent No. RE38442  
GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESS: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PassSeq Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/798,641  
FILING DATE: 02-Mar-2001  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,495  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacLeod, Janet M.  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..108  
SEQUENCE DESCRIPTION: SEQ ID NO: 31;  
US-09-798-641-31

Query Match 100.0%; Score 20; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 4 TTCCGACCCCAACTACTC 23

## RESULT 18

US-08-690-495-31  
Sequence 31, Application US/08690495  
Patent No. 5876924

GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASSEQ Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,495  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacLeod, Janet M.  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
US-08-690-495-31

Query Match 100.0%; Score 20; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 4 TTCCGACCCCAACTACTC 23

## RESULT 19

US-08-690-494-31  
Sequence 31, Application US/08690494  
Patent No. 5842391

GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brumbaugh, Graves, Donohue & Raymond

STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASSEQ Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,494  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacLeod, Janet M.  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
US-08-690-494-31

Query Match 100.0%; Score 20; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 4 TTCCGACCCCAACTACTC 23

## RESULT 20

US-09-299-217-31  
Sequence 31, Application US/09299217  
Patent No. 6569647

GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASSEQ Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,217  
FILING DATE: 23-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,494  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacLeod, Janet M.  
REGISTRATION NUMBER: 35,263

REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
US-09-299-217-31  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
Query Match 100.0%; Score 20; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
Db 4 TTGCGACCCCAACTACTC 23  
RESULT 21  
US-09-728-265-31  
Sequence 31, Application US/09728265  
Patent No. 6593086  
GENERAL INFORMATION:  
APPLICANT: Zhang, David Y.  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD.  
TITLE OF INVENTION: RAMIFICATION-EXTENSION AMPLIFICATION METHOD (RAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Stroock & Stroock & Lavan  
STREET: 180 Maiden Lane  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10038  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PCDOS/MSDOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/728,265  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pokocilow, Steven B  
REGISTRATION NUMBER: 26,405  
REFERENCE/DOCKET NUMBER: Old 29545A/PCT/USA-B // New 251305/0018  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212806-6663  
TELEFAX: 2128066006  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
US-09-728-265-31  
Query Match 100.0%; Score 20; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 4 TTGCGACCCCAACTACTC 23  
RESULT 22  
PCT-US95-07671-31  
Sequence 31, Application PC/TUS9507671  
GENERAL INFORMATION:  
APPLICANT: Zhang, David Y.  
TITLE OF INVENTION: LIGATION-DEPENDENT AMPLIFICATION FOR THE  
DETECTION OF INFECTIOUS PATHOGENS AND ABNORMAL GENES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07671  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Seide, Rochelle K.  
REGISTRATION NUMBER: 32,300  
REFERENCE/DOCKET NUMBER: 29545-A-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2626  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
PCT-US95-07671-31  
Query Match 100.0%; Score 20; DB 5; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
Db 4 TTGCGACCCCAACTACTC 23  
RESULT 23  
US-08-244-116B-12/C  
Sequence 12, Application US/08244116B  
Patent No. 5763159  
GENERAL INFORMATION:  
APPLICANT: Simmonds, Peter  
APPLICANT: Chan, Shiu-Wan  
APPLICANT: Yap, Peng L.  
TITLE OF INVENTION: Hepatitis-C Virus Testing  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.  
STREET: 1211 East Morehead Street  
CITY: Charlotte  
STATE: No. 5763159th Carolina

COUNTRY: United States  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,116B  
FILING DATE: 15-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02143  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stbley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 1749-125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 704-377-1561  
TELEFAX: 704-334-2014  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Hepatitis-C virus  
US-08-244-116B-12

Query Match 100.0%; Score 20; DB 1; Length 194;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
DB 189 TTGCGACCCACACTACTC 170

RESULT 24  
US-09-034-205-37/c  
Sequence 37, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neel, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
DB 199 TTGCGACCCACACTACTC 180

RESULT 25  
US-08-934-097A-37/c  
Sequence 37, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neel, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 26

US-08-851-588-37/C  
Sequence 37, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION/DOCKET NUMBER: 40,027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 27

US-09-677-218B-37/C  
Sequence 37, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68

## CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION/DOCKET NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-677-218B-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 28

US-09-677-192-37/C  
Sequence 37, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 29

US-09-402-618B-37/c  
Sequence 37, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-37

Query Match 100.0%; Score 20; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 30

US-09-825-574-37/c  
Sequence 37, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Karmin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-825-574-37

Query Match 100.0%; Score 20; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 31

US-09-676-768-37/c  
Sequence 37, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear



MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-676-768-37

Query Match 100.0%; Score 20; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 199 TTGCGACCCCAACTACTC 180

RESULT 32  
US-09-034-205-32/c  
Sequence 32, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-32  
Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 206 TTGCGACCCCAACTACTC 187

RESULT 33  
US-09-034-205-36/c  
Sequence 36, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-36  
Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 206 TTGCGACCCCAACTACTC 187

RESULT 34  
US-08-934-097A-32/c  
Sequence 32, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
STRUCTURE PROBING WITH STRUCTURE-BRIDGING  
OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-32

Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 35  
US-08-934-097A-36/C  
Sequence 36, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Meri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-36

Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 36  
US-08-851-588-32/C  
Sequence 32, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-32

Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 37  
US-08-851-588-36/C  
Sequence 36, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-36  
Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187  
RESULT 38  
US-09-677-218B-32/c  
Sequence 32, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
US-09-677-218B-32  
Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187  
RESULT 39  
US-09-677-218B-36/c  
Sequence 36, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

```

; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-677-218B-36

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 239;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 206 TTGGGACCCCAACTACTC 187

RESULT 40
US-09-677-192-32/c
; Sequence 32, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 32
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-32

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 239;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 206 TTGGGACCCCAACTACTC 187

RESULT 41
US-09-677-192-36/c
; Sequence 36, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 36
; LENGTH: 239
; TYPE: DNA
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; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-36

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 239;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 206 TTGGGACCCCAACTACTC 187

RESULT 42
US-09-402-618B-32/c
; Sequence 32, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 32
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-32

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 239;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 206 TTGGGACCCCAACTACTC 187

RESULT 43
US-09-402-618B-36/c
; Sequence 36, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 36
; LENGTH: 239
; TYPE: DNA
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ORGANISM: Hepatitis C virus  
US-09-402-618B-36

Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

## RESULT 44

US-09-825-574-32/c  
Sequence 32, Application US/09825574  
Patent No. 6709819

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-825-574-32

Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 45  
US-09-825-574-36/c

Sequence 36, Application US/09825574  
Patent No. 6709819

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-825-574-36

Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

## RESULT 46

US-09-676-768-32/c  
Sequence 32, Application US/09676768  
Patent No. 6780585

GENERAL INFORMATION:

APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-676-768-32

Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
|||  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 47  
US-09-676-768-36/c  
Sequence 36, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
STRUCTURE-PROBING  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-676-768-36

Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
|||  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 48  
US-09-034-205-33/c  
Sequence 33, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: /desc = "DNA"  
US-09-034-205-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 207 TTGGGACCCCAACTACTC 188

## RESULT 49

US-09-034-205-35/c  
; Sequence 35, Application US/09034205  
; Patent No. 6194149  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Nerl, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034,205  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-09-034-205-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 207 TTGGGACCCCAACTACTC 188

## RESULT 50

US-09-034-205-38/c  
; Sequence 38, Application US/09034205  
; Patent No. 6194149  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Nerl, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034,205  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-09-034-205-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

## RESULT 51

US-08-934-097A-33/c  
; Sequence 33, Application US/08934097A  
; Patent No. 6210880  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Nerl, Bruce P.  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; TITLE OF INVENTION: Structure Probing With Structure-Bridging  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,097A  
; FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 207 TTGGGACCCCACTACTC 188

RESULT 52  
US-08-934-097A-35/C  
Sequence 35, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neiri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 207 TTGGGACCCCACTACTC 188

RESULT 53  
US-08-934-097A-38/C  
Sequence 38, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neiri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 208 TTGGGACCCCACTACTC 189

RESULT 54  
US-08-934-097A-33/C  
Sequence 33, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neiri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-33



APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
DB 207 TTGCGACCCCACTACTC 188

RESULT 55  
US-08-851-588-35/c  
Sequence 35, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588

FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
DB 207 TTGCGACCCCACTACTC 188

RESULT 56  
US-08-851-588-38/c  
Sequence 38, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-38



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELEPHONE: (415) 397-8338  
TELEFAX: (415) 705-8410  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-677-218B-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 60  
US-09-677-192-33/c  
Sequence 33, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 33  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 207 TTGCGACCCCAACTACTC 188

RESULT 61  
US-09-677-192-35/c

Sequence 35, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 35  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 207 TTGCGACCCCAACTACTC 188

RESULT 62  
US-09-677-192-38/c  
Sequence 38, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 38  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 63  
US-09-402-618B-33/c  
Sequence 33, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 33  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-33

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 207 TTCCGACCCCAACTACTC 188

RESULT 64  
US-09-402-618B-35/c  
Sequence 35, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-35

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 207 TTCCGACCCCAACTACTC 188

RESULT 65  
US-09-402-618B-38/c  
Sequence 38, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 38  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-38

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 208 TTCCGACCCCAACTACTC 189

RESULT 66  
US-09-825-574-33/c  
Sequence 33, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-825-574-33

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

## RESULT 67

US-09-825-574-35/C  
Sequence 35, Application US/09825574  
Patent No. 6709819

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Karin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 397-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-09-825-574-35

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

RESULT 68  
US-09-825-574-38/C

Sequence 38, Application US/09825574  
Patent No. 6709819

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Karin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-825-574-38

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

## RESULT 69

US-09-676-768-33/C  
Sequence 33, Application US/09676768  
Patent No. 6780585

GENERAL INFORMATION:

APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/676,768  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-676-768-33

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTGGGACCCCACTACTC 20  
Db 207 TTGGGACCCCACTACTC 188

RESULT 70  
US-09-676-768-35/c  
Sequence 35, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamlichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-676-768-35

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTGGGACCCCACTACTC 20  
Db 207 TTGGGACCCCACTACTC 188

RESULT 71  
US-09-676-768-38/c  
Sequence 38, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamlichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-676-768-38

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

RESULT 72  
US-09-034-205-26/c  
Sequence 26, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-26

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

RESULT 73  
US-09-034-205-27/c  
Sequence 27, Application US/09034205  
Patent No. 6194149

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-27

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

RESULT 74  
US-09-034-205-29/c  
Sequence 29, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-29

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 75  
US-09-034-205-31/c  
Sequence 31, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"  
US-09-034-205-31

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 76  
US-08-934-097A-26/c  
Sequence 26, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
STRUCTURE PROBING WITH STRUCTURE-BRIDGING  
OLIGONUCLEOTIDES.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-26

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 77  
US-08-934-097A-27/c  
Sequence 27, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.



APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ. ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-27

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 78  
US-08-934-097A-29/C  
Sequence 29, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ. ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ. ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-29

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 79  
US-08-934-097A-31/C  
Sequence 31, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ. ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-31

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
Db 208 TTCGGACCCCAACTACTC 189

RESULT 80  
US-08-851-588-26/c  
Sequence 26, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-26

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
Db 208 TTCGGACCCCAACTACTC 189

RESULT 81  
US-08-851-588-27/c  
Sequence 27, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-27

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
Db 208 TTCGGACCCCAACTACTC 189

RESULT 82  
US-08-851-588-29/c  
Sequence 29, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-29

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 83  
US-08-851-588-31/c  
Sequence 31, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-31

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 84  
US-09-677-218B-26/c  
Sequence 26, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Neri, Bruce P.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-677-218B-26

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 85

US-09-677-218B-27/c  
; Sequence 27, Application US/09677218B  
; Patent No. 6355437  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; Fors, Lance  
; Nerl, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/677,218B  
; FILING DATE: 02-Oct-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/034,205  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
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; SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-677-218B-27  
Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
DB 208 TTCCGACCCCAACTACTC 189  
RESULT 86  
US-09-677-218B-29/c  
; Sequence 29, Application US/09677218B  
; Patent No. 6355437  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; Fors, Lance  
; Nerl, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-677-218B-29  
Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
DB 208 TTCCGACCCCAACTACTC 189  
RESULT 87  
US-09-677-218B-31/c  
; Sequence 31, Application US/09677218B  
; Patent No. 6355437  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; Fors, Lance  
; Nerl, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/677,218B  
; FILING DATE: 02-Oct-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/034,205  
; FILING DATE: <Unknown>

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ATTORNEY/AGENT INFORMATION:
; NAME: Macknight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-677-218b-31

Query Match          100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 88
US-09-677-192-26/c
; Sequence 26, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-26

Query Match          100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 89
US-09-677-192-27/c
; Sequence 27, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-27
```

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CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-27

Query Match          100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 90
US-09-677-192-29/c
; Sequence 29, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-29

Query Match          100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 91
US-09-677-192-31/c
; Sequence 31, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31
; LENGTH: 244
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; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-31

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 244;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20
Db 208 TTCCGACCCCAACTACTC 189

RESULT 92
US-09-402-618B-26/c
; Sequence 26, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-26

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 244;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20
Db 208 TTCCGACCCCAACTACTC 189

RESULT 93
US-09-402-618B-27/c
; Sequence 27, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus

; ORGANISM: Hepatitis C virus
US-09-402-618B-27

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 244;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20
Db 208 TTCCGACCCCAACTACTC 189

RESULT 94
US-09-402-618B-29/c
; Sequence 29, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-29

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 244;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20
Db 208 TTCCGACCCCAACTACTC 189

RESULT 95
US-09-402-618B-31/c
; Sequence 31, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
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US-09-402-618B-31

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 96  
US-09-402-618B-124  
; Sequence 124, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/09/402,618B  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 124  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-402-618B-124

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
DB 37 TTGGGACCCCAACTACTC 56

RESULT 97  
US-09-402-618B-125  
; Sequence 125, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/09/402,618B  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 125  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-402-618B-125

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
DB 37 TTGGGACCCCAACTACTC 56

RESULT 98  
US-09-402-618B-127  
; Sequence 127, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/09/402,618B  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 127  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-402-618B-127

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
DB 37 TTGGGACCCCAACTACTC 56

RESULT 99  
US-09-402-618B-128  
; Sequence 128, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/09/402,618B  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 128  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-402-618B-128

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 80.0%; Pred. No. 0.0029;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCACTACTC 20  
Db 37 TTCCGACCCCACTACTC 56

## RESULT 100

US-09-825-574-26/c

Sequence 26, Application US/09825574

Patent No. 6709819

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Fors, Lance P.

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid

Structure Probing With Structure-Bridging Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-825-574-26

Query Match

Best Local Similarity 100.0%; Score 20; DB 4; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCACTACTC 20  
Db 208 TTCCGACCCCACTACTC 189

## RESULT 101

US-09-825-574-27/c

Sequence 27, Application US/09825574

Patent No. 6709819

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance P.

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid

Structure Probing With Structure-Bridging Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-825-574-27

Query Match

Best Local Similarity 100.0%; Score 20; DB 4; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCACTACTC 20  
Db 208 TTCCGACCCCACTACTC 189

## RESULT 102

US-09-825-574-29/c

Sequence 29, Application US/09825574

Patent No. 6709819

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance P.

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid

Structure Probing With Structure-Bridging Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA



ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-825-574-29

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 208 TTGGGACCCCACTACTC 189

RESULT 103  
US-09-825-574-31/c  
Sequence 31, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-825-574-31

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 208 TTGGGACCCCACTACTC 189

RESULT 104  
US-09-676-768-26/c  
Sequence 26, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 26;  
US-09-676-768-26

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 105

US-09-676-768-27/c  
Sequence 27, Application US/09676768  
Patent No. 6780585

GENERAL INFORMATION:  
APPLICANT: Dong, Fang

Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:

ADDRESSES: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94104  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 27;  
US-09-676-768-27

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 106  
US-09-676-768-29/c

Sequence 29, Application US/09676768  
Patent No. 6780585

GENERAL INFORMATION:  
APPLICANT: Dong, Fang

Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:

ADDRESSES: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94104  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 29;  
US-09-676-768-29

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 107  
US-09-676-768-31/c

Sequence 31, Application US/09676768  
Patent No. 6780585

GENERAL INFORMATION:  
APPLICANT: Dong, Fang

Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:

ADDRESSES: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-676-768-31

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACACTACTC 20  
DB 208 TTGGGACCCACACTACTC 189

RESULT 108  
US-08-441-971-33/C  
Sequence 33, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:

APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: (ATCC # 40394)  
INDIVIDUAL ISOLATE: hcvt  
US-08-441-971-33

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACACTACTC 20  
DB 186 TTGGGACCCACACTACTC 167

RESULT 109  
US-08-441-971-34/C  
Sequence 34, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-441-971-34

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
DB 186 TTGCGAGCCCACTACTC 167

RESULT 110  
US-08-441-971-35/c  
Sequence 35, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-441-971-35

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCACTACTC 20

DB 186 TTGCGAGCCCACTACTC 167

RESULT 111  
US-08-441-971-36/c  
Sequence 36, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp2  
US-08-441-971-36

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
DB 186 TTGCGAGCCCACTACTC 167

RESULT 112  
US-08-441-971-37/c  
Sequence 37, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147

```

CORRESPONDENCE ADDRESS:
ADDRESS: Wolf, Greenfield & Sacke, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,971
FILING DATE: 16-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,653
FILING DATE:
APPLICATION NUMBER: US/07/881,528
FILING DATE:
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janluk, Anthony J.
REGISTRATION NUMBER: 29, 809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: gm2
US-08-441-971-37

Query Match 100.0%; Score 20; DB 3; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 TTGGGACCCCAACTACTC 20
Db 186 TTGGGACCCCAACTACTC 167

RESULT 113
US-08-441-971-38/c
Sequence 38, Application US/08441971
Parent No. 6071693
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/441,971
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,653
FILING DATE:
APPLICATION NUMBER: US/07/881,528
FILING DATE:
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 121
US-08-441-971-38

Query Match 100.0%; Score 20; DB 3; Length 252;
Best Local Similarity 100.0%; Pctd. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 TTCCGACCCACACTACTC 20
Db 186 TTCCGACCCACACTACTC 167

RESULT 114
US-08-441-971-39/c
Sequence 39, Application US/08441971
Patent No. 6071693
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,971
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,653
FILING DATE:
APPLICATION NUMBER: US/07/881,528
FILING DATE:
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809

```

REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us4  
US-08-441-971-39

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
DB 186 TTCCGACCCCACTACTC 167

RESULT 115  
US-08-441-971-40/C  
Sequence 40, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: jh1  
US-08-441-971-40

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
DB 186 TTCCGACCCCACTACTC 167

RESULT 116  
US-08-441-971-41/C  
Sequence 41, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: nac5  
US-08-441-971-41

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
DB 186 TTCCGACCCCACTACTC 167

RESULT 117

US-08-441-971-42/c  
; Sequence 42, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIORITY INFORMATION:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: arg2  
; US-08-441-971-42  
  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167  
  
RESULT 118  
US-08-441-971-43/c  
; Sequence 43, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts

COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIORITY INFORMATION:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: sp1  
; US-08-441-971-43  
  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167  
  
RESULT 119  
US-08-441-971-44/c  
; Sequence 44, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIORITY INFORMATION:  
; APPLICATION NUMBER: US/08/221,653

;; FILING DATE: US/07/881,528  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ ID NO: 44:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: gh1  
US-08-441-971-44

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167

RESULT 120  
US-08-441-971-45/c  
; Sequence 45, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL

;; INFORMATION FOR SEQ ID NO: 45:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: 115  
US-08-441-971-45

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167

RESULT 121  
US-08-441-971-48/c  
; Sequence 48, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: 621  
US-08-441-971-48

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;



Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
|||||  
Db 186 TTGGGACCCACACTACTC 167

## RESULT 122

US-08-441-971-49/c  
; Sequence 49, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-May-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: GJ61329  
US-08-441-971-49

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
|||||  
Db 186 TTGGGACCCACACTACTC 167

RESULT 123  
US-08-221-653-33/c  
; Sequence 33, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha

;; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
;; DIAGNOSTICS AND THERAPEUTICS  
;; NUMBER OF SEQUENCES: 147  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
;; STREET: 600 Atlantic Avenue  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02210

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: MS-DOS Version 3.3  
;; SOFTWARE: WordPerfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/221,653  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/881,528  
;; FILING DATE:  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ ID NO: 33:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE: (ATCC # 40394)  
;; INDIVIDUAL ISOLATE: hcvi  
US-08-221-653-33

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
|||||  
Db 186 TTGGGACCCACACTACTC 167

RESULT 124  
US-08-221-653-34/c  
; Sequence 34, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/221,653  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/881,528  
;; FILING DATE:  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ ID NO: 34:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: us5  
;; US-08-221-653-34

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGAGCCCACTACTC 20  
DB 186 TTGGGAGCCCACTACTC 167

;; RESULT 125  
;; US-08-221-653-35/c  
;; Sequence 35, Application US/08221653  
;; Patent No. 6190864  
;; GENERAL INFORMATION:  
;; APPLICANT: Tai-An Cha  
;; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
;; NUMBER OF SEQUENCES: 147  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: Wolf, Greenfield & Sacks, P.C.  
;; STREET: 600 Atlantic Avenue  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02210  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: MS-DOS Version 3.3  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/221,653  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/881,528  
;; FILING DATE:  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500

;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ ID NO: 35:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: aus1  
;; US-08-221-653-35

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGAGCCCACTACTC 20  
DB 186 TTGGGAGCCCACTACTC 167

;; RESULT 126  
;; US-08-221-653-36/c  
;; Sequence 36, Application US/08221653  
;; Patent No. 6190864  
;; GENERAL INFORMATION:  
;; APPLICANT: Tai-An Cha  
;; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
;; NUMBER OF SEQUENCES: 147  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: Wolf, Greenfield & Sacks, P.C.  
;; STREET: 600 Atlantic Avenue  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02210  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: MS-DOS Version 3.3  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/221,653  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/881,528  
;; FILING DATE:  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ ID NO: 36:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: sp2  
;; US-08-221-653-36

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20  
Db 186 TTGGGAGCCCAACTACTC 167

RESULT 127  
US-08-221-653-37/C  
Sequence 37, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-221-653-37

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20  
Db 186 TTGGGAGCCCAACTACTC 167

RESULT 128  
US-08-221-653-38/C  
Sequence 38, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653

NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 121  
US-08-221-653-38

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20  
Db 186 TTGGGAGCCCAACTACTC 167

RESULT 129  
US-08-221-653-39/C  
Sequence 39, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653

;; FILING DATE: 435  
;; CLASSIFICATION: 435  
;; PRIORITY APPLICATION DATA: US/07/881,528  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELETYPE: EZEKIEL  
;; INFORMATION FOR SEQ ID NO: 39:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: us4  
;; US-08-221-653-39

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGAGCCCACTACTC 20  
Db 186 TTGCGAGCCCACTACTC 167

RESULT 130  
US-08-221-653-40/c  
; Sequence 40, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF INVENTIONS: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELETYPE: EZEKIEL

;; INFORMATION FOR SEQ ID NO: 40:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: jh1  
;; US-08-221-653-40

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGAGCCCACTACTC 20  
Db 186 TTGCGAGCCCACTACTC 167

RESULT 131  
US-08-221-653-41/c  
; Sequence 41, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF INVENTIONS: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELETYPE: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: nac5  
; US-08-221-653-41

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCACACTACTC 20  
|||  
Db 186 TTGGGACCCACACTACTC 167

RESULT 132  
US-08-221-653-42/C  
; Sequence 42, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: arg2  
; US-08-221-653-42  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: bpl  
; US-08-221-653-43  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 134  
US-08-221-653-44/C  
; Sequence 44, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 9h1  
US-08-221-653-44

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCACACTACTC 20  
Db 186 TTCCGACCCACACTACTC 167

RESULT 135  
US-08-221-653-45/c  
Sequence 45, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:

LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 115  
US-08-221-653-45

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCACACTACTC 20  
Db 186 TTCCGACCCACACTACTC 167

RESULT 136  
US-08-221-653-48/c  
Sequence 48, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 821  
US-08-221-653-48

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCACACTACTC 20

Db 186 TTCGCGACCCCAACTACTC 167

## RESULT 137

US-08-221-653-49/c

Sequence 49, Application US/08221653

Patent No. 6190864

## GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacke, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

APPLICATION NUMBER: 07/697,326

FILING DATE: 8 May 1991

ATTORNEY/AGENT INFORMATION:

NAME: Janluk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: g161329

US-08-221-653-49

Query Match 100.0%; Score 20; DB 3; Length 252;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGCGACCCCAACTACTC 20

Db 186 TTCGCGACCCCAACTACTC 167

## RESULT 138

US-08-442-144A-33/c

Sequence 33, Application US/08442144A

Patent No. 6214583

## GENERAL INFORMATION:

APPLICANT: Tai-An Cha

APPLICANT: Eileen Beall

APPLICANT: Bruce Irvine

APPLICANT: Janice Kolberg

APPLICANT: Michael S. Urdea

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: California

COUNTRY: USA

ZIP: 94608-2916

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 Inch

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows NT

SOFTWARE: Microsoft Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/442,144A

FILING DATE: MAY 16, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/221,653

FILING DATE: APRIL 1, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Doreen Yalco Trujillo

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CHIR-0121

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

TELEX:

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 Nucleotides

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: hcvi (ATCC# 40394)

US-08-442-144A-33

## Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 252;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGCGACCCCAACTACTC 20

Db 186 TTCGCGACCCCAACTACTC 167

## RESULT 139

US-08-442-144A-34/c

Sequence 34, Application US/08442144A

Patent No. 6214583

## GENERAL INFORMATION:

APPLICANT: Tai-An Cha

APPLICANT: Eileen Beall

APPLICANT: Bruce Irvine

APPLICANT: Janice Kolberg

APPLICANT: Michael S. Urdea

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: California

COUNTRY: USA

ZIP: 94608-2916

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 Inch

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows NT

SOFTWARE: Microsoft Word 97

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-442-144A-34

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
Db 186 TTGGGACCCACACTACTC 167

RESULT 140  
US-08-442-144A-35/C  
Sequence 35, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-442-144A-35

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
Db 186 TTGGGACCCACACTACTC 167

RESULT 141  
US-08-442-144A-36/C  
Sequence 36, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: SP2  
US-08-442-144A-36



Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
DB 186 TTCGGACCCCAACTACTC 167

## RESULT 142

US-08-442-144A-37/c

; Sequence 37, Application US/08442144A

; Patent No. 6214583

; GENERAL INFORMATION:

; APPLICANT: Tai-An Cha

; APPLICANT: Eileen Beall

; APPLICANT: Bruce Irvine

; APPLICANT: Janice Kolberg

; APPLICANT: Michael S. Urdea

; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

; NUMBER OF SEQUENCES: 148

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: California

; COUNTRY: USA

; ZIP: 94608-2916

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 Inch

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows NT

; SOFTWARE: Microsoft Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/442,144A

; FILING DATE: MAY 16, 1995

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/221,653

; FILING DATE: APRIL 1, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Doreen Yalco Trujillo

; REGISTRATION NUMBER: 35,719

; REFERENCE/DOCKET NUMBER: CHIR-0121

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; TELEX:

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 Nucleotides

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; MOLECULE TYPE: DNA

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: gm2

; US-08-442-144A-37

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
DB 186 TTCGGACCCCAACTACTC 167

## RESULT 143

US-08-442-144A-38/c

; Sequence 38, Application US/08442144A

; Patent No. 6214583

; GENERAL INFORMATION:

; APPLICANT: Tai-An Cha

; APPLICANT: Eileen Beall

; APPLICANT: Bruce Irvine

; APPLICANT: Janice Kolberg

; APPLICANT: Michael S. Urdea

; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

; NUMBER OF SEQUENCES: 148

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: California

; COUNTRY: USA

; ZIP: 94608-2916

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 Inch

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows NT

; SOFTWARE: Microsoft Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/442,144A

; FILING DATE: MAY 16, 1995

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/221,653

; FILING DATE: APRIL 1, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Doreen Yalco Trujillo

; REGISTRATION NUMBER: 35,719

; REFERENCE/DOCKET NUMBER: CHIR-0121

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; TELEX:

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 Nucleotides

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; MOLECULE TYPE: DNA

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: 121

; US-08-442-144A-38

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
DB 186 TTCGGACCCCAACTACTC 167

## RESULT 144

US-08-442-144A-39/c

; Sequence 39, Application US/08442144A

; Patent No. 6214583

; GENERAL INFORMATION:

; APPLICANT: Tai-An Cha

; APPLICANT: Eileen Beall

; APPLICANT: Bruce Irvine

; APPLICANT: Janice Kolberg

; APPLICANT: Michael S. Urdea

; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

; NUMBER OF SEQUENCES: 148

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us4  
US-08-442-144A-39

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 145  
US-08-442-144A-40/c  
Sequence 40, Application US/08442144A  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: jh1  
US-08-442-144A-40

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 146  
US-08-442-144A-41/c  
Sequence 41, Application US/08442144A  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides

TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: nacs  
US-08-442-144A-41

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

RESULT 147  
US-08-442-144A-42/c  
Sequence 42, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Udea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko TTUJ1110  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: arg2  
US-08-442-144A-42

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

DB 186 TTGGGACCCCAACTACTC 167

RESULT 148  
US-08-442-144A-43/c  
Sequence 43, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Udea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko TTUJ1110  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp1  
US-08-442-144A-43

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

RESULT 149  
US-08-442-144A-44/c  
Sequence 44, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg

APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yalko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ghl  
US-08-442-144A-44

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
DB 186 TTGCGACCCCAACTACTC 167

RESULT 150  
US-08-442-144A-45/C  
Sequence 45, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yalko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 115  
US-08-442-144A-45

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
DB 186 TTGCGACCCCAACTACTC 167

RESULT 151  
US-08-442-144A-48/C  
Sequence 48, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yalko Trujillo  
REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 821  
US-08-442-144A-48

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 186 TTGGGACCCCACTACTC 167

RESULT 152  
US-08-442-144A-49/c  
Sequence 49, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yalco Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 9j61329  
US-08-442-144A-49

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 186 TTGGGACCCCACTACTC 167

RESULT 153  
US-08-441-970-33/c  
Sequence 33, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: (ATCC # 40394)  
INDIVIDUAL ISOLATE: hc1  
US-08-441-970-33

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 186 TTGGGACCCCACTACTC 167

RESULT 154  
US-08-441-970-34/c  
Sequence 34, Application US/08441970

Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEU  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-441-970-34  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCCGACCCCACTACTC 20  
Db 186 TTCCGACCCCACTACTC 167  
RESULT 155  
US-08-441-970-35/c  
Sequence 35, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEU  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-441-970-35

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCCGACCCCACTACTC 20  
Db 186 TTCCGACCCCACTACTC 167

RESULT 156  
US-08-441-970-36/c  
Sequence 36, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp2  
US-08-441-970-36

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 186 TTGGGACCCCACTACTC 167

RESULT 157  
US-08-441-970-37/c  
Sequence 37, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-441-970-37

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 186 TTGGGACCCCACTACTC 167

RESULT 158  
US-08-441-970-38/c  
Sequence 38, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 121  
US-08-441-970-38

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 186 TTGGGACCCCACTACTC 167

RESULT 159  
US-08-441-970-39/c  
Sequence 39, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:

APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us4  
US-08-441-970-39  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TTGCGACCCCACTACTC 20  
Db 186 TTGCGACCCCACTACTC 167  
RESULT 160  
US-08-441-970-40/c  
Sequence 40, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:

SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: jh1  
US-08-441-970-40  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TTGCGACCCCACTACTC 20  
Db 186 TTGCGACCCCACTACTC 167  
RESULT 161  
US-08-441-970-41/c  
Sequence 41, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:



TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: nacs  
US-08-441-970-41

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 162  
US-08-441-970-42/C  
Sequence 42, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: arg2  
US-08-441-970-42

Query Match 100.0%; Score 20; DB 3; Length 252;

Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 163  
US-08-441-970-43/C  
Sequence 43, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: spi  
US-08-441-970-43

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 164  
US-08-441-970-44/C  
Sequence 44, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ghl  
US-08-441-970-44

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
DB 186 TTCCGACCCCAACTACTC 167

RESULT 165  
US-08-441-970-45/C  
Sequence 45, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: i15  
US-08-441-970-45

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
DB 186 TTCCGACCCCAACTACTC 167

RESULT 166  
US-08-441-970-48/C  
Sequence 48, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441

TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 821  
US-08-441-970-48

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 167  
US-08-441-970-49/c  
Sequence 49, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441, 970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 MAY 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 9161329  
US-08-441-970-49

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 168  
US-08-483-695-1/c  
Sequence 1, Application US/08483695  
Patent No. 5866139  
GENERAL INFORMATION:  
APPLICANT: Brecht, Christian  
APPLICANT: Kremdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,265  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-483-695-1

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 169  
US-08-483-695-24/c  
Sequence 24, Application US/08483695  
Patent No. 5866139  
GENERAL INFORMATION:  
APPLICANT: Brecht, Christian  
APPLICANT: Kremdorf, Dina

APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
ADDRESSER: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695.  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-483-695-24  
Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 TTGGGACCCCACTACTC 20  
Db 193 TTGGGACCCCACTACTC 174  
RESULT 170  
US-08-483-695-25/c  
Sequence 25, Application US/08483695  
Patent No. 5866139  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
ADDRESSER: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-483-695-25  
Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 TTGGGACCCCACTACTC 20  
Db 193 TTGGGACCCCACTACTC 174  
RESULT 171  
US-08-483-695-26/c  
Sequence 26, Application US/08483695  
Patent No. 5866139  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
ADDRESSER: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882

;; FILING DATE: 06-JUN-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Meyers, Kenneth J.  
;; REGISTRATION NUMBER: 25,146  
;; REFERENCE/DOCKET NUMBER: 05286-0001-00000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-408-4000  
;; TELEFAX: 202-408-4400  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 256 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: Other  
;; DESCRIPTION: cDNA to genomic RNA  
;; US-08-483-695-26

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 172  
US-07-965-285-1/c  
; Sequence 1, Application US/07965285  
; Patent No. 5879904  
; GENERAL INFORMATION:  
; APPLICANT: Brecht, Christian  
; APPLICANT: Kremendorf, Dina  
; TITLE OF INVENTION: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; TITLE OF INVENTION: Applications  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/965,285  
; FILING DATE: 18-MAR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 06 882  
; FILING DATE: 06-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other

;; DESCRIPTION: cDNA to genomic RNA  
;; US-07-965-285-1

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 173  
US-07-965-285-24/c  
; Sequence 24, Application US/07965285  
; Patent No. 5879904  
; GENERAL INFORMATION:  
; APPLICANT: Brecht, Christian  
; APPLICANT: Kremendorf, Dina  
; TITLE OF INVENTION: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; TITLE OF INVENTION: Applications  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/965,285  
; FILING DATE: 18-MAR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 06 882  
; FILING DATE: 06-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; DESCRIPTION: cDNA to genomic RNA  
;; US-07-965-285-24

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 174  
US-07-965-285-25/c  
; Sequence 25, Application US/07965285

Patent No. 5879904  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-07-965-285-25

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
|||||  
Db 193 TTGCGACCCACACTACTC 174

RESULT 175  
US-07-965-285-26/C  
Sequence 26, Application US/07965285  
Patent No. 5879904  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-07-965-285-26

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
|||||  
Db 193 TTGCGACCCACACTACTC 174

RESULT 176  
US-08-487-231-1/C  
Sequence 1, Application US/08487231  
Patent No. 5819454  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,231  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-487-231-1

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 177  
US-08-487-231-24/c  
Sequence 24, Application US/08487231  
Patent No. 5919454  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremendorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,231  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-487-231-24

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 178  
US-08-487-231-25/c  
Sequence 25, Application US/08487231  
Patent No. 5919454  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremendorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,231  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-487-231-25

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 193 TTCCGACCCCAACTACTC 174

## RESULT 179

US-08-487-231-26/c  
; Sequence 26, Application US/08487231  
; Patent No. 5919454  
; GENERAL INFORMATION:  
; APPLICANT: Brechot, Christian  
; APPLICANT: Kremsdorf, Dina  
; APPLICANT: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: 1300 I Street, N.W.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,231  
; FILING DATE: 07-JUNE-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,285  
; FILING DATE: 18-MAR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 06 882  
; FILING DATE: 06-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; DESCRIPTION: cDNA to genomic RNA  
US-08-487-231-26

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 193 TTCCGACCCCAACTACTC 174

RESULT 180  
US-09-201-912-1/c  
; Sequence 1, Application US/09201912  
; Patent No. 6210962

## GENERAL INFORMATION:

; APPLICANT: Brechot, Christian  
; APPLICANT: Kremsdorf, Dina  
; APPLICANT: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: 1300 I Street, N.W.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/201,912  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,285  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; DESCRIPTION: cDNA to genomic RNA  
US-09-201-912-1

Query Match 100.0%; Score 20; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 193 TTCCGACCCCAACTACTC 174

## RESULT 181

US-09-201-912-24/c  
; Sequence 24, Application US/09201912  
; Patent No. 6210962  
; GENERAL INFORMATION:  
; APPLICANT: Brechot, Christian  
; APPLICANT: Kremsdorf, Dina  
; APPLICANT: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: 1300 I Street, N.W.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA



ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,912  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,285  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-09-201-912-24

Query Match 100.0%; Score 20; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 193 TTGGGACCCCACTACTC 174

RESULT 182  
US-09-201-912-25/C  
Sequence 25, Application US/09201912  
Patent No. 6210962  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremesdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,912  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,285  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-09-201-912-25

Query Match 100.0%; Score 20; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 193 TTGGGACCCCACTACTC 174

RESULT 183  
US-09-201-912-26/C  
Sequence 26, Application US/09201912  
Patent No. 6210962  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremesdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,912  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,285  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-09-201-912-26

Query Match 100.0%; Score 20; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 193 TTGGGACCCCAACTACTC 174

RESULT 184  
US-08-757-653-121/c  
; Sequence 121, Application US/08757653  
; Patent No. 5843669

GENERAL INFORMATION:  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Lyamichev, Victor I.  
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,653  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02565  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-653-121

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 218 TTGGGACCCCAACTACTC 199

RESULT 185  
US-08-757-653-123/c  
; Sequence 123, Application US/08757653  
; Patent No. 5843669

GENERAL INFORMATION:  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Lyamichev, Victor I.  
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,653  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02565  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-653-123

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 218 TTGGGACCCCAACTACTC 199

RESULT 186  
US-08-757-653-126/c  
; Sequence 126, Application US/08757653  
; Patent No. 5843669

GENERAL INFORMATION:  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Lyamichev, Victor I.  
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,653  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02565  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-757-653-126

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGGACCCCAACTACTC 20  
Db 218 TTCCGGACCCCAACTACTC 199

RESULT 187  
US-08-757-653-127

; Sequence 127, Application US/08757653  
; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/757,653

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ingolia, Diane E.

; REGISTRATION NUMBER: 40,027

; REFERENCE/DOCKET NUMBER: FORS-02565

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 127:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 281 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-757-653-127

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGGACCCCAACTACTC 20  
Db 64 TTCCGGACCCCAACTACTC 83

RESULT 188  
US-08-757-653-128

; Sequence 128, Application US/08757653  
; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/757,653

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ingolia, Diane E.

; REGISTRATION NUMBER: 40,027

; REFERENCE/DOCKET NUMBER: FORS-02565

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 128:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 281 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-757-653-128

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGGACCCCAACTACTC 20  
Db 64 TTCCGGACCCCAACTACTC 83

RESULT 189

US-08-757-653-129

; Sequence 129, Application US/08757653  
; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,653  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02565  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-653-129

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
Db 64 TTGGGACCCACACTACTC 83

RESULT 190  
US-08-757-653-132  
Sequence 132, Application US/08757653  
Patent No. 5843669  
GENERAL INFORMATION:  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Lyamichev, Natasha  
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,653  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02565  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-653-132

Query Match 100.0%; Score 20; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGGGACCCACACTACTC 20  
Db 64 TTGGGACCCACACTACTC 83

RESULT 191  
US-08-520-946-121/C  
Sequence 121, Application US/08520946  
Patent No. 6372424  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
APPLICANT: LYAMICHEV, VICTOR I.  
APPLICANT: OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,946  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-520-946-121

Query Match 100.0%; Score 20; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
Db 218 TTGGGACCCACACTACTC 199

RESULT 192  
US-08-520-946-123/C  
Sequence 123, Application US/08520946  
Patent No. 6372424  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
APPLICANT: LYAMICHEV, VICTOR I.  
APPLICANT: OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL

```
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,946
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-123

Query Match      100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGCGACCCCAACTACTC 20
DB      218 TTGCGACCCCAACTACTC 199

RESULT 193
US-08-520-946-126/c
Sequence 126, Application US/08520946
Patent No. 6372424
GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,946
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
```

```
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-126

Query Match      100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGCGACCCCAACTACTC 20
DB      218 TTGCGACCCCAACTACTC 199

RESULT 194
US-08-520-946-127
Sequence 127, Application US/08520946
Patent No. 6372424
GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,946
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
TELEFAX: (415) 705-8410
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-127

Query Match      100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGCGACCCCAACTACTC 20
DB      64 TTGCGACCCCAACTACTC 83

RESULT 195
US-08-520-946-128
Sequence 128, Application US/08520946
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; Patent No. 6372424
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; APPLICANT: LYAMICHEV, VICTOR I.
; APPLICANT: OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; TITLE OF INVENTION: PATHOGENS
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,946
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-520-946-128

Query Match      100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 TTGGGACCCCACTACTC 20
Db      64 TTGGGACCCCACTACTC 83

RESULT 196
US-08-520-946-129
; Sequence 129; Application US/08520946
; Patent No. 6372424
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; APPLICANT: LYAMICHEV, VICTOR I.
; APPLICANT: OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; TITLE OF INVENTION: PATHOGENS
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,946
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-520-946-132

Query Match      100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICATION NUMBER: US/08/520,946
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-520-946-129

Query Match      100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 TTGGGACCCCACTACTC 20
Db      64 TTGGGACCCCACTACTC 83

RESULT 197
US-08-520-946-132
; Sequence 132; Application US/08520946
; Patent No. 6372424
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; APPLICANT: LYAMICHEV, VICTOR I.
; APPLICANT: OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; TITLE OF INVENTION: PATHOGENS
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,946
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-520-946-132

Query Match      100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

## RESULT 198

US-09-655-378A-121/C

Sequence 121, Application US/09655378A

Patent No. 6673616

GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN &amp; CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/655,378A

FILING DATE: 05-Sep-2000

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 121:

US-09-655-378A-121

Query Match

Best Local Similarity 100.0%; Score 20; DB 4; Length 281;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20

Db 218 TTGGGACCCCACTACTC 199

RESULT 199

US-09-655-378A-123/C

Sequence 123, Application US/09655378A

Patent No. 6673616

GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN &amp; CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/655,378A

FILING DATE: 05-Sep-2000

CLASSIFICATION: &lt;Unknown&gt;

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/655,378A

FILING DATE: 05-Sep-2000

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 123:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 123:

US-09-655-378A-123

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Best Local Similarity 100.0%; Score 20; DB 4; Length 281;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 218 TTGGGACCCCACTACTC 199

RESULT 200

US-09-655-378A-126/C

Sequence 126, Application US/09655378A

Patent No. 6673616

GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN &amp; CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/655,378A

FILING DATE: 05-Sep-2000

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:  
US-09-655-378A-126.

Query Match 100.0%; Score 20; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 218 TTGCGAGCCCAACTACTC 199

Search completed: April 25, 2005, 13:47:39  
Job time : 104.316 secs



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OM nucleic - nucleic search, using bw model

Run on: April 25, 2005, 13:45:46 ; Search time 280.526 Seconds  
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432.833 Million cell updates/sec

Title: US-08-887-505B-28

Perfect score: 20

Sequence: 1 TTTCGGACCCACACTACTC 20

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Minimum DB seq length: 0

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Post-Processing: Listing first 1000 summaries

Database : Published Applications NA.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 233	20	100.0	9632	18	US-10-475-989-2	Sequence 2, Appl	C 306	19	95.0	177	9	US-09-899-302-72	Sequence 72, Appl
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C 235	20	100.0	9646	9	US-09-238-076-1	Sequence 1, Appl	C 308	19	95.0	177	9	US-09-899-302-74	Sequence 74, Appl
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C 254	19	95.0	19	18	US-10-667-271-854	Sequence 854, App	C 327	19	95.0	177	10	US-09-899-044-74	Sequence 74, Appl
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C 256	19	95.0	19	18	US-10-819-564-2	Sequence 2, Appl	C 329	19	95.0	177	10	US-09-899-044-76	Sequence 76, Appl
C 257	19	95.0	40	18	US-10-318-416B-25	Sequence 25, Appl	C 330	19	95.0	177	10	US-09-899-044-77	Sequence 77, Appl
C 258	19	95.0	177	9	US-09-294-121A-57	Sequence 57, Appl	C 331	19	95.0	177	10	US-09-899-044-78	Sequence 78, Appl
C 259	19	95.0	177	9	US-09-294-121A-58	Sequence 58, Appl	C 332	19	95.0	177	10	US-09-899-044-79	Sequence 79, Appl
C 260	19	95.0	177	9	US-09-294-121A-61	Sequence 61, Appl	C 333	19	95.0	177	10	US-09-899-044-80	Sequence 80, Appl
C 261	19	95.0	177	9	US-09-294-121A-62	Sequence 62, Appl	C 334	19	95.0	177	10	US-09-899-044-81	Sequence 81, Appl
C 262	19	95.0	177	9	US-09-294-121A-65	Sequence 65, Appl	C 335	19	95.0	177	18	US-10-822-711-57	Sequence 57, Appl
C 263	19	95.0	177	9	US-09-294-121A-66	Sequence 66, Appl	C 336	19	95.0	177	18	US-10-822-711-58	Sequence 58, Appl
C 264	19	95.0	177	9	US-09-294-121A-67	Sequence 67, Appl	C 337	19	95.0	177	18	US-10-822-711-61	Sequence 61, Appl
C 265	19	95.0	177	9	US-09-294-121A-68	Sequence 68, Appl	C 338	19	95.0	177	18	US-10-822-711-62	Sequence 62, Appl
C 266	19	95.0	177	9	US-09-294-121A-69	Sequence 69, Appl	C 339	19	95.0	177	18	US-10-822-711-65	Sequence 65, Appl
C 267	19	95.0	177	9	US-09-294-121A-70	Sequence 70, Appl	C 340	19	95.0	177	18	US-10-822-711-67	Sequence 67, Appl
C 268	19	95.0	177	9	US-09-294-121A-72	Sequence 72, Appl	C 341	19	95.0	177	18	US-10-822-711-68	Sequence 68, Appl
C 269	19	95.0	177	9	US-09-294-121A-73	Sequence 73, Appl	C 342	19	95.0	177	18	US-10-822-711-69	Sequence 69, Appl
C 270	19	95.0	177	9	US-09-294-121A-74	Sequence 74, Appl	C 343	19	95.0	177	18	US-10-822-711-70	Sequence 70, Appl
C 271	19	95.0	177	9	US-09-294-121A-75	Sequence 75, Appl	C 344	19	95.0	177	18	US-10-822-711-72	Sequence 72, Appl
C 272	19	95.0	177	9	US-09-294-121A-76	Sequence 76, Appl	C 345	19	95.0	177	18	US-10-822-711-73	Sequence 73, Appl
C 273	19	95.0	177	9	US-09-294-121A-77	Sequence 77, Appl	C 346	19	95.0	177	18	US-10-822-711-74	Sequence 74, Appl
C 274	19	95.0	177	9	US-09-294-121A-78	Sequence 78, Appl	C 347	19	95.0	177	18	US-10-822-711-75	Sequence 75, Appl
C 275	19	95.0	177	9	US-09-294-121A-79	Sequence 79, Appl	C 348	19	95.0	177	18	US-10-822-711-76	Sequence 76, Appl
C 276	19	95.0	177	9	US-09-294-121A-80	Sequence 80, Appl	C 349	19	95.0	177	18	US-10-822-711-77	Sequence 77, Appl
C 277	19	95.0	177	9	US-09-899-082A-57	Sequence 57, Appl	C 350	19	95.0	177	18	US-10-822-711-78	Sequence 78, Appl
C 278	19	95.0	177	9	US-09-899-082A-58	Sequence 58, Appl	C 351	19	95.0	177	18	US-10-822-711-79	Sequence 79, Appl
C 279	19	95.0	177	9	US-09-899-082A-59	Sequence 59, Appl	C 352	19	95.0	177	18	US-10-822-711-80	Sequence 80, Appl
C 280	19	95.0	177	9	US-09-899-082A-61	Sequence 61, Appl	C 353	19	95.0	178	9	US-09-294-121A-59	Sequence 59, Appl
C 281	19	95.0	177	9	US-09-899-082A-62	Sequence 62, Appl	C 354	19	95.0	178	9	US-09-294-121A-60	Sequence 60, Appl
C 282	19	95.0	177	9	US-09-899-082A-65	Sequence 65, Appl	C 355	19	95.0	178	9	US-09-294-121A-71	Sequence 71, Appl
C 283	19	95.0	177	9	US-09-899-082A-66	Sequence 66, Appl	C 356	19	95.0	178	9	US-09-294-121A-81	Sequence 81, Appl
C 284	19	95.0	177	9	US-09-899-082A-67	Sequence 67, Appl	C 357	19	95.0	178	9	US-09-899-082A-59	Sequence 59, Appl
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C 286	19	95.0	177	9	US-09-899-082A-69	Sequence 69, Appl	C 359	19	95.0	178	9	US-09-899-082A-71	Sequence 71, Appl
C 287	19	95.0	177	9	US-09-899-082A-70	Sequence 70, Appl	C 360	19	95.0	178	9	US-09-899-082A-81	Sequence 81, Appl
C 288	19	95.0	177	9	US-09-899-082A-72	Sequence 72, Appl	C 361	19	95.0	178	9	US-09-899-302-59	Sequence 59, Appl
C 289	19	95.0	177	9	US-09-899-082A-73	Sequence 73, Appl	C 362	19	95.0	178	9	US-09-899-302-60	Sequence 60, Appl
C 290	19	95.0	177	9	US-09-899-082A-74	Sequence 74, Appl	C 363	19	95.0	178	9	US-09-899-302-71	Sequence 71, Appl
C 291	19	95.0	177	9	US-09-899-082A-75	Sequence 75, Appl	C 364	19	95.0	178	9	US-09-899-302-81	Sequence 81, Appl
C 292	19	95.0	177	9	US-09-899-082A-76	Sequence 76, Appl	C 365	19	95.0	178	10	US-09-899-044-59	Sequence 59, Appl
C 293	19	95.0	177	9	US-09-899-082A-77	Sequence 77, Appl	C 366	19	95.0	178	10	US-09-899-044-60	Sequence 60, Appl
C 294	19	95.0	177	9	US-09-899-082A-78	Sequence 78, Appl	C 367	19	95.0	178	10	US-09-899-044-71	Sequence 71, Appl
C 295	19	95.0	177	9	US-09-899-082A-80	Sequence 80, Appl	C 368	19	95.0	178	10	US-09-899-044-81	Sequence 81, Appl
C 296	19	95.0	177	9	US-09-899-302-57	Sequence 57, Appl	C 369	19	95.0	178	18	US-10-822-711-59	Sequence 59, Appl
C 297	19	95.0	177	9	US-09-899-302-58	Sequence 58, Appl	C 370	19	95.0	178	18	US-10-822-711-60	Sequence 60, Appl
C 298	19	95.0	177	9	US-09-899-302-61	Sequence 61, Appl	C 371	19	95.0	178	18	US-10-822-711-71	Sequence 71, Appl
C 299	19	95.0	177	9	US-09-899-302-62	Sequence 62, Appl	C 372	19	95.0	178	18	US-10-822-711-81	Sequence 81, Appl
C 300	19	95.0	177	9	US-09-899-302-65	Sequence 65, Appl	C 373	18	8	US-08-887-505-112	Sequence 112, App		
C 301	19	95.0	177	9	US-09-899-302-66	Sequence 66, Appl	C 374	18	8	US-08-887-505-115	Sequence 115, App		
C 302	19	95.0	177	9	US-09-899-302-67	Sequence 67, Appl	C 375	18	90.0	19	18	US-10-667-271-150	Sequence 150, App
C 303	19	95.0	177	9	US-09-899-302-68	Sequence 68, Appl	C 376	18	90.0	19	18	US-10-667-271-151	Sequence 151, App











C 961 12 60.0 807 18 US-10-363-345A-17135 Sequence 17135, A  
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C 963 12 60.0 807 19 US-10-363-483A-17135 Sequence 17135, A  
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C 965 12 60.0 812 18 US-10-363-345A-21711 Sequence 21711, A  
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C 969 12 60.0 817 18 US-10-363-345A-22095 Sequence 22095, A  
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C 973 12 60.0 822 17 US-10-363-483A-22095 Sequence 22095, A  
C 974 12 60.0 825 17 US-10-424-599-87321 Sequence 87321, A  
C 975 12 60.0 826 18 US-10-425-115-52498 Sequence 52498, A  
C 976 12 60.0 826 18 US-10-425-115-52498 Sequence 52498, A  
C 977 12 60.0 828 17 US-10-027-632-14440 Sequence 14440, A  
C 978 12 60.0 828 17 US-10-027-632-14440 Sequence 14440, A  
C 979 12 60.0 863 13 US-10-027-632-261782 Sequence 261782, A  
C 980 12 60.0 863 13 US-10-027-632-261782 Sequence 261782, A  
C 981 12 60.0 863 13 US-10-027-632-261782 Sequence 261782, A  
C 982 12 60.0 863 13 US-10-027-632-261782 Sequence 261782, A  
C 983 12 60.0 863 17 US-10-027-632-261782 Sequence 261782, A  
C 984 12 60.0 863 17 US-10-027-632-261782 Sequence 261782, A  
C 985 12 60.0 863 17 US-10-027-632-261782 Sequence 261782, A  
C 986 12 60.0 870 11 US-09-997-722-3 Sequence 261785, A  
C 987 12 60.0 876 13 US-10-024-066-1 Sequence 3, Appl  
C 988 12 60.0 880 18 US-10-425-115-111217 Sequence 111217, A  
C 989 12 60.0 916 18 US-10-363-345A-26589 Sequence 26589, A  
C 990 12 60.0 916 18 US-10-363-345A-26589 Sequence 26589, A  
C 991 12 60.0 916 19 US-10-363-483A-26589 Sequence 26589, A  
C 992 12 60.0 916 19 US-10-363-483A-26589 Sequence 26589, A  
C 993 12 60.0 917 18 US-10-767-701-9820 Sequence 9820, A  
C 994 12 60.0 930 18 US-09-510-332-61 Sequence 61, Appl  
C 995 12 60.0 930 18 US-10-770-127-61 Sequence 61, Appl  
C 996 12 60.0 930 18 US-10-962-365-61 Sequence 61, Appl  
C 997 12 60.0 954 9 US-09-938-842A-2570 Sequence 2570, A  
C 998 12 60.0 954 11 US-09-938-842A-2570 Sequence 2570, A  
C 999 12 60.0 962 18 US-10-363-345A-18907 Sequence 18907, A  
C 1000 12 60.0 962 18 US-10-363-345A-18908 Sequence 18908, A

## ALIGNMENTS

RESULT 1  
US-08-887-505-28  
Sequence 28, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner Ann-Louise  
REGISTRATION NUMBER: 33,523  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-5000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-28

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 TTGGGACCCGACACTCTC 20  
DB 1 TTGGGACCCGACACTCTC 20

RESULT 2  
US-08-887-505-119  
Sequence 119, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-119

Query Match  
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;  
Pred. No. 0.017;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGGAGCCCAACTACTC 20  
Db 1 TTCGGAGCCCAACTACTC 20

RESULT 3  
US-08-887-505-120  
Sequence 120, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keirner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO

ANTI-SENSE: YES  
US-08-887-505-120

Query Match  
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;  
Pred. No. 0.017;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGGAGCCCAACTACTC 20  
Db 1 TTCGGAGCCCAACTACTC 20

RESULT 4  
US-08-887-505-121  
Sequence 121, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keirner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-121

Query Match  
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;  
Pred. No. 0.017;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGGAGCCCAACTACTC 20  
Db 1 TTCGGAGCCCAACTACTC 20

RESULT 5  
US-08-887-505-122  
; Sequence 122, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-122

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.017;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
Db 1 UUGCGACCCACACUACUC 20

RESULT 6  
US-08-887-505-123  
; Sequence 123, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.

; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 123:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-123

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.017;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCACACTACTC 20  
Db 1 UUGCGACCCACACUACUC 20

RESULT 7  
US-08-887-505-124  
; Sequence 124, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-124

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.017;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCCGACCCCACTACTC 20  
Db 1 UUCGCGACCCACACUACUC 20

RESULT 8  
US-08-887-505-125  
Sequence 125, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 125:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-125

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.017;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCCGACCCCACTACTC 20  
Db 1 UUCGCGACCCACACUACUC 20

RESULT 9  
US-08-887-505-126  
Sequence 126, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 126:

## SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-126

## Query Match

Best Local Similarity 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
1 TTGCGAGCCCAACTACTC 20  
Db 1 TTGCGAGCCCAACTACTC 20

## RESULT 10

US-08-887-505-127

; Sequence 127, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:

APPLICANT: Kilukkie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-5000  
TELEFAX: (617) 526-6000

## INFORMATION FOR SEQ ID NO: 127:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-127

## Query Match

100.0%; Score 20; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
1 TTGCGAGCCCAACTACTC 20  
Db 1 TTGCGAGCCCAACTACTC 20

## RESULT 11

US-08-887-505-128

; Sequence 128, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:

APPLICANT: Kilukkie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000

## INFORMATION FOR SEQ ID NO: 128:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-128

## Query Match

100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
1 TTGCGAGCCCAACTACTC 20  
Db 1 TTGCGAGCCCAACTACTC 20

## RESULT 12

US-08-887-505-129

; Sequence 129, Application US/08887505

Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-129

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCAACTACTC 20  
Db 1 TTCCGACCCAACTACTC 20

RESULT 13  
US-08-887-505-130  
Sequence 130, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-130

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCAACTACTC 20  
Db 1 TTCCGACCCAACTACTC 20

RESULT 14  
US-08-887-505-75  
Sequence 75, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-75

Query Match 100.0%; Score 20; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
DB 3 TTGCGAGCCCAACTACTC 22

RESULT 15  
US-08-887-505-131  
Sequence 131, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 131:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-131

Query Match 100.0%; Score 20; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
DB 1 TTGCGAGCCCAACTACTC 20

RESULT 16  
US-10-407-952-4/c  
Sequence 4, Application US/10407952  
Publication No. US20030232074A1  
GENERAL INFORMATION:  
APPLICANT: Lipford, Grayson  
APPLICANT: Bauer, Stefan  
TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides  
FILE REFERENCE: C01041.70037 US  
CURRENT APPLICATION NUMBER: US/10/407,952  
CURRENT FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: US 60/421,966  
PRIOR FILING DATE: 2002-10-29  
PRIOR APPLICATION NUMBER: US 60/370,515  
PRIOR FILING DATE: 2002-04-04  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 27  
TYPE: RNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-407-952-4

Query Match 100.0%; Score 20; DB 17; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
DB 23 TTGCGAGCCCAACTACTC 4

RESULT 17  
US-10-475-024-20/c  
Sequence 20, Application US/10475024  
Publication No. US20040219545A1  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Welch, Ellen  
TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA  
FILE REFERENCE: 10589-007-999  
CURRENT APPLICATION NUMBER: US/10/475,024  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: 60/282,965

PRIOR FILING DATE: 2001-04-11  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 20  
LENGTH: 27  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-475-024-20

Query Match 100.0%; Score 20; DB 18; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 23 TTGGGACCCCAACTACTC 4

RESULT 18  
US-08-887-505-68  
Sequence 68, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-68  
Query Match 100.0%; Score 20; DB 8; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 1 TTGGGACCCCAACTACTC 20

RESULT 19  
US-08-887-505-74  
Sequence 74, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-74  
Query Match 100.0%; Score 20; DB 8; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 20  
US-10-332-626-3/c  
Sequence 3, Application US/10332626  
Publication No. US20040073380A1

GENERAL INFORMATION:  
APPLICANT: Joseph D. Puglisi  
TITLE OF INVENTION: Structural Targets of Hepatitis C Virus  
FILE REFERENCE: STAN-196  
CURRENT FILING DATE: 2003-09-08  
PRIOR APPLICATION NUMBER: PCT/US01/21871  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,673  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 29  
TYPE: RNA  
ORGANISM: Hepatitis C virus  
US-10-332-626-3

Query Match 100.0%; Score 20; DB 17; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 24 TTGGGACCCCAACTACTC 5

## RESULT 21

US-09-790-417-181/c  
Sequence 181, Application US/09790417  
Patent No. US20010031470A1  
GENERAL INFORMATION:  
APPLICANT: Shultz, John W.  
APPLICANT: Lewis, Martin K.  
APPLICANT: Lieppe, Donna  
APPLICANT: Mandrekas, Michelle  
APPLICANT: Kephart, Daniel  
APPLICANT: Rhodes, Richard B.  
APPLICANT: Andrews, Christine A.  
APPLICANT: Hartnett, James R.  
APPLICANT: Gu, Trent  
APPLICANT: Olson, Ryan J.  
APPLICANT: Wood, Keith W.  
APPLICANT: Welch, Roy  
TITLE OF INVENTION: Nucleic Acid Detection  
FILE REFERENCE: Pro-103 6868/75528  
CURRENT APPLICATION NUMBER: US/09/790,417  
CURRENT FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 09/358,972  
PRIOR FILING DATE: 1999-07-21  
PRIOR APPLICATION NUMBER: 09/042,287  
PRIOR FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 181  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
FEATURE:  
OTHER INFORMATION: probe for Hepatitis C  
US-09-790-417-181

Query Match 100.0%; Score 20; DB 9; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 29 TTGGGACCCCAACTACTC 10

## RESULT 22

US-09-780-863-43/c  
Sequence 43, Application US/09780863  
Publication No. US20030203358A1  
GENERAL INFORMATION:  
APPLICANT: Shultz, John W.  
APPLICANT: Lewis, Martin K.  
APPLICANT: Lieppe, Donna  
APPLICANT: Mandrekas, Michelle  
APPLICANT: Kephart, Daniel  
APPLICANT: Rhodes, Richard B.  
APPLICANT: Andrews, Christine A.  
APPLICANT: Hartnett, James R.  
APPLICANT: Gu, Trent  
APPLICANT: Wood, Keith W.  
APPLICANT: Welch, Roy  
TITLE OF INVENTION: EXOGENOUS NUCLEIC ACID DETECTION  
FILE REFERENCE: EXOGENOUS NUCLEIC ACID DETECTION  
CURRENT APPLICATION NUMBER: US/09/780,863  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/406,147  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/252,436  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/042,287  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 43  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-780-863-43

Query Match 100.0%; Score 20; DB 10; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 29 TTGGGACCCCAACTACTC 10

## RESULT 23

US-10-318-416B-6/c  
Sequence 6, Application US/10318416B  
Publication No. US20040115643A1  
GENERAL INFORMATION:  
APPLICANT: Lizardi, Paul M.  
APPLICANT: Grishanov, Oleg G.  
TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF  
FILE REFERENCE: 25006.001201  
CURRENT APPLICATION NUMBER: US/10/318,416B  
CURRENT FILING DATE: 2002-12-12  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/note =  
US-10-318-416B-6

Query Match 100.0%; Score 20; DB 18; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 31 TTGGGACCCCAACTACTC 12



```
RESULT 24
US-10-318-416B-18/c
; Sequence 18, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.001201
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-318-416B-18

Query Match      100.0%; Score 20; DB 18; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20
Db 31 TTGGGAGCCCAACTACTC 12

RESULT 25
US-10-318-416B-19/c
; Sequence 19, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.001201
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-318-416B-19

Query Match      100.0%; Score 20; DB 18; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20
Db 31 TTGGGAGCCCAACTACTC 12

RESULT 26
US-09-870-939-1/c
; Sequence 1, Application US/09870939
; Publication No. US20020192650A1
; GENERAL INFORMATION:
; APPLICANT: AMORESE, DOUGLAS A.
; APPLICANT: SHANNON, KAREN W.
; APPLICANT: COLLINS, PATRICK J.
```

```
; APPLICANT: WOLBER, PAUL K.
; TITLE OF INVENTION: COMPOSITE ARRAYS
; FILE REFERENCE: 10010791-1
; CURRENT APPLICATION NUMBER: US/09/870,939
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-870-939-1

Query Match      100.0%; Score 20; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20
Db 24 TTGGGAGCCCAACTACTC 5

RESULT 27
US-09-728-265-31
; Sequence 31, Application US/09728265
; Publication No. US20020182598A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:
; TITLE OF INVENTION: RAMIFICATION-EXTENSION AMPLIFICATION METHOD (RAM)
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroock & Stroock & Lavan
; STREET: 180 Maiden Lane
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10038
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/728,265
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pokocillow, Steven B
; REGISTRATION NUMBER: 26,405
; REFERENCE/DOCKET NUMBER: Old 29545APCT/USA-B // New 251305/0018
; TELEPHONE: 212806-6663
; TELEFAX: 2128066006
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..108
US-09-728-265-31

Query Match      100.0%; Score 20; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20
Db 4 TTGGGAGCCCAACTACTC 23
```

```
RESULT 28
US-09-978-261A-31
; Sequence 31, Application US/09978261A
; Publication No. US20030175706A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHODS
; FILE REFERENCE: A29545-A-PCT-USA-A 070165.0601
; CURRENT APPLICATION NUMBER: US/09/978,261A
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/263,937
; PRIOR FILING DATE: 1994-06-22
; PRIOR APPLICATION NUMBER: 08/596,331
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/690,495
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: 08/909,031
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 09/728,265
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-978-261A-31

Query Match          100.0%; Score 20; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20
DB 4 TTGCGAGCCCACTACTC 23

RESULT 29
US-10-309-438-31
; Sequence 31, Application US/10309438
; Publication No. US20030190604A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; APPLICANT: Brandwein, Maragat
; APPLICANT: Hsu, Terence C.H.
; TITLE OF INVENTION: Nucleic Acid Amplification Method: Ramification-extension
; FILE REFERENCE: 251305/0031
; CURRENT APPLICATION NUMBER: US/10/309,438
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 09/299,217
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 08/690,494
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: US 08/596,331
; PRIOR FILING DATE: 1996-05-20
; PRIOR APPLICATION NUMBER: PCT/US95/07671
; PRIOR FILING DATE: 1995-06-14
; PRIOR APPLICATION NUMBER: 08/263,937
; PRIOR FILING DATE: 1994-06-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-10-309-438-31
```

```
Query Match          100.0%; Score 20; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20
DB 4 TTGCGAGCCCACTACTC 23

RESULT 30
US-10-719-480-31
; Sequence 31, Application US/10719480
; Publication No. US20040137484A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; APPLICANT: Yi, Jizuo
; APPLICANT: Zhang, Wandu
; TITLE OF INVENTION: Nucleic Acid Amplification Methods
; FILE REFERENCE: 251305/0040
; CURRENT APPLICATION NUMBER: US/10/719,480
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 09/978,261
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/US02/32754
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-10-719-480-31

Query Match          100.0%; Score 20; DB 18; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20
DB 4 TTGCGAGCCCACTACTC 23

RESULT 31
US-10-396-964-12/c
; Sequence 12, Application US/10396964
; Publication No. US20030198946A1
; GENERAL INFORMATION:
; APPLICANT: Simmonds, Peter
; APPLICANT: Chan, Shu-Wan
; APPLICANT: Yap, Peng L.
; TITLE OF INVENTION: Hepatitis-C Virus Testing
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: NO. US20030198946A1th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/396,964
; FILING DATE: 23-MARCH-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,116B
```

```

; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02143
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-334-2014
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis-C virus
US-10-396-964-12

Query Match      100.0%; Score 20; DB 16; Length 194;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTCCGACCCCAACTACTC 20
        ||||||||||||||||
Db      189 TTCCGACCCCAACTACTC 170

RESULT 32
US-10-688-272-19/c
; Sequence 19, Application US/10688272
; Publication No. US20040091924A1
; GENERAL INFORMATION:
; APPLICANT: Genematrix Inc.; Kim, Nam-Keun
; TITLE OF INVENTION: Method for detecting base mutation
; FILE REFERENCE: 11281-014-999
; CURRENT APPLICATION NUMBER: US/10/688,272
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: KR2002-0063832
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: KR2003-0061066
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 19
; LENGTH: 226
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Resulting PCR fragment
US-10-688-272-19

Query Match      100.0%; Score 20; DB 17; Length 226;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTCCGACCCCAACTACTC 20
        ||||||||||||||||
Db      200 TTCCGACCCCAACTACTC 181

RESULT 33
US-10-688-272-22/c
; Sequence 22, Application US/10688272
; Publication No. US20040091924A1
; GENERAL INFORMATION:
; APPLICANT: Genematrix Inc.; Kim, Nam-Keun
```

```

; TITLE OF INVENTION: Method for detecting base mutation
; FILE REFERENCE: 11281-014-999
; CURRENT APPLICATION NUMBER: US/10/688,272
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: KR2002-0063832
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: KR2003-0061066
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 22
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Resulting PCR fragment
US-10-688-272-22

Query Match      100.0%; Score 20; DB 17; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTCCGACCCCAACTACTC 20
        ||||||||||||||||
Db      204 TTCCGACCCCAACTACTC 185

RESULT 34
US-10-688-272-23
; Sequence 23, Application US/10688272
; Publication No. US20040091924A1
; GENERAL INFORMATION:
; APPLICANT: Genematrix Inc.; Kim, Nam-Keun
; TITLE OF INVENTION: Method for detecting base mutation
; FILE REFERENCE: 11281-014-999
; CURRENT APPLICATION NUMBER: US/10/688,272
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: KR2002-0063832
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: KR2003-0061066
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 23
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Resulting PCR fragment
US-10-688-272-23

Query Match      100.0%; Score 20; DB 17; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTCCGACCCCAACTACTC 20
        ||||||||||||||||
Db      27 TTCCGACCCCAACTACTC 46

RESULT 35
US-09-825-574-37/c
; Sequence 37, Application US/09825574
; Patent No. US20020119454A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; Forz, Lance
; Neel, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing With Structure-Bridging
; Oligonucleotides.
; NUMBER OF SEQUENCES: 51
```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-825-574-37

Query Match 100.0%; Score 20; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 199 TTGGGACCCCAACTACTC 180

RESULT 36  
US-09-882-945A-37/c  
Sequence 37, Application US/09882945A  
Publication No. US2003014353A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/09/882,945A  
PRIORITY FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-882-945A-37

Query Match 100.0%; Score 20; DB 10; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 199 TTGGGACCCCAACTACTC 180

RESULT 37  
US-10-807-114-37/c  
Sequence 37, Application US/10807114  
Publication No. US2004023502A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/10/807,114  
PRIORITY FILING DATE: 2004-03-23  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-807-114-37

Query Match 100.0%; Score 20; DB 18; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 199 TTGGGACCCCAACTACTC 180

RESULT 38  
US-10-655-362-37/c  
Sequence 37, Application US/10655362  
Publication No. US2005014163A1  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/10/655,362  
PRIORITY FILING DATE: 2003-09-04  
PRIORITY FILING DATE: 2000-07-18  
PRIORITY FILING DATE: PCT/US98/03194  
PRIORITY FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-10-655-362-37

Query Match 100.0%; Score 20; DB 19; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 199 TTGGGACCCCAACTACTC 180

## RESULT 39

US-09-825-574-32/c  
; Sequence 32, Application US/09825574  
; Patent No. US20020119454A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Neri, Bruce P.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-825-574-32

Query Match 100.0%; Score 20; DB 9; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 40

US-09-825-574-36/c

; Sequence 36, Application US/09825574

; Patent No. US20020119454A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-825-574-36

Query Match 100.0%; Score 20; DB 9; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 41

US-09-882-945A-32/c

; Sequence 32, Application US/09882945A

; Publication No. US20030143535A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor

APPLICANT: Allawi, Halim

APPLICANT: Dong, Fang

APPLICANT: Neri, Bruce

APPLICANT: Vener, Tatiana

TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

FILE REFERENCE: FORS-04586

CURRENT APPLICATION NUMBER: US/09/882,945A

NUMBER OF SEQ ID NOS: 334

SOFTWARE: Patentin version 3.0

SEQ ID NO: 32

LENGTH: 239

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-882-945A-32

Query Match 100.0%; Score 20; DB 10; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 42

US-09-882-945A-36/c  
; Sequence 36, Application US/09882945A  
; Publication No. US2003014355A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-882-945A-36

Query Match 100.0%; Score 20; DB 10; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 43

US-10-807-114-32/c  
; Sequence 32, Application US/10807114  
; Publication No. US20040235024A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/10/807,114  
; CURRENT FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US/09/882,945  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 32  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-807-114-32

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 44  
US-10-807-114-36/c  
; Sequence 36, Application US/10807114  
; Publication No. US20040235024A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/10/807,114  
; CURRENT FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US/09/882,945  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-807-114-36

Query Match 100.0%; Score 20; DB 18; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 45  
US-10-655-362-32/c  
; Sequence 32, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 32  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-32

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

## RESULT 46

US-10-655-362-36/C  
; Sequence 36, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-36

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

## RESULT 47

US-10-927-520-9/C  
; Sequence 9, Application US/10927520  
; Publication No. US20050069870A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: New HCV clade and prototype sequences thereof  
; FILE REFERENCE: 157  
; CURRENT APPLICATION NUMBER: US/10/927,520  
; CURRENT FILING DATE: 2004-08-27  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-10-927-520-9

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 200 TTGGGACCCCAACTACTC 181

## RESULT 48

US-10-927-520-10/C

; Sequence 10, Application US/10927520  
; Publication No. US20050069870A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: New HCV clade and prototype sequences thereof  
; FILE REFERENCE: 157  
; CURRENT APPLICATION NUMBER: US/10/927,520  
; CURRENT FILING DATE: 2004-08-27  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-10-927-520-10

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 200 TTGGGACCCCAACTACTC 181

## RESULT 49

US-09-825-574-33/C  
; Sequence 33, Application US/09825574  
; Patent No. US20020119454A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; APPLICANT: Brow, Mary Ann D.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-825-574-33

Query Match 100.0%; Score 20; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

RESULT 50

US-09-825-574-35/C

; Sequence 35, Application US/09825574  
; Patent No. US20020119454A1  
; GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Karin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-09-825-574-35

Query Match 100.0%; Score 20; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

RESULT 51

US-09-825-574-38/C

; Sequence 38, Application US/09825574

Patent No. US20020119454A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Karin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-825-574-38

Query Match 100.0%; Score 20; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 52

US-09-882-945A-33/C

; Sequence 33, Application US/09882945A

; Publication No. US20030143535A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor

APPLICANT: Allawi, Hatim

APPLICANT: Dong, Fang

APPLICANT: Neri, Bruce

APPLICANT: Vener, Tatiana

TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

FILE REFERENCE: FORS-04586

CURRENT APPLICATION NUMBER: US/09/882,945A

NUMBER OF SEQ ID NOS: 334

SOFTWARE: PatentIn version 3.0

SEQ ID NO 33



/ LENGTH: 240  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic  
US-09-882-945A-33

Query Match 100.0%; Score 20; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 207 TTGGGACCCCAACTACTC 188

RESULT 53  
US-09-882-945A-35/c  
/ Sequence 35, Application US/09882945A  
/ Publication No. US20030143535A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Lyamichev, Victor  
/ APPLICANT: Allawi, Hatim  
/ APPLICANT: Dong, Fang  
/ APPLICANT: Neri, Bruce  
/ APPLICANT: Vener, Tatiana  
/ TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
/ FILE REFERENCE: FORS-04586  
/ CURRENT APPLICATION NUMBER: US/09/882,945A  
/ CURRENT FILING DATE: 2001-06-15  
/ NUMBER OF SEQ ID NOS: 334  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 35  
/ LENGTH: 240  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic  
US-09-882-945A-35

Query Match 100.0%; Score 20; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 207 TTGGGACCCCAACTACTC 188

RESULT 54  
US-09-882-945A-38/c  
/ Sequence 38, Application US/09882945A  
/ Publication No. US20030143535A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Lyamichev, Victor  
/ APPLICANT: Allawi, Hatim  
/ APPLICANT: Dong, Fang  
/ APPLICANT: Neri, Bruce  
/ APPLICANT: Vener, Tatiana  
/ TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
/ FILE REFERENCE: FORS-04586  
/ CURRENT APPLICATION NUMBER: US/09/882,945A  
/ CURRENT FILING DATE: 2001-06-15  
/ NUMBER OF SEQ ID NOS: 334  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 38  
/ LENGTH: 240  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic  
US-09-882-945A-38

Query Match 100.0%; Score 20; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

RESULT 55  
US-10-807-114-33/c  
/ Sequence 33, Application US/10807114  
/ Publication No. US20040235024A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Lyamichev, Victor  
/ APPLICANT: Allawi, Hatim  
/ APPLICANT: Dong, Fang  
/ APPLICANT: Neri, Bruce  
/ APPLICANT: Vener, Tatiana  
/ TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
/ FILE REFERENCE: FORS-04586  
/ CURRENT APPLICATION NUMBER: US/10/807,114  
/ CURRENT FILING DATE: 2004-03-23  
/ PRIOR APPLICATION NUMBER: US/09/882,945  
/ PRIOR FILING DATE: 2001-06-15  
/ NUMBER OF SEQ ID NOS: 334  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 33  
/ LENGTH: 240  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic  
US-10-807-114-33

Query Match 100.0%; Score 20; DB 18; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 207 TTGGGACCCCAACTACTC 188

RESULT 56  
US-10-807-114-35/c  
/ Sequence 35, Application US/10807114  
/ Publication No. US20040235024A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Lyamichev, Victor  
/ APPLICANT: Allawi, Hatim  
/ APPLICANT: Dong, Fang  
/ APPLICANT: Neri, Bruce  
/ APPLICANT: Vener, Tatiana  
/ TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
/ FILE REFERENCE: FORS-04586  
/ CURRENT APPLICATION NUMBER: US/10/807,114  
/ CURRENT FILING DATE: 2004-03-23  
/ PRIOR APPLICATION NUMBER: US/09/882,945  
/ PRIOR FILING DATE: 2001-06-15  
/ NUMBER OF SEQ ID NOS: 334  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 35  
/ LENGTH: 240  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic  
US-10-807-114-35

Query Match 100.0%; Score 20; DB 18; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
|||||  
Db 207 TTCCGACCCCACTACTC 188

## RESULT 57

US-10-807-114-38/c  
; Sequence 38, Application US/10807114  
; Publication No. US20040235024A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/10/807,114  
; PRIOR FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US/09/882,945  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-807-114-38

Query Match 100.0%; Score 20; DB 18; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
|||||  
Db 208 TTCCGACCCCACTACTC 189

## RESULT 58

US-10-655-362-33/c  
; Sequence 33, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; PRIOR FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 33  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-33

Query Match 100.0%; Score 20; DB 19; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
|||||  
Db 207 TTCCGACCCCACTACTC 188

## RESULT 59

US-10-655-362-35/c  
; Sequence 35, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleor  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; PRIOR FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-35

Query Match 100.0%; Score 20; DB 19; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
|||||  
Db 207 TTCCGACCCCACTACTC 188

## RESULT 60

US-10-655-362-38/c  
; Sequence 38, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; PRIOR FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-38

Query Match 100.0%; Score 20; DB 19; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACACTACTC 20  
DB 208 TTGCGAGCCCAACACTACTC 189

RESULT 61  
US-10-087-631B-10/c

Sequence 10, Application US/10087631B  
Publication No. US20030054372A1  
GENERAL INFORMATION:

APPLICANT: JAEGER, STEPHAN  
TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A  
FILE REFERENCE: 1803-335-999  
CURRENT APPLICATION NUMBER: US/10/087,631B  
CURRENT FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 241  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence derived by  
US-10-087-631B-10  
OTHER INFORMATION: amplification of HCV type 1 using primers ST280 and ST778

Query Match 100.0%; Score 20; DB 14; Length 241;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACACTACTC 20  
DB 208 TTGCGAGCCCAACACTACTC 189

RESULT 62  
US-10-419-022-10/c

Sequence 10, Application US/10419022  
Publication No. US20030165982A1  
GENERAL INFORMATION:

APPLICANT: JAEGER, STEPHAN  
TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A  
FILE REFERENCE: 1803-335-999  
CURRENT APPLICATION NUMBER: US/10/419,022  
CURRENT FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: US/10/087,631B  
PRIOR FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 241  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence derived by  
US-10-419-022-10  
OTHER INFORMATION: amplification of HCV type 1 using primers ST280 and ST778

Query Match 100.0%; Score 20; DB 16; Length 241;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACACTACTC 20  
DB 208 TTGCGAGCCCAACACTACTC 189

RESULT 63  
US-09-825-574-26/c

Sequence 26, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-825-574-26

Query Match 100.0%; Score 20; DB 9; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACACTACTC 20  
DB 208 TTGCGAGCCCAACACTACTC 189

RESULT 64  
US-09-825-574-27/c

Sequence 27, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid

Structure Probing With Structure-Bridging

Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ADDRESS: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-825-574-27

Query Match 100.0%; Score 20; DB 9; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 65  
US-09-825-574-29/c  
Sequence 29, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-825-574-29

Query Match 100.0%; Score 20; DB 9; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 66  
US-09-825-574-31/c  
Sequence 31, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-825-574-31
```

```
Query Match          100.0%; Score 20; DB 9; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGCGACCCCAACTACTC 20
DB      208 TTGCGACCCCAACTACTC 189
```

```
RESULT 67
US-09-882-945A-26/c
; Sequence 26, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 26
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-26
```

```
Query Match          100.0%; Score 20; DB 10; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGCGACCCCAACTACTC 20
DB      208 TTGCGACCCCAACTACTC 189
```

```
RESULT 68
US-09-882-945A-27/c
; Sequence 27, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 27
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-27
```

```
Query Match          100.0%; Score 20; DB 10; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGCGACCCCAACTACTC 20
DB      208 TTGCGACCCCAACTACTC 189
```

```
RESULT 69
US-09-882-945A-29/c
; Sequence 29, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 29
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-29
```

```
Query Match          100.0%; Score 20; DB 10; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGCGACCCCAACTACTC 20
DB      208 TTGCGACCCCAACTACTC 189
```

```
RESULT 70
US-09-882-945A-31/c
; Sequence 31, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 31
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-31
```

```
Query Match          100.0%; Score 20; DB 10; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGCGACCCCAACTACTC 20
```

Db 208 TTGGGACCCCAACTACTC 189

RESULT 71  
US-10-688-272-16/c

; Sequence 16, Application US/10688272

; Publication No. US20040091924A1

; GENERAL INFORMATION:

; APPLICANT: Genentech Inc.; Klm, Nam-Keun

; TITLE OF INVENTION: Method for detecting base mutation

; FILE REFERENCE: 11281-014-999

; CURRENT APPLICATION NUMBER: US/10/688,272

; PRIOR FILING DATE: 2003-10-17

; PRIOR APPLICATION NUMBER: KR2002-0063832

; PRIOR FILING DATE: 2003-09-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn 1.71

; SEQ ID NO 16

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: 5'Noncoding region of HCV

US-10-688-272-16

Query Match

Best Local Similarity 100.0%; Score 20; DB 17; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 72

US-10-807-114-26/c

; Sequence 26, Application US/10807114

; Publication No. US20040235024A1

; GENERAL INFORMATION:

; APPLICANT: Lyamichev, Victor

; APPLICANT: Allawi, Hatim

; APPLICANT: Dong, Fang

; APPLICANT: Neri, Bruce

; APPLICANT: Vener, Tatiana

; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

; FILE REFERENCE: FORS-04586

; CURRENT APPLICATION NUMBER: US/10/807,114

; PRIOR FILING DATE: 2004-03-23

; PRIOR APPLICATION NUMBER: US/09/882,945

; PRIOR FILING DATE: 2001-06-15

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 26

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-807-114-26

Query Match

Best Local Similarity 100.0%; Score 20; DB 18; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 73

US-10-807-114-27/c

; Sequence 27, Application US/10807114

; Publication No. US20040235024A1

; GENERAL INFORMATION:

; APPLICANT: Lyamichev, Victor

; APPLICANT: Allawi, Hatim

; APPLICANT: Dong, Fang

; APPLICANT: Neri, Bruce

; APPLICANT: Vener, Tatiana

; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

; FILE REFERENCE: FORS-04586

; CURRENT APPLICATION NUMBER: US/10/807,114

; PRIOR FILING DATE: 2004-03-23

; PRIOR APPLICATION NUMBER: US/09/882,945

; PRIOR FILING DATE: 2001-06-15

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 27

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-807-114-27

Query Match

Best Local Similarity 100.0%; Score 20; DB 18; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 74

US-10-807-114-29/c

; Sequence 29, Application US/10807114

; Publication No. US20040235024A1

; GENERAL INFORMATION:

; APPLICANT: Lyamichev, Victor

; APPLICANT: Allawi, Hatim

; APPLICANT: Dong, Fang

; APPLICANT: Neri, Bruce

; APPLICANT: Vener, Tatiana

; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

; FILE REFERENCE: FORS-04586

; CURRENT APPLICATION NUMBER: US/10/807,114

; PRIOR FILING DATE: 2004-03-23

; PRIOR APPLICATION NUMBER: US/09/882,945

; PRIOR FILING DATE: 2001-06-15

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 29

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-807-114-29

Query Match

Best Local Similarity 100.0%; Score 20; DB 18; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 75

US-10-807-114-31/c

; Sequence 31, Application US/10807114

; Publication No. US20040235024A1

; GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neil, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/10/807,114  
CURRENT FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: US/09/882,945  
PRIOR FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 244  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-807-114-31

Query Match 100.0%; Score 20; DB 18; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
DB 208 TTCCGGACCCCAACTACTC 189

RESULT 76  
US-10-655-362-26/c

Sequence 26, Application US/10655362  
Publication No. US20050014163A1  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/10/655,362  
CURRENT FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: US/09/402,618B  
PRIOR FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 26  
LENGTH: 244  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-10-655-362-26

Query Match 100.0%; Score 20; DB 19; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
DB 208 TTCCGGACCCCAACTACTC 189

RESULT 77  
US-10-655-362-27/c  
Sequence 27, Application US/10655362  
Publication No. US20050014163A1  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/10/655,362  
CURRENT FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: US/09/402,618B  
PRIOR FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 27  
LENGTH: 244  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-10-655-362-27

Query Match 100.0%; Score 20; DB 19; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
DB 208 TTCCGGACCCCAACTACTC 189

RESULT 78  
US-10-655-362-29/c  
Sequence 29, Application US/10655362  
Publication No. US20050014163A1  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/10/655,362  
CURRENT FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: US/09/402,618B  
PRIOR FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 29  
LENGTH: 244  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-10-655-362-29

Query Match 100.0%; Score 20; DB 19; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
DB 208 TTCCGGACCCCAACTACTC 189

RESULT 79  
US-10-655-362-31/c

```
; Sequence 31, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-31
```

```
Query Match 100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTGGGACCCCAACTACTC 20
Db 208 TTGGGACCCCAACTACTC 189
```

```
RESULT 80
US-10-655-362-124
; Sequence 124, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-124
```

```
Query Match 100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTGGGACCCCAACTACTC 20
Db 37 TTGGGACCCCAACTACTC 56
```

```
RESULT 81
US-10-655-362-125
; Sequence 125, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 125
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-125
```

```
Query Match 100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTGGGACCCCAACTACTC 20
Db 37 TTGGGACCCCAACTACTC 56
```

```
RESULT 82
US-10-655-362-127
; Sequence 127, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 127
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-127
```

```
Query Match 100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTGGGACCCCAACTACTC 20
```



Db 37 TTGGGACCCCAACTACTC 56

RESULT 83  
US-10-655-362-128  
; Sequence 128, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichay, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neel, Bruce  
; APPLICANT: Brown, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 128  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-128

Query Match 100.0%; Score 20; DB 19; Length 244;  
Best Local Similarity 80.0%; Pred. No. 0.014;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 37 TTGGGACCCCAACTACTC 56

RESULT 84  
US-10-292-129-13/c  
; Sequence 13, Application US/10292129  
; Publication No. US20030148267A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Emmett Vance  
; APPLICANT: Chung, Raymond Taeyong  
; TITLE OF INVENTION: SCREENING ASSAY FOR HEPATITIS C VIRUS  
; FILE REFERENCE: 00786-539001  
; CURRENT APPLICATION NUMBER: US/10/292,129  
; CURRENT FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: US 60/345,405  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 263  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-292-129-13

Query Match 100.0%; Score 20; DB 15; Length 263;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 217 TTGGGACCCCAACTACTC 198

RESULT 85  
US-09-940-925A-121/c  
; Sequence 121, Application US/09940925A  
; Publication No. US20030054338A1  
; GENERAL INFORMATION:  
; APPLICANT: BROW, MARY ANN D.  
; APPLICANT: LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/940,925A

FILING DATE: 10-Jun-2002

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 121:

US-09-940-925A-121

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 218 TTGGGACCCCAACTACTC 199

RESULT 86  
US-09-940-925A-123/c  
; Sequence 123, Application US/09940925A  
; Publication No. US20030054338A1  
; GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
APPLICANT: LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-09-940-925A-123

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 281;
Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCACTACTC 20
DB 218 TTGGCGACCCCACTACTC 199

RESULT 87
US-09-940-925A-126/c
Sequence 126, Application US/09940925A
Publication No. US20030054338A1
GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
PATHOGENS
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
```

```
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-09-940-925A-126

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 281;
Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCACTACTC 20
DB 218 TTGGCGACCCCACTACTC 199

RESULT 88
US-09-940-925A-127
Sequence 127, Application US/09940925A
Publication No. US20030054338A1
GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
PATHOGENS
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 127:
US-09-940-925A-127

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 281;
Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCACTACTC 20
DB 64 TTGGCGACCCCACTACTC 83

RESULT 89
US-09-940-925A-128
Sequence 128, Application US/09940925A
Publication No. US20030054338A1
GENERAL INFORMATION:
```

APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 128:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
US-09-940-925A-128

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

RESULT 90  
US-09-940-925A-129  
Sequence 129, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A

FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-09-940-925A-129

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

RESULT 91  
US-09-940-925A-132  
Sequence 132, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-09-940-925A-132

Query Match 100.0%; Score 20; DB 10; Length 281;

Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

## RESULT 92

US-09-941-193A-121/c  
; Sequence 121, Application US/09941193A  
; Publication No. US20030108873A1  
; GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/941,193A

FILING DATE: 28-Aug-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 121:

US-09-941-193A-121

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 218 TTGGGACCCCACTACTC 199

## RESULT 93

US-09-941-193A-123/c  
; Sequence 123, Application US/09941193A  
; Publication No. US20030108873A1  
; GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/941,193A

FILING DATE: 28-Aug-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 123:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 123:

US-09-941-193A-123

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 218 TTGGGACCCCACTACTC 199

## RESULT 94

US-09-941-193A-126/c  
; Sequence 126, Application US/09941193A  
; Publication No. US20030108873A1  
; GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/941,193A

FILING DATE: 28-Aug-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 126:  
US-09-941-193A-126

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 218 TTCCGACCCCAACTACTC 199

RESULT 95  
US-09-941-193A-127  
Sequence 127, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 127:  
US-09-941-193A-127

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 64 TTCCGACCCCAACTACTC 83

RESULT 96  
US-09-941-193A-128  
Sequence 128, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 128:  
SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
US-09-941-193A-128

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 64 TTCCGACCCCAACTACTC 83

RESULT 97  
US-09-941-193A-129  
Sequence 129, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-09-941-193A-129

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACACTACTC 20  
Db 64 TTGGGACCCCAACACTACTC 83

RESULT 98  
US-09-941-193A-132  
Sequence 132, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-09-941-193A-132

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACACTACTC 20  
Db 64 TTGGGACCCCAACACTACTC 83

RESULT 99  
US-09-940-925A-124/c  
Sequence 124, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 124:  
US-09-940-925A-124

Query Match 100.0%; Score 20; DB 10; Length 282;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACACTACTC 20  
Db 219 TTGGGACCCCAACACTACTC 200

RESULT 100  
US-09-940-925A-130  
Sequence 130, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.

LYMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 130:  
US-09-940-925A-130

Query Match 100.0%; Score 20; DB 10; Length 282;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCACACTACTC 20  
|||||  
Db 64 TTGGGACCCACACTACTC 83

RESULT 101  
US-09-941-193A-124/C  
Sequence 124, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001

CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 124:  
US-09-941-193A-124

Query Match 100.0%; Score 20; DB 10; Length 282;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCACACTACTC 20  
|||||  
Db 219 TTGGGACCCACACTACTC 200

RESULT 102  
US-09-941-193A-130  
Sequence 130, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 130:  
US-09-941-193A-130

Query Match 100.0%; Score 20; DB 10; Length 282;  
Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 64 TTGGGACCCCAACTACTC 83

## RESULT 103

US-09-825-574-21/c  
; Sequence 21, Application US/09825574  
; Patent No. US2002019454A1

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8358

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-825-574-21

Query Match 100.0%; Score 20; DB 9; Length 286;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||

Db 222 TTGGGACCCCAACTACTC 203

## RESULT 104

US-09-882-945A-21/c

; Sequence 21, Application US/09882945A

; Publication No. US20030143535A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.

APPLICANT: Allawi, Hatim

APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana

TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

FILE REFERENCE: FORS-04586

CURRENT APPLICATION NUMBER: US/09/882,945A

CURRENT FILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 334

SOFTWARE: PatentIn version 3.0

SEQ ID NO 21

LENGTH: 286

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-882-945A-21

Query Match 100.0%; Score 20; DB 10; Length 286;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||

Db 222 TTGGGACCCCAACTACTC 203

## RESULT 105

US-10-807-114-21/c

; Sequence 21, Application US/10807114

; Publication No. US20040235024A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

APPLICANT: Allawi, Hatim

APPLICANT: Dong, Fang

APPLICANT: Neri, Bruce

APPLICANT: Vener, Tatiana

TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

FILE REFERENCE: FORS-04586

CURRENT APPLICATION NUMBER: US/10/807,114

CURRENT FILING DATE: 2004-03-23

PRIOR APPLICATION NUMBER: US/09/882,945

PRIOR FILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 334

SOFTWARE: PatentIn version 3.0

SEQ ID NO 21

LENGTH: 286

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-807-114-21

Query Match 100.0%; Score 20; DB 18; Length 286;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||

Db 222 TTGGGACCCCAACTACTC 203

## RESULT 106

US-10-655-362-21/c

; Sequence 21, Application US/10655362

; Publication No. US20050014163A1

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor I.

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd



APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/10/655,362  
CURRENT FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: US/09/402,618B  
PRIOR FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 21  
LENGTH: 286  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-10-655-362-21

Query Match 100.0%; Score 20; DB 19; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 222 TTGGGACCCCAACTACTC 203

RESULT 107  
US-09-825-574-20/c  
Sequence 20, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Karin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-825-574-20

Query Match 100.0%; Score 20; DB 9; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 222 TTGGGACCCCAACTACTC 203

RESULT 108  
US-09-825-574-23/c  
Sequence 23, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Karin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-09-825-574-23

Query Match 100.0%; Score 20; DB 9; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 222 TTGGGACCCCAACTACTC 203

RESULT 109  
US-09-882-945A-20/c

```
; Sequence 20, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-20
```

```
Query Match          100.0%; Score 20; DB 10; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGCGACCCCAACTACTC 20
DB      222 TTGCGACCCCAACTACTC 203
```

```
RESULT 110
US-09-882-945A-23/C
; Sequence 23, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-23
```

```
Query Match          100.0%; Score 20; DB 10; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 TTGCGACCCCAACTACTC 20
DB      222 TTGCGACCCCAACTACTC 203
```

```
RESULT 111
US-10-807-114-20/C
; Sequence 20, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
```

```
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-807-114-20
```

```
Query Match          100.0%; Score 20; DB 18; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGCGACCCCAACTACTC 20
DB      222 TTGCGACCCCAACTACTC 203
```

```
RESULT 112
US-10-807-114-23/C
; Sequence 23, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-807-114-23
```

```
Query Match          100.0%; Score 20; DB 18; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 TTGCGACCCCAACTACTC 20
DB      222 TTGCGACCCCAACTACTC 203
```

```
RESULT 113
US-10-655-362-20/C
; Sequence 20, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
```

```

; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-20

Query Match      100.0%; Score 20; DB 19; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGGACCCCAACTACTC 20
        |||
Db      222 TTGGGACCCCAACTACTC 203

RESULT 114
US-10-655-362-23/c
; Sequence 23, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neill, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-655-362-23

Query Match      100.0%; Score 20; DB 19; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGGACCCCAACTACTC 20
        |||
Db      222 TTGGGACCCCAACTACTC 203

RESULT 115
US-09-345-761-7/c
; Sequence 7, Application US/09345761
; Patent No. US20010053518A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
```

```

; APPLICANT: ISHIZUKA, Tetsuya
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/09/345,761
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 298
; TYPE: RNA
; ORGANISM: Synthetic Construct
US-09-345-761-7

Query Match      100.0%; Score 20; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGGACCCCAACTACTC 20
        |||
Db      261 TTGGGACCCCAACTACTC 242

RESULT 116
US-10-687-588-7/c
; Sequence 7, Application US/10687588
; Publication No. US20040115718A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
; APPLICANT: ISHIZUKA, Tetsuya
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/10/687,588
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/09/345,761
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 298
; TYPE: RNA
; ORGANISM: Synthetic Construct
US-10-687-588-7

Query Match      100.0%; Score 20; DB 18; Length 298;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGGACCCCAACTACTC 20
        |||
Db      261 TTGGGACCCCAACTACTC 242

RESULT 117
US-10-230-381-1/c
; Sequence 1, Application US/10230381
; Publication No. US20030152591A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New hepatitis C virus genotype 13, and its use as prophylactic,
; FILE REFERENCE: INNX-124-BP
; CURRENT APPLICATION NUMBER: US/10/230,381
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 299
; TYPE: DNA
```

ORGANISM: hepatitis C virus  
US-10-230-381-1

Query Match 100.0%; Score 20; DB 16; Length 299;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 233 TTGGGACCCCAACTACTC 214

RESULT 118  
US-09-345-761-6/c  
Sequence 6, Application US/09345761  
Patent No. US2001005318A1  
GENERAL INFORMATION:  
APPLICANT: ISHIGURO, Takahiko  
APPLICANT: SAITOH, Juichi  
APPLICANT: ISHIZUKA, Tetsuya  
TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID  
FILE REFERENCE: Q54969  
CURRENT APPLICATION NUMBER: US/09/345,761  
CURRENT FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: JP 10-186434  
PRIOR FILING DATE: 1998-07-01  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 315  
TYPE: DNA  
ORGANISM: Synthetic Construct  
US-09-345-761-6

Query Match 100.0%; Score 20; DB 9; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 278 TTGGGACCCCAACTACTC 259

RESULT 119  
US-10-687-588-6/c  
Sequence 6, Application US/10687588  
Publication No. US20040115718A1  
GENERAL INFORMATION:  
APPLICANT: ISHIGURO, Takahiko  
APPLICANT: SAITOH, Juichi  
APPLICANT: ISHIZUKA, Tetsuya  
TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID  
FILE REFERENCE: Q54969  
CURRENT APPLICATION NUMBER: US/10/687,588  
CURRENT FILING DATE: 2003-10-20  
PRIOR APPLICATION NUMBER: US/09/345,761  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: JP 10-186434  
PRIOR FILING DATE: 1998-07-01  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 315  
TYPE: DNA  
ORGANISM: Synthetic Construct  
US-10-687-588-6

Query Match 100.0%; Score 20; DB 18; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 278 TTGGGACCCCAACTACTC 259

RESULT 120  
US-09-882-945A-240/c  
Sequence 240, Application US/09882945A  
Publication No. US20030143535A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/09/882,945A  
CURRENT FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 240  
LENGTH: 328  
TYPE: RNA  
ORGANISM: Hepatitis C virus  
US-09-882-945A-240

Query Match 100.0%; Score 20; DB 10; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 257 TTGGGACCCCAACTACTC 238

RESULT 121  
US-09-882-945A-242/c  
Sequence 242, Application US/09882945A  
Publication No. US20030143535A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/09/882,945A  
CURRENT FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 242  
LENGTH: 328  
TYPE: RNA  
ORGANISM: Hepatitis C virus  
US-09-882-945A-242

Query Match 100.0%; Score 20; DB 10; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 257 TTGGGACCCCAACTACTC 238

RESULT 122  
US-09-882-945A-245/c  
Sequence 245, Application US/09882945A  
Publication No. US20030143535A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang

```

; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-09-882-945A-245

Query Match          100.0%; Score 20; DB 10; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 257 TTGGGACCCCAACTACTC 238

RESULT 123
US-10-475-024-18/c
; Sequence 18, Application US/10475024
; Publication No. US20040219545A1
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Welch, Ellen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA
; FILE REFERENCE: 10589-007-999
; CURRENT APPLICATION NUMBER: US/10/475,024
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/282,965
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-475-024-18

Query Match          100.0%; Score 20; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 263 TTGGGACCCCAACTACTC 244

RESULT 124
US-10-807-114-240/c
; Sequence 240, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
```

```

; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-240

Query Match          100.0%; Score 20; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 257 TTGGGACCCCAACTACTC 238

RESULT 125
US-10-807-114-242/c
; Sequence 242, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 242
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-242

Query Match          100.0%; Score 20; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 257 TTGGGACCCCAACTACTC 238

RESULT 126
US-10-807-114-245/c
; Sequence 245, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-245

Query Match          100.0%; Score 20; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 257 TTGGGACCCCAACTACTC 238

RESULT 127  
US-09-940-244-45/C  
Sequence 45, Application US/09940244  
Publication No. US20030044796A1  
GENERAL INFORMATION:  
APPLICANT: Neri, Bruce P.  
APPLICANT: Hall, Jeff G.  
APPLICANT: Lyamichev, Victor  
APPLICANT: Smith, Lloyd M.  
TITLE OF INVENTION: Reactions on Dendrimers  
FILE REFERENCE: FORS-06478  
CURRENT APPLICATION NUMBER: US/09/940,244  
CURRENT FILING DATE: 2002-05-06  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 45  
LENGTH: 337  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-940-244-45

Query Match 100.0%; Score 20; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 274 TTGGGACCCCAACTACTC 255

RESULT 128  
US-09-982-667-56/C  
Sequence 56, Application US/09982667  
Publication No. US20030096245A1  
GENERAL INFORMATION:  
APPLICANT: Prudent, James R.  
Hall, Jeff G.  
Lyamichev, Victor I.  
TITLE OF INVENTION: Invasive Cleavage Of Nucleic Acids  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,667  
FILING DATE: 18-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/756,386  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/682,853  
FILING DATE: 12-JUL-1996  
APPLICATION NUMBER: US 08/599,491  
FILING DATE: 24-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027

NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE//DOCKET NUMBER: FORS-02564  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: RNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-09-982-667-56

Query Match 100.0%; Score 20; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 274 TTGGGACCCCAACTACTC 255

RESULT 129  
US-10-033-297-45/C  
Sequence 45, Application US/10033297  
Publication No. US20020187486A1  
GENERAL INFORMATION:  
APPLICANT: Hall, Jeff G.  
Lyamichev, Victor I.  
Maer, Andrea L.  
Brow, Mary Ann D.  
TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple  
Sequential Invasive Cleavages  
NUMBER OF SEQUENCES: 163  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/033,297  
FILING DATE: 12-No. US20020187486A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,597  
FILING DATE: 09-Jul-1999  
APPLICATION NUMBER: US/08/823,516  
FILING DATE: 24-MAR-1997  
APPLICATION NUMBER: PCT/US97/01072  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 08/759,038  
FILING DATE: 02-DEC-1996  
APPLICATION NUMBER: US 08/758,314  
FILING DATE: 02-DEC-1996  
APPLICATION NUMBER: US 08/756,386  
FILING DATE: 29-NOV-1996  
APPLICATION NUMBER: US 08/682,853  
FILING DATE: 12-JUL-1996  
APPLICATION NUMBER: US 08/599,491  
FILING DATE: 24-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02736  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020187486A1 Relevant  
MOLECULE TYPE: RNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-10-033-297-45

Query Match 100.0%; Score 20; DB 13; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
Db 274 TTGCGACCCCACTACTC 255

RESULT 130  
US-10-081-806-56/c  
Sequence 56, Application US/10081806  
Publication No. US20020197623A1  
GENERAL INFORMATION:  
APPLICANT: Prudent, James R.  
Hall, Jeff G.  
Lyamichev, Victor I.  
TITLE OF INVENTION: Invasive Cleavage Of Nucleic Acids  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/081,806  
FILING DATE: 22-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,386  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/682,853  
FILING DATE: 12-JUL-1996  
APPLICATION NUMBER: US 08/599,491  
FILING DATE: 24-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02564  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020197623A1 Relevant  
MOLECULE TYPE: RNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-10-081-806-56

Query Match 100.0%; Score 20; DB 13; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
Db 274 TTGCGACCCCACTACTC 255

RESULT 131  
US-10-142-283-136/c  
Sequence 136, Application US/10142283  
Publication No. US20030152942A1  
GENERAL INFORMATION:  
APPLICANT: Fors, Lance  
Neil, Bruce P.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: de Arruda Indis, Monika  
APPLICANT: Roeven, Robert  
TITLE OF INVENTION: Nucleic Acid Detection in Pooled Samples  
FILE REFERENCE: FORS-07219  
CURRENT APPLICATION NUMBER: US/10/142,283  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: 60/326,549  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 60/289,764  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 136  
LENGTH: 337  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-142-283-136

Query Match 100.0%; Score 20; DB 16; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
Db 274 TTGCGACCCCACTACTC 255

RESULT 132  
US-10-290-386-45/c  
Sequence 45, Application US/10290386  
Publication No. US20030152971A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
Neil, Bruce P.  
APPLICANT: Hall, Jeff G.  
APPLICANT: Lukowiak, Andrew A.  
TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences  
FILE REFERENCE: FORS-07459  
CURRENT APPLICATION NUMBER: US/10/290,386  
CURRENT FILING DATE: 2002-11-07  
PRIOR APPLICATION NUMBER: 60/361,060  
PRIOR FILING DATE: 2002-02-27  
PRIOR APPLICATION NUMBER: 60/344,946  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 09/713,601  
PRIOR FILING DATE: 2000-11-15  
PRIOR APPLICATION NUMBER: 09/381,212  
PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 09/350,309  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: 08/823,516  
PRIOR FILING DATE: 1997-03-24  
PRIOR APPLICATION NUMBER: 08/759,038  
PRIOR FILING DATE: 1996-12-02

```
; PRIOR APPLICATION NUMBER: 08/756,386
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: 08/682,853
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/599,491
; PRIOR FILING DATE: 1996-01-24
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 337
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-290-386-45

Query Match          100.0%; Score 20; DB 16; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20
    |||||
Db 274 TTCCGACCCCACTACTC 255

RESULT 133
US-10-356-861-45/C
; Sequence 45, Application US/10356861
; Publication No. US20040072182A1
; GENERAL INFORMATION:
; APPLICANT: Victor, Lyamichev
; APPLICANT: Neri, Bruce P.
; APPLICANT: Hall, Jeff
; APPLICANT: Lukowiak, Andrew A.
; TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences
; FILE REFERENCE: FORS-07813
; CURRENT APPLICATION NUMBER: US/10/356,861
; CURRENT FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 337
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-356-861-45

Query Match          100.0%; Score 20; DB 17; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20
    |||||
Db 274 TTCCGACCCCACTACTC 255

RESULT 134
US-10-309-584-45/C
; Sequence 45, Application US/10309584
; Publication No. US20040214174A1
; GENERAL INFORMATION:
; APPLICANT: Neri, Bruce P.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Smith, Lloyd M.
; TITLE OF INVENTION: Reactions on Dendrimers
; FILE REFERENCE: FORS-06478
; CURRENT APPLICATION NUMBER: US/10/309,584
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US/09/940,244
; PRIOR FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 422
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-309-584-45

Query Match          100.0%; Score 20; DB 18; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20
    |||||
Db 274 TTCCGACCCCACTACTC 255

RESULT 135
US-10-897-793-45/C
; Sequence 45, Application US/10897793
; Publication No. US20050003432A1
; GENERAL INFORMATION:
; APPLICANT: Hall, Jeff G.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Mast, Andrea L.
; APPLICANT: Brow, Mary Ann D.
; TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
;                               Sequential Invasive Cleavages
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/897,793
; FILING DATE: 23-Jul-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/01072
; FILING DATE: 21-JAN-1997
; APPLICATION NUMBER: US 08/759,038
; FILING DATE: 02-DEC-1996
; APPLICATION NUMBER: US 08/758,314
; FILING DATE: 02-DEC-1996
; APPLICATION NUMBER: US 08/756,386
; FILING DATE: 29-NOV-1996
; APPLICATION NUMBER: US 08/682,853
; FILING DATE: 12-JUL-1996
; APPLICATION NUMBER: US 08/599,491
; FILING DATE: 24-JAN-1996
; APPLICATION NUMBER: US 08/323,516
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: McKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
```



TOPOLOGY: not relevant  
MOLECULE TYPE: RNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-10-897-793-45

Query Match 100.0%; Score 20; DB 18; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
DB 274 TTGGGACCCCAACTACTC 255

RESULT 136  
US-10-783-557-45/c  
Sequence 45, Application US/10783557  
Publication No. US20050048527A1  
GENERAL INFORMATION:  
APPLICANT: Allawi, Hatim T.  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Ma, Wu-Po  
APPLICANT: Neel, Bruce P.  
APPLICANT: Lyamichev, Victor I.  
TITLE OF INVENTION: Endonuclease-Substrate Complexes  
FILE REFERENCE: FORS-08907  
CURRENT APPLICATION NUMBER: US/10/783,557  
CURRENT FILING DATE: 2004-02-20  
NUMBER OF SEQ ID NOS: 533  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 45  
LENGTH: 337  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-783-557-45

Query Match 100.0%; Score 20; DB 19; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
DB 274 TTGGGACCCCAACTACTC 255

RESULT 137  
US-09-814-292-44/c  
Sequence 44, Application US/09814292  
Patent No. US20020120117A1  
GENERAL INFORMATION:  
APPLICANT: Yu, De-Chao  
APPLICANT: Zhang, Hong  
APPLICANT: Henderson, Daniel R.  
TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN  
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING  
TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND  
FILE REFERENCE: 348022001500  
CURRENT APPLICATION NUMBER: US/09/814,292  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/191,861  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 44  
LENGTH: 341  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-292-44

Query Match 100.0%; Score 20; DB 9; Length 341;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
DB 275 TTGGGACCCCAACTACTC 256

RESULT 138  
US-09-814-357-3/c  
Sequence 3, Application US/09814357  
Publication No. US20030068307A1  
GENERAL INFORMATION:  
APPLICANT: Yu, De-Chao  
APPLICANT: Chen, Yu  
APPLICANT: Henderson, Daniel R.  
TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA  
TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,  
FILE REFERENCE: 348022001600  
CURRENT APPLICATION NUMBER: US/09/814,357  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 60/192,015  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 341  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-357-3

Query Match 100.0%; Score 20; DB 10; Length 341;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
DB 275 TTGGGACCCCAACTACTC 256

RESULT 139  
US-09-814-351-3/c  
Sequence 3, Application US/09814351  
Publication No. US20030148520A1  
GENERAL INFORMATION:  
APPLICANT: Yu, De-Chao  
APPLICANT: Li, Yuanhao  
APPLICANT: Henderson, Daniel R.  
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
FILE REFERENCE: 348022001700  
CURRENT APPLICATION NUMBER: US/09/814,351  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/192,156  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 341  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-351-3

Query Match 100.0%; Score 20; DB 10; Length 341;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 140  
US-10-259-275-35/c  
; Sequence 35, Application US/10259275  
; Publication No. US20030125541A1  
; GENERAL INFORMATION:  
; APPLICANT: Lemov, Stanley M.  
; APPLICANT: Yi, Minkyung  
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
; FILE REFERENCE: 265,0007 0120  
; CURRENT APPLICATION NUMBER: US/10/259,275  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/171,909  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 09/747,419  
; PRIOR FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/325,236  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/338,123  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 341  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: nucleotide sequence of 5' NTR  
US-10-259-275-35

Query Match 100.0%; Score 20; DB 15; Length 341;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 141  
US-10-132-295-1/c  
; Sequence 1, Application US/10132295  
; Publication No. US20030124550A1  
; GENERAL INFORMATION:  
; APPLICANT: BML, Inc.  
; TITLE OF INVENTION: METHOD OF SCREENING DRUG FOR HEPATITIS C  
; FILE REFERENCE: 069614  
; CURRENT APPLICATION NUMBER: US/10/132,295  
; CURRENT FILING DATE: 2002-04-26  
; PRIOR APPLICATION NUMBER: JP 2001-329728  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 347  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-132-295-1

Query Match 100.0%; Score 20; DB 15; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 142  
US-09-877-526A-48/c  
; Sequence 48, Application US/09877526A  
; Patent No. US20020102568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: Usman, Nassim  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Haebertli, Pete  
; APPLICANT: Chowitra, Bharat  
; APPLICANT: Blatt, Larry  
; APPLICANT: Vaish, Narendra  
; TITLE OF INVENTION: A Process for the Detection of Nucleic Acid Using Nucleic Acid C

; FILE REFERENCE: MEH800-816-C (700/002)  
; CURRENT APPLICATION NUMBER: US/09/877,526A  
; CURRENT FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: 60/187,128  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 48  
; LENGTH: 366  
; TYPE: RNA  
; ORGANISM: Hepatitis C virus  
US-09-877-526A-48

Query Match 100.0%; Score 20; DB 9; Length 366;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 143  
US-09-992-160-48/c  
; Sequence 48, Application US/09992160  
; Publication No. US2003008295A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: Usman, Nassim  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Haebertli, Pete  
; APPLICANT: Chowitra, Bharat  
; APPLICANT: Blatt, Larry  
; TITLE OF INVENTION: Nucleic Acid Sensor Molecules  
; FILE REFERENCE: MEH800-816-D (700/004)  
; CURRENT APPLICATION NUMBER: US/09/992,160  
; CURRENT FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 48  
; LENGTH: 366  
; TYPE: RNA  
; ORGANISM: Hepatitis C virus  
US-09-992-160-48

Query Match 100.0%; Score 20; DB 10; Length 366;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 144  
US-09-740-332-9701/c

```
Sequence 9701, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9701
; LENGTH: 366
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: HCV 5' UTR
US-09-740-332-9701

Query Match          100.0%; Score 20; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 276 TTGGGACCCCAACTACTC 257

RESULT 145
US-09-817-879-9701/c
; Sequence 9701, Application US/09817879
; Publication No. US2003017131A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9701
; LENGTH: 366
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: HCV 5' UTR
US-09-817-879-9701

Query Match          100.0%; Score 20; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 276 TTGGGACCCCAACTACTC 257

RESULT 146
US-10-056-761-48/c
; Sequence 48, Application US/10056761
; Publication No. US20030065155A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: MCSIWigen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haeblerl, Pete
```

```
APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Nucleic Acid Sensor Molecules
; FILE REFERENCE: MBH00-816-E (700/005)
; CURRENT APPLICATION NUMBER: US/10/056,761
; CURRENT FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 366
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-10-056-761-48

Query Match          100.0%; Score 20; DB 14; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 147
US-10-422-050-48/c
; Sequence 48, Application US/10422050
; Publication No. US20040009510A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Seiwert, Scott
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules
; FILE REFERENCE: 700/013 (MBH 00-816-M)
; CURRENT APPLICATION NUMBER: US/10/422,050
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/US 02/35529
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/286,492
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 10/283,858
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 10/056,761
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/992,160
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 09/877,526
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/800,594
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 366
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-10-422-050-48

Query Match          100.0%; Score 20; DB 17; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 148
US-10-669-841-16198/c
```

```
; Sequence 16198, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/04205 (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 16198
; LENGTH: 366
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: HCV 5' UTR
; US-10-669-841-16198

Query Match          100.0%; Score 20; DB 18; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20
Db 276 TTCCGACCCCACTACTC 257

RESULT 149
US-10-324-409B-32/c
; Sequence 32, Application US/10324409B
; Publication No. US2004008680A1
; GENERAL INFORMATION:
; APPLICANT: Sampson, et al.
; TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
; FILE REFERENCE: 2003309-0028
; CURRENT APPLICATION NUMBER: US/10/324,409B
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
```

```
; LENGTH: 374
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotides
; OTHER INFORMATION: 1-335 for the Hepatitis C Virus Genome.
; US-10-324-409B-32

Query Match          100.0%; Score 20; DB 17; Length 374;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20
Db 263 TTCCGACCCCACTACTC 244

RESULT 150
US-10-626-879-9/c
; Sequence 9, Application US/10626879
; Publication No. US20050058982A1
; GENERAL INFORMATION:
; APPLICANT: HAN, JANG
; APPLICANT: SEO, MI YOUNG
; APPLICANT: HOUGHTON, MICHAEL
; TITLE OF INVENTION: MODIFIED SMALL INTERFERING RNA MOLECULES AND METHODS OF USE
; FILE REFERENCE: 072121-0189-REG
; CURRENT APPLICATION NUMBER: US/10/626,879
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/470,230
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/461,838
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/398,605
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 383
; TYPE: RNA
; ORGANISM: Hepatitis C virus
; US-10-626-879-9

Query Match          100.0%; Score 20; DB 19; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20
Db 275 TTCCGACCCCACTACTC 256

RESULT 151
US-10-332-626-1/c
; Sequence 1, Application US/10332626
; Publication No. US20040073380A1
; GENERAL INFORMATION:
; APPLICANT: Joseph D. Pugliesi
; TITLE OF INVENTION: Structural Targets of Hepatitis C Virus
; FILE REFERENCE: STAN-196
; CURRENT APPLICATION NUMBER: US/10/332,626
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: PCT/US01/21371
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,673
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 384
; TYPE: RNA
; ORGANISM: Hepatitis C virus
```

US-10-332-626-1

Query Match 100.0%; Score 20; DB 17; Length 384;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
|||||  
Db 276 TTGGGACCCCACTACTC 257

RESULT 152

US-09-940-925A-122/c

Sequence 122, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:

LENGTH: 386 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 122:

US-09-940-925A-122

Query Match 100.0%; Score 20; DB 10; Length 386;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
|||||  
Db 323 TTGGGACCCCACTACTC 304

RESULT 153

US-09-941-193A-122/c

Sequence 122, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:

LENGTH: 386 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 122:

US-09-941-193A-122

Query Match 100.0%; Score 20; DB 10; Length 386;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
|||||  
Db 323 TTGGGACCCCACTACTC 304

RESULT 154

US-10-276-513-5/c

Sequence 5, Application US/10276513  
Publication No. US20030143528A1  
GENERAL INFORMATION:

APPLICANT: KOHARA, MICHINORI  
APPLICANT: MATSUZAKI, JUNICHI

APPLICANT: OKAMOTO, KOUICHI  
APPLICANT: KATSUME, ASAO

TITLE OF INVENTION: VECTOR FOR ANALYSING REPLICATION MECHANISM OF RNA VIRUS AND USE  
FILE REFERENCE: 382.1038

CURRENT APPLICATION NUMBER: US/10/276,513  
PRIOR FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: PCT/JP01/04033  
PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: JP 2000-142451  
PRIOR FILING DATE: 2000-05-15

NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5  
LENGTH: 393

TYPE: DNA  
ORGANISM: Hepatitis C Virus

US-10-276-513-5

Query Match 100.0%; Score 20; DB 15; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 287 TTGGGACCCCAACTACTC 268

## RESULT 155

US-10-276-513-4/c  
; Sequence 4, Application US/10276513  
; Publication No. US20030143528A1  
; GENERAL INFORMATION:  
; APPLICANT: KOHARA, MICHINORI  
; APPLICANT: MATSUZAKI, JUNICHI  
; APPLICANT: OKAMOTO, KOUICHI  
; APPLICANT: KATSUME, ASAO  
; TITLE OF INVENTION: VECTOR FOR ANALYSING REPLICATION MECHANISM OF RNA VIRUS AND USE T  
; FILE REFERENCE: 382.1038  
; CURRENT APPLICATION NUMBER: US/10/276,513  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: PCT/JPO1/04033  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: JP 2000-142451  
; PRIOR FILING DATE: 2000-05-15  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 412  
; TYPE: DNA  
; ORGANISM: Hepatitis C Virus  
US-10-276-513-4

Query Match 100.0%; Score 20; DB 15; Length 412;  
Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 306 TTGGGACCCCAACTACTC 287

RESULT 156  
US-09-851-138-59/c  
; Sequence 59, Application US/09851138  
; Publication No. US20020183508A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: STUYVER, LIEVEN  
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES  
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
; AGENTS

NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210-4433

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word 6.0 / ASCII text output

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/851,138  
FILING DATE: 09-May-2001

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,075  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 94870166.9  
FILING DATE: 21 Oct 1994

APPLICATION NUMBER: EP 95870076.7  
FILING DATE: 28 Jun 1995  
ATTORNEY/AGENT INFORMATION:

NAME: KAMMERER, PATRICIA A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: INNS:004  
INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:  
LENGTH: 652 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-851-138-59

Query Match 100.0%; Score 20; DB 9; Length 652;  
Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 172 TTGGGACCCCAACTACTC 153

RESULT 157  
US-09-853-409-37/c  
; Sequence 37, Application US/09853409  
; Publication No. US20030171313A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Kevin P.  
; APPLICANT: Hanecek, Ronnie C.  
; APPLICANT: Dotz, F. Andrew  
; APPLICANT: Kwoh, T. Jesse

TITLE OF INVENTION: Compositions and Methods for Treatment of Hepatitis C  
; FILE REFERENCE: ISPH-0569  
; CURRENT APPLICATION NUMBER: US/09/853,409  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 08/988,321  
; PRIOR FILING DATE: 1997-12-10  
; PRIOR APPLICATION NUMBER: 08/650,093  
; PRIOR FILING DATE: 1996-05-17  
; PRIOR APPLICATION NUMBER: 08/452,841  
; PRIOR FILING DATE: 1995-05-30  
; PRIOR APPLICATION NUMBER: 08/397,330  
; PRIOR FILING DATE: 1995-03-09  
; PRIOR APPLICATION NUMBER: 07/945,289  
; PRIOR FILING DATE: 1992-09-10  
; PRIOR APPLICATION NUMBER: 09/690,936  
; PRIOR FILING DATE: 2000-10-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 685  
; TYPE: RNA  
; ORGANISM: Hepatitis C Virus  
US-09-853-409-37

Query Match 100.0%; Score 20; DB 10; Length 685;  
Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 274 TTGGGACCCCAACTACTC 255

RESULT 158  
US-10-457-304-37/c  
; Sequence 37, Application US/10457304  
; Publication No. US20040033978A1  
; GENERAL INFORMATION:

APPLICANT: Anderson, Kevin P.  
APPLICANT: Hanecak, Ronnie C.  
APPLICANT: No. US20040033978A1aki, Chikateru  
APPLICANT: Dorr, F. Andrew  
APPLICANT: Kwoh, T. Jesse  
TITLE OF INVENTION: Compositions and Methods for Treatment of Hepatitis C  
FILE REFERENCE: ISPH-0569  
CURRENT APPLICATION NUMBER: US/10/457,304  
CURRENT FILING DATE: 2003-06-09  
PRIOR APPLICATION NUMBER: US/09/853,409  
PRIOR FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 08/988,321  
PRIOR FILING DATE: 1997-12-10  
PRIOR APPLICATION NUMBER: 08/650,093  
PRIOR FILING DATE: 1996-05-17  
PRIOR APPLICATION NUMBER: 08/452,841  
PRIOR FILING DATE: 1995-05-30  
PRIOR APPLICATION NUMBER: 08/397,330  
PRIOR FILING DATE: 1995-03-09  
PRIOR APPLICATION NUMBER: 07/945,289  
PRIOR FILING DATE: 1992-09-10  
PRIOR APPLICATION NUMBER: 09/690,936  
PRIOR FILING DATE: 2000-10-18  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1.  
SEQ ID NO 37  
LENGTH: 685  
TYPE: RNA  
ORGANISM: Hepatitis C virus  
US-10-457-304-37

Query Match 100.0%; Score 20; DB 17; Length 685;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGAGCCCAACTACTC 20  
DB 274 TTGGGAGCCCAACTACTC 255

RESULT 159  
US-10-454-293-37/c  
Sequence 37, Application US/10454293  
Publication No. US20040049021A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Kevin P.  
APPLICANT: Hanecak, Ronnie C.  
APPLICANT: No. US20040049021A1aki, Chikateru  
APPLICANT: Dorr, F. Andrew  
APPLICANT: Kwoh, T. Jesse  
TITLE OF INVENTION: Compositions and Methods for Treatment of Hepatitis C  
FILE REFERENCE: ISPH-0743  
CURRENT APPLICATION NUMBER: US/10/454,293  
CURRENT FILING DATE: 2003-06-04  
PRIOR APPLICATION NUMBER: 09/853,409  
PRIOR FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 08/988,321  
PRIOR FILING DATE: 1997-12-10  
PRIOR APPLICATION NUMBER: 08/650,093  
PRIOR FILING DATE: 1996-05-17  
PRIOR APPLICATION NUMBER: 08/452,841  
PRIOR FILING DATE: 1995-05-30  
PRIOR APPLICATION NUMBER: 08/397,330  
PRIOR FILING DATE: 1995-03-09  
PRIOR APPLICATION NUMBER: 07/945,289  
PRIOR FILING DATE: 1992-09-10  
PRIOR APPLICATION NUMBER: 09/690,936  
PRIOR FILING DATE: 2000-10-18  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1.  
SEQ ID NO 37

LENGTH: 685  
TYPE: RNA  
ORGANISM: Hepatitis C virus  
US-10-454-293-37

Query Match 100.0%; Score 20; DB 17; Length 685;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGAGCCCAACTACTC 20  
DB 274 TTGGGAGCCCAACTACTC 255

RESULT 160  
US-10-066-130-20  
Sequence 20, Application US/10066130  
Publication No. US20030175663A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase  
FILE REFERENCE: PH-7171 NP  
CURRENT APPLICATION NUMBER: US/10/066,130  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 60/265,437  
PRIOR FILING DATE: 2001-01-31  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 2327  
TYPE: DNA  
ORGANISM: viral  
US-10-066-130-20

Query Match 100.0%; Score 20; DB 16; Length 2327;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGAGCCCAACTACTC 20  
DB 2053 TTGGGAGCCCAACTACTC 2072

RESULT 161  
US-10-734-801-20  
Sequence 20, Application US/10734801  
Publication No. US20040126388A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase  
FILE REFERENCE: PH-7171-DIV  
CURRENT APPLICATION NUMBER: US/10/734,801  
CURRENT FILING DATE: 2003-12-12  
PRIOR APPLICATION NUMBER: US 60/265,437  
PRIOR FILING DATE: 2001-01-31  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 2327  
TYPE: DNA  
ORGANISM: viral  
US-10-734-801-20

Query Match 100.0%; Score 20; DB 18; Length 2327;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGAGCCCAACTACTC 20  
DB 2053 TTGGGAGCCCAACTACTC 2072

```
RESULT 162
; US-10-066-130-19
; Sequence 19, Application US/10066130
; Publication No. US20030175683A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171 NP
; CURRENT APPLICATION NUMBER: US/10/066,130
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/265,437
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: viral
; US-10-066-130-19

Query Match          100.0%; Score 20; DB 16; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 2400 TTGGGACCCCAACTACTC 2419

RESULT 163
; US-10-734-801-19
; Sequence 19, Application US/10734801
; Publication No. US20040126388A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171-DIV
; CURRENT APPLICATION NUMBER: US/10/734,801
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/265,437
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: viral
; US-10-734-801-19

Query Match          100.0%; Score 20; DB 18; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 2400 TTGGGACCCCAACTACTC 2419

RESULT 164
; US-10-066-130-18
; Sequence 18, Application US/10066130
; Publication No. US20030175683A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171 NP
; CURRENT APPLICATION NUMBER: US/10/066,130
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/265,437
```

```
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 2771
; TYPE: DNA
; ORGANISM: viral
; US-10-066-130-18

Query Match          100.0%; Score 20; DB 16; Length 2771;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 2400 TTGGGACCCCAACTACTC 2419

RESULT 165
; US-10-734-801-18
; Sequence 18, Application US/10734801
; Publication No. US20040126388A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171-DIV
; CURRENT APPLICATION NUMBER: US/10/734,801
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/265,437
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 2771
; TYPE: DNA
; ORGANISM: viral
; US-10-734-801-18

Query Match          100.0%; Score 20; DB 18; Length 2771;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 2400 TTGGGACCCCAACTACTC 2419

RESULT 166
; US-10-066-130-17
; Sequence 17, Application US/10066130
; Publication No. US20030175683A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171 NP
; CURRENT APPLICATION NUMBER: US/10/066,130
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/265,437
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: viral
; US-10-066-130-17

Query Match          100.0%; Score 20; DB 16; Length 5860;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      2400 TTGGGACCCCAACTACTC 2419

RESULT 167
US-10-734-801-17
; Sequence 17, Application US/10734801
; Publication No. US20040126388A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171-DIV
; CURRENT APPLICATION NUMBER: US/10/734,801
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/265,437
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Viral
US-10-734-801-17

Query Match      100.0%; Score 20; DB 18; Length 5860;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      2400 TTGGGACCCCAACTACTC 2419

RESULT 168
US-10-434-842-16/c
; Sequence 16, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FCA4 Replicon Sequence
US-10-434-842-16

Query Match      100.0%; Score 20; DB 17; Length 7989;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      275 TTGGGACCCCAACTACTC 256

RESULT 169
US-10-639-150-1/c
; Sequence 1, Application US/10639150

Publication No. US20040121975A1
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: HEPATITIS C VIRUS ASSAYS
; FILE REFERENCE: D0224 NP
; CURRENT APPLICATION NUMBER: US/10/639,150
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: US 60/402,661
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HCV Replicon
US-10-639-150-1

Query Match      100.0%; Score 20; DB 18; Length 7989;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      275 TTGGGACCCCAACTACTC 256

RESULT 170
US-10-897-648-17/c
; Sequence 17, Application US/10897648
; Publication No. US20050043266A1
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha
; TITLE OF INVENTION: SHORT INTERFERING RNA AS AN ANTIVIRAL AGENT FOR HEPATITIS C
; FILE REFERENCE: A-835
; CURRENT APPLICATION NUMBER: US/10/897,648
; CURRENT FILING DATE: 2004-07-22
; PRIOR APPLICATION NUMBER: 60/490,204
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-897-648-17

Query Match      100.0%; Score 20; DB 19; Length 7989;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      275 TTGGGACCCCAACTACTC 256

RESULT 171
US-10-005-469-1/c
; Sequence 1, Application US/10005469
; Publication No. US20020155133A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RI
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/10/005,469
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
```

; SEQ ID NO 1  
; LENGTH: 7992  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCV replicon I377/NS3-3'UTR  
US-10-005-469-1

Query Match 100.0%; Score 20; DB 13; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 172  
US-10-005-469-2/c  
; Sequence 2, Application US/10005469  
; Publication No. US20020155133A1  
; GENERAL INFORMATION:  
; APPLICANT: ANADYS Pharmaceuticals, Inc.  
; APPLICANT: Bichko, Vadim  
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
; FILE REFERENCE: 0342/1H395US1  
; CURRENT APPLICATION NUMBER: US/10/005,469  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US 60/245,866  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 7992  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCV Replicon RNA from cell line HCVR2  
US-10-005-469-2

Query Match 100.0%; Score 20; DB 13; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 173  
US-10-005-469-4/c  
; Sequence 4, Application US/10005469  
; Publication No. US20020155133A1  
; GENERAL INFORMATION:  
; APPLICANT: ANADYS Pharmaceuticals, Inc.  
; APPLICANT: Bichko, Vadim  
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
; FILE REFERENCE: 0342/1H395US1  
; CURRENT APPLICATION NUMBER: US/10/005,469  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US 60/245,866  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 7992  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCV Replicon RNA from cell line HCVR9  
US-10-005-469-4

Query Match 100.0%; Score 20; DB 13; Length 7992;

Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 174  
US-10-005-469-5/c  
; Sequence 5, Application US/10005469  
; Publication No. US20020155133A1  
; GENERAL INFORMATION:  
; APPLICANT: ANADYS Pharmaceuticals, Inc.  
; APPLICANT: Bichko, Vadim  
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
; FILE REFERENCE: 0342/1H395US1  
; CURRENT APPLICATION NUMBER: US/10/005,469  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US 60/245,866  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 7992  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCV Replicon from cell line HCVR22  
US-10-005-469-5

Query Match 100.0%; Score 20; DB 13; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 175  
US-10-005-469-6/c  
; Sequence 6, Application US/10005469  
; Publication No. US20020155133A1  
; GENERAL INFORMATION:  
; APPLICANT: ANADYS Pharmaceuticals, Inc.  
; APPLICANT: Bichko, Vadim  
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
; FILE REFERENCE: 0342/1H395US1  
; CURRENT APPLICATION NUMBER: US/10/005,469  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US 60/245,866  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 7992  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCV Replicon from cell line HCVR24  
US-10-005-469-6

Query Match 100.0%; Score 20; DB 13; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 176

```
US-10-434-842-1/c
; Sequence 1, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV1b-based chimeric replicon
US-10-434-842-1
Query Match      100.0%; Score 20; DB 17; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20
DB 275 TTCCGGACCCCAACTACTC 256

RESULT 177
US-10-434-842-2/c
; Sequence 2, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV2 subgenomic HCV replicon
US-10-434-842-2
Query Match      100.0%; Score 20; DB 17; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20
DB 275 TTCCGGACCCCAACTACTC 256

RESULT 178
US-10-434-842-4/c
; Sequence 4, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
```

```
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCVR9 subgenomic HCV replicon
US-10-434-842-4
Query Match      100.0%; Score 20; DB 17; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20
DB 275 TTCCGGACCCCAACTACTC 256

RESULT 179
US-10-434-842-5/c
; Sequence 5, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCVR2 subgenomic HCV replicon
US-10-434-842-5
Query Match      100.0%; Score 20; DB 17; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20
DB 275 TTCCGGACCCCAACTACTC 256

RESULT 180
US-10-434-842-6/c
; Sequence 6, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
```

FILE REFERENCE: 0342/1H395US3  
CURRENT APPLICATION NUMBER: US/10/434,842  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: US 10/233,307  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 10/005,469  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCVR24 subgenomic HCV replicon  
US-10-434-842-6

Query Match 100.0%; Score 20; DB 17; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 181  
US-10-434-842-15/c  
Sequence 15, Application US/10/434842  
Publication No. US20040005549A1  
GENERAL INFORMATION:  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US3  
CURRENT APPLICATION NUMBER: US/10/434,842  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: US 10/233,307  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 10/005,469  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: FCAL Replicon Sequence  
US-10-434-842-15

Query Match 100.0%; Score 20; DB 17; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 182  
US-10-434-842-17/c  
Sequence 17, Application US/10/434842  
Publication No. US20040005549A1  
GENERAL INFORMATION:  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US3  
CURRENT APPLICATION NUMBER: US/10/434,842  
CURRENT FILING DATE: 2003-05-09

PRIOR APPLICATION NUMBER: US 10/233,307  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 10/005,469  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: FCA22 Replicon Sequence  
US-10-434-842-17

Query Match 100.0%; Score 20; DB 17; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 183  
US-10-005-469-3/c  
Sequence 3, Application US/10005469  
Publication No. US2002015513A1  
GENERAL INFORMATION:  
APPLICANT: ANADYS Pharmaceuticals, Inc.  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R  
FILE REFERENCE: 0342/1H395US1  
CURRENT APPLICATION NUMBER: US/10/005,469  
CURRENT FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 7995  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCV Replicon RNA from cell line HCVR8  
US-10-005-469-3

Query Match 100.0%; Score 20; DB 13; Length 7995;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 184  
US-10-434-842-3/c  
Sequence 3, Application US/10/434842  
Publication No. US20040005549A1  
GENERAL INFORMATION:  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US3  
CURRENT APPLICATION NUMBER: US/10/434,842  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: US 10/233,307  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 10/005,469  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07

NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 7995  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCVr8 subgenomic HCV replicon  
US-10-434-842-3

Query Match 100.0%; Score 20; DB 17; Length 7995;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

RESULT 185  
US-10-475-989-3/c  
; Sequence 3, Application US/10475989  
; Publication No. US20040142320A1  
; GENERAL INFORMATION:  
; APPLICANT: CNRS  
; TITLE OF INVENTION: PROCESS FOR THE REPLICATION OF THE HEPATITIS C VIRUS  
; FILE REFERENCE: MOB 01 AA CNR GENO  
; CURRENT APPLICATION NUMBER: US/10/475,989  
; PRIOR FILING DATE: 2003-10-27  
; PRIOR APPLICATION NUMBER: FR 01/05732  
; PRIOR FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 8451  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: replicon obtained by fusion of a hygromycin B  
US-10-475-989-3

Query Match 100.0%; Score 20; DB 18; Length 8451;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

RESULT 186  
US-10-029-907-6/c  
; Sequence 6, Application US/10029907  
; Publication No. US20020142350A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)

US-10-029-907-6

Query Match 100.0%; Score 20; DB 13; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

RESULT 187  
US-10-029-907-7/c  
; Sequence 7, Application US/10029907  
; Publication No. US20020142350A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-029-907-7

Query Match 100.0%; Score 20; DB 13; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

RESULT 188  
US-10-029-907-24/c  
; Sequence 24, Application US/10029907  
; Publication No. US20020142350A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-029-907-24

Query Match 100.0%; Score 20; DB 13; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 275 TTGCGACCCCAACTACTC 256

RESULT 189  
US-10-029-907-25/c  
; Sequence 25, Application US/10029907  
; Publication No. US20020142350A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-029-907-25

Query Match 100.0%; Score 20; DB 13; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 190  
US-10-309-561-6/c  
; Sequence 6, Application US/10309561  
; Publication No. US20030148348A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/309,561  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-309-561-6

Query Match 100.0%; Score 20; DB 15; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 191

US-10-309-561-7/c  
; Sequence 7, Application US/10309561  
; Publication No. US20030148348A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/309,561  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-309-561-7

Query Match 100.0%; Score 20; DB 15; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 192  
US-10-309-561-24/c  
; Sequence 24, Application US/10309561  
; Publication No. US20030148348A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/309,561  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-309-561-24

Query Match 100.0%; Score 20; DB 15; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 193  
US-10-309-561-25/c  
; Sequence 25, Application US/10309561  
; Publication No. US20030148348A1

```

; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/309,561
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-309-561-25

Query Match          100.0%; Score 20; DB 15; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 194
US-10-789-355-6/c
; Sequence 6, Application US/10789355
; Publication No. US2004018033A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-789-355-6

Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 195
US-10-789-355-7/c
; Sequence 7, Application US/10789355
; Publication No. US2004018033A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
```

```

; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-789-355-7

Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 196
US-10-789-355-24/c
; Sequence 24, Application US/10789355
; Publication No. US2004018033A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-789-355-24

Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 197
US-10-789-355-25/c
; Sequence 25, Application US/10789355
; Publication No. US2004018033A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
```

```
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-686-835-25
```

```
Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGAGCCCAACTACTC 20
        |||||
Db      275 TTGGGAGCCCAACTACTC 256
```

```
RESULT 198
US-10-686-835-6/c
; Sequence 6, Application US/10686835
; Publication No. US20040203020A1
; GENERAL INFORMATION:
; APPLICANT: Kukolj, George and Pause, Armin
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083-2-C1
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-686-835-6
```

```
Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGAGCCCAACTACTC 20
        |||||
Db      275 TTGGGAGCCCAACTACTC 256
```

```
RESULT 199
US-10-686-835-7/c
; Sequence 7, Application US/10686835
; Publication No. US20040203020A1
; GENERAL INFORMATION:
; APPLICANT: Kukolj, George and Pause, Armin
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083-2-C1
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 10/029,907
; PRIOR FILING DATE: 2001-12-21
```

```
; PRIOR APPLICATION NUMBER: US 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-686-835-7
```

```
Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGAGCCCAACTACTC 20
        |||||
Db      275 TTGGGAGCCCAACTACTC 256
```

```
RESULT 200
US-10-686-835-24/c
; Sequence 24, Application US/10686835
; Publication No. US20040203020A1
; GENERAL INFORMATION:
; APPLICANT: Kukolj, George and Pause, Armin
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083-2-C1
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-686-835-24
```

```
Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGAGCCCAACTACTC 20
        |||||
Db      275 TTGGGAGCCCAACTACTC 256
```

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Search completed: April 25, 2005, 16:27:21
Job time : 300.526 secs
```



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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:42 ; Search time 779.211 Seconds  
(without alignments)  
.1119.330 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18  
Sequence: 1 GGGGUCCTCGAGNNNNNN 18

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hg: \*  
3: gb\_in: \*  
4: gb\_cm: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	6 AX803675	AX803675 Sequence
2	18	100.0	24	6 AX803704	AX803704 Sequence
3	16	88.9	65130	2 AC026845	AC026845 Homo sapi
4	16	88.9	132013	2 CR354556	CR354556 Homo sapi
5	16	88.9	132597	2 AC074014	AC074014 Homo sapi
6	16	88.9	155605	2 BX927307	BX927307 Homo sapi
7	16	88.9	162408	2 CR752651	CR752651 Homo sapi
8	16	88.9	166622	2 CR774197	CR774197 Homo sapi
9	16	88.9	172578	2 CR812468	CR812468 Homo sapi
10	16	88.9	177849	2 BX927353	BX927353 Homo sapi
11	16	88.9	178025	2 CR752654	CR752654 Homo sapi
12	16	88.9	184628	2 AC133391	AC133391 Homo sapi
13	16	88.9	189909	2 CR735108	CR735108 Homo sapi
14	16	88.9	198047	2 CR376763	CR376763 Homo sapi
15	16	88.9	213402	2 BX901895	BX901895 Homo sapi
16	16	88.9	215185	2 BX927073	BX927073 Homo sapi
17	16	88.9	221924	2 CR388047	CR388047 Homo sapi
18	16	88.9	222876	2 AC068379	AC068379 Homo sapi
19	16	88.9	228022	2 BX927188	BX927188 Homo sapi

20	C	88.9	256581	2	CR394526	CR394526 Danio rer
21	16	83.3	29	6	AX528761	AX528761 Sequence
22	C	83.3	29	6	AX528762	AX528762 Sequence
23	15	83.3	62373	2	AC129972	AC129972 Felis cat
24	15	83.3	72483	2	AC101265	AC101265 Mus muscu
25	15	83.3	84720	2	AC115635	Continuation (5 of
26	15	83.3	110000	2	AC097780	AC097780 Rattus no
27	15	83.3	150670	2	AC143037	AC143037 Macaca mu
28	C	83.3	161787	2	AC105679	AC105679 Rattus no
29	15	83.3	211680	2	CR385082	CR385082 Danio rer
30	15	83.3	222685	2	AC130029	AC130029 Rattus no
31	15	83.3	235173	2	AC112325	AC112325 Rattus no
32	14	77.8	27	6	AX037200	AX037200 Sequence
33	14	77.8	27	6	AX037201	AX037201 Sequence
34	14	77.8	27	6	AX037202	AX037202 Sequence
35	14	77.8	27	6	AX037203	AX037203 Sequence
36	14	77.8	27	6	AX037204	AX037204 Sequence
37	14	77.8	27	6	AX037205	AX037205 Sequence
38	14	77.8	27	6	AX037206	AX037206 Sequence
39	14	77.8	27	6	AX037207	AX037207 Sequence
40	14	77.8	27	6	AX037208	AX037208 Sequence
41	14	77.8	27	6	AX037209	AX037209 Sequence
42	14	77.8	27	6	AX037210	AX037210 Sequence
43	14	77.8	27	6	AX037211	AX037211 Sequence
44	14	77.8	27	6	AX037212	AX037212 Sequence
45	14	77.8	27	6	AX037213	AX037213 Sequence
46	14	77.8	27	6	AX037214	AX037214 Sequence
47	14	77.8	27	6	AX037215	AX037215 Sequence
48	14	77.8	49739	2	AC100909	AC100909 Mus muscu
49	14	77.8	55662	2	AC100333	AC100333 Mus muscu
50	14	77.8	59918	2	AC100339	AC100339 Mus muscu
51	14	77.8	62676	2	AC125441	AC125441 Mus muscu
52	14	77.8	64345	2	AC062003	AC062003 Homo sapi
53	14	77.8	65174	2	AC025214	AC025214 Homo sapi
54	14	77.8	66795	2	AC100485	AC100485 Mus muscu
55	14	77.8	67822	2	AC027792	AC027792 Homo sapi
56	14	77.8	73882	2	AC102023	AC102023 Mus muscu
57	14	77.8	81233	2	AC021390	AC021390 Homo sapi
58	14	77.8	83547	2	AC022890	AC022890 Homo sapi
59	14	77.8	85440	2	AC034264	AC034264 Mus muscu
60	14	77.8	88940	2	AC138602	AC138602 Mus muscu
61	14	77.8	110000	2	AC095920	Continuation (4 of
62	14	77.8	110000	2	AC096315	Continuation (4 of
63	14	77.8	110000	2	AC112872	AC112872 Rattus no
64	14	77.8	133614	2	AC025433	AC025433 Homo sapi
65	14	77.8	150695	2	AC023576	AC023576 Homo sapi
66	14	77.8	151097	2	AC142149	AC142149 Rattus no
67	14	77.8	151448	2	AC074261	AC074261 Homo sapi
68	14	77.8	152420	2	BX927200	BX927200 Danio rer
69	14	77.8	154474	2	AC117546	AC117546 Mus muscu
70	14	77.8	154696	2	AC025626	AC025626 Homo sapi
71	14	77.8	158981	2	AC144021	AC144021 Macaca mu
72	14	77.8	159732	2	AL627241	AL627241 Rattus no
73	14	77.8	161829	2	AC027535	AC027535 Homo sapi
74	14	77.8	163732	2	BX908804	BX908804 Danio rer
75	14	77.8	173423	2	AC026082	AC026082 Homo sapi
76	14	77.8	173705	2	CR339046	CR339046 Danio rer
77	14	77.8	175056	2	AP002368	AP002368 Homo sapi
78	14	77.8	176565	2	AC144311	AC144311 Macaca mu
79	14	77.8	177380	2	AC151062	AC151062 Bos tauru
80	14	77.8	178472	2	AC125597	AC125597 Rattus no
81	14	77.8	180506	2	BX927248	BX927248 Danio rer
82	14	77.8	184869	2	AC015622	AC015622 Homo sapi
83	14	77.8	187478	2	BX927379	BX927379 Danio rer
84	14	77.8	188931	2	AC121358	AC121358 Mus muscu
85	14	77.8	189756	2	CR356244	CR356244 Danio rer
86	14	77.8	189787	2	CR293534	CR293534 Danio rer
87	14	77.8	191602	2	AC068920	AC068920 Homo sapi
88	14	77.8	194513	2	CR524482	CR524482 Danio rer
89	14	77.8	202456	2	AC150020	AC150020 Papio anu
90	14	77.8	210310	2	CR749177	CR749177 Danio rer
91	14	77.8	210481	2	CR376743	CR376743 Danio rer
92	14	77.8	213181	2	AC122949	AC122949 Rattus no

C 93	14	77.8	215479	2	AC125694	Rattus no	166	72.2	71396	2	AC100674	AC100674	Mus muscu
C 94	14	77.8	215604	2	CR376804	Danio rer	167	72.2	72969	2	AC026581	AC026581	AC026581
C 95	14	77.8	216013	2	BX927238	Danio rer	168	72.2	73173	2	AC025146	AC025146	AC025146
C 96	14	77.8	217309	2	BX901905	Danio rer	169	72.2	75974	2	AC090991	AC090991	AC090991
C 97	14	77.8	222632	2	AC106115	Rattus no	170	72.2	76113	2	AC023453	AC023453	AC023453
C 98	14	77.8	222961	2	CR382363	Danio rer	171	72.2	76856	2	AC021526	AC021526	AC021526
C 99	14	77.8	224370	2	AC097049	Rattus no	172	72.2	76856	2	AC021526	AC021526	AC021526
C 100	14	77.8	224022	2	BX927188	Danio rer	173	72.2	84680	2	AC015735	AC015735	AC015735
C 101	14	77.8	224022	2	BX927188	Danio rer	174	72.2	84680	2	AC015735	AC015735	AC015735
C 102	14	77.8	224990	2	AC107590	Rattus no	175	72.2	90108	2	AC021611	AC021611	AC021611
C 103	14	77.8	231366	2	BX950179	Danio rer	176	72.2	92726	6	AX658818	AX658818	AX658818
C 104	14	77.8	241934	2	AC110826	Rattus no	177	72.2	99591	2	AC013392	AC013392	AC013392
C 105	14	77.8	244594	2	AC131536	Rattus no	178	72.2	99591	2	AC013392	AC013392	AC013392
C 106	14	77.8	245318	2	AC112470	Rattus no	179	72.2	99630	2	AC142060	AC142060	AC142060
C 107	14	77.8	247436	2	AC117977	Rattus no	180	72.2	110000	2	AC091367	AC091367	AC091367
C 108	14	77.8	248358	2	CR812481	Danio rer	181	72.2	110000	2	AC107093	AC107093	AC107093
C 109	14	77.8	250161	2	AC122944	Rattus no	182	72.2	110000	2	AC130665	AC130665	AC130665
C 110	14	77.8	256409	2	AC127927	Rattus no	183	72.2	110000	2	AC145312	AC145312	AC145312
C 111	14	77.8	259219	2	AC111204	Rattus no	184	72.2	110000	2	AC055725	AC055725	AC055725
C 112	14	77.8	272053	2	AC128915	Rattus no	185	72.2	116585	2	AL139153	AL139153	AL139153
C 113	14	77.8	276376	2	AC106994	Rattus no	186	72.2	118540	2	AC013324	AC013324	AC013324
C 114	14	77.8	278311	2	AC095110	Rattus no	187	72.2	133669	2	AL155675	AL155675	AL155675
C 115	14	77.8	292735	2	AC132498	Rattus no	188	72.2	133669	2	AC007835	AC007835	AC007835
C 116	14	77.8	303281	2	AC097975	Rattus no	189	72.2	140714	2	AC007835	AC007835	AC007835
C 117	14	77.8	303894	2	AC105854	Rattus no	190	72.2	143907	2	AC141318	AC141318	AC141318
C 118	13	72.2	21	6	AX555067	Sequence	191	72.2	144832	2	AC141318	AC141318	AC141318
C 119	13	72.2	21	6	AX555067	Sequence	192	72.2	145009	2	AC141318	AC141318	AC141318
C 120	13	72.2	21	6	AX555067	Sequence	193	72.2	145555	2	AC141318	AC141318	AC141318
C 121	13	72.2	27	6	AX037233	Sequence	194	72.2	147552	2	AC141318	AC141318	AC141318
C 122	13	72.2	27	6	AX037217	Sequence	195	72.2	147552	2	AC141318	AC141318	AC141318
C 123	13	72.2	27	6	AX037218	Sequence	196	72.2	147552	2	AC141318	AC141318	AC141318
C 124	13	72.2	27	6	AX037219	Sequence	197	72.2	147552	2	AC141318	AC141318	AC141318
C 125	13	72.2	27	6	AX037220	Sequence	198	72.2	147552	2	AC141318	AC141318	AC141318
C 126	13	72.2	27	6	AX037221	Sequence	199	72.2	147552	2	AC141318	AC141318	AC141318
C 127	13	72.2	27	6	AX037222	Sequence	200	72.2	147552	2	AC141318	AC141318	AC141318
C 128	13	72.2	27	6	AX037223	Sequence	201	72.2	147552	2	AC141318	AC141318	AC141318
C 129	13	72.2	27	6	AX037224	Sequence	202	72.2	147552	2	AC141318	AC141318	AC141318
C 130	13	72.2	27	6	AX037225	Sequence	203	72.2	147552	2	AC141318	AC141318	AC141318
C 131	13	72.2	27	6	AX037226	Sequence	204	72.2	147552	2	AC141318	AC141318	AC141318
C 132	13	72.2	27	6	AX037227	Sequence	205	72.2	147552	2	AC141318	AC141318	AC141318
C 133	13	72.2	27	6	AX037228	Sequence	206	72.2	147552	2	AC141318	AC141318	AC141318
C 134	13	72.2	27	6	AX037229	Sequence	207	72.2	147552	2	AC141318	AC141318	AC141318
C 135	13	72.2	27	6	AX037230	Sequence	208	72.2	147552	2	AC141318	AC141318	AC141318
C 136	13	72.2	27	6	AX037231	Sequence	209	72.2	147552	2	AC141318	AC141318	AC141318
C 137	13	72.2	27	6	AX037232	Sequence	210	72.2	147552	2	AC141318	AC141318	AC141318
C 138	13	72.2	761	11	G06767	human STS	211	72.2	162821	2	AC115841	AC115841	AC115841
C 139	13	72.2	784	6	BD021433	Novel gen	212	72.2	164866	2	AC091102	AC091102	AC091102
C 140	13	72.2	30040	2	BD101371	Novel gen	213	72.2	165490	2	AC025326	AC025326	AC025326
C 141	13	72.2	41107	2	AC055941	Homo sapi	214	72.2	167797	2	AC151841	AC151841	AC151841
C 142	13	72.2	45685	2	AC087168	Homo sapi	215	72.2	173396	2	AC136059	AC136059	AC136059
C 143	13	72.2	51920	2	CER08A5	282281 Caenorhabdi	216	72.2	174938	2	AC141887	AC141887	AC141887
C 144	13	72.2	52867	2	AC021293	Homo sapi	217	72.2	176502	2	AC141887	AC141887	AC141887
C 145	13	72.2	56611	2	AC111183	Homo sapi	218	72.2	176100	2	AC141390	AC141390	AC141390
C 146	13	72.2	57736	2	AC101344	Mus muscu	219	72.2	181668	2	AC026644	AC026644	AC026644
C 147	13	72.2	58465	2	AC107514	Homo sapi	220	72.2	182741	2	AC120426	AC120426	AC120426
C 148	13	72.2	59550	2	AC100999	Mus muscu	221	72.2	183478	2	AC099123	AC099123	AC099123
C 149	13	72.2	60323	2	AC087334	Homo sapi	222	72.2	186294	2	AC021108	AC021108	AC021108
C 150	13	72.2	61582	2	AC100819	Rattus no	223	72.2	187114	2	AC026598	AC026598	AC026598
C 151	13	72.2	61837	2	AC100831	Homo sapi	224	72.2	187175	2	AC104579	AC104579	AC104579
C 152	13	72.2	62138	2	AC099931	Mus muscu	225	72.2	188789	2	AC090087	AC090087	AC090087
C 153	13	72.2	63831	2	AC100902	Mus muscu	226	72.2	191212	2	AC129856	AC129856	AC129856
C 154	13	72.2	64919	2	AC124644	Mus muscu	227	72.2	191372	2	CR548630	CR548630	CR548630
C 155	13	72.2	64962	2	AC100429	Mus muscu	228	72.2	192525	2	AC102475	AC102475	AC102475
C 156	13	72.2	65158	2	AC100675	Mus muscu	229	72.2	192707	2	EX465841	EX465841	EX465841
C 157	13	72.2	65199	2	AC090157	Homo sapi	230	72.2	193354	2	AC025152	AC025152	AC025152
C 158	13	72.2	66086	2	AC012249	Mus muscu	231	72.2	193605	2	AC026905	AC026905	AC026905
C 159	13	72.2	67572	2	AC120428	Homo sapi	232	72.2	199993	2	AC137386	AC137386	AC137386
C 160	13	72.2	67572	2	AC117553	Mus muscu	233	72.2	201302	2	AC120896	AC120896	AC120896
C 161	13	72.2	68315	2	AC117553	Mus muscu	234	72.2	201989	2	AC073169	AC073169	AC073169
C 162	13	72.2	68315	2	AC100130	Mus muscu	235	72.2	202091	2	AC150434	AC150434	AC150434
C 163	13	72.2	68732	2	AC091036	Homo sapi	236	72.2	204401	2	AC105524	AC105524	AC105524
C 164	13	72.2	68951	2	AC100065	Mus muscu	237	72.2	206860	2	AC025689	AC025689	AC025689
C 165	13	72.2	70557	2	AC090143	Homo sapi	238	72.2	207408	2	AC068618	AC068618	AC068618

C 239	13	72.2 211251	2	AC121029	Rattus no	312	12	66.7	18	6	AX803689	AX803689 Sequence
240	13	72.2 212116	2	AC029973	Homo sapi	313	12	66.7	18	6	AX803690	AX803690 Sequence
241	13	72.2 214434	2	AC125695	Rattus no	314	12	66.7	18	6	AX803691	AX803691 Sequence
242	13	72.2 214508	2	AC103532	Rattus no	C 315	12	66.7	20	6	A52659	A52659 Sequence 4
243	13	72.2 215373	2	AC128023	Rattus no	C 316	12	66.7	20	6	AR031224	AR031224 Sequence
C 244	13	72.2 215373	2	AC128023	Rattus no	C 317	12	66.7	20	6	AR145040	AR145040 Sequence
245	13	72.2 216915	2	AC125580	Rattus no	C 318	12	66.7	20	6	AR167021	AR167021 Sequence
246	13	72.2 220006	2	AC084068	Mus muscu	319	12	66.7	20	6	AR167022	AR167022 Sequence
C 247	13	72.2 220103	2	AC073781	Mus muscu	320	12	66.7	20	6	AR167023	AR167023 Sequence
248	13	72.2 226190	2	AC095562	Rattus no	321	12	66.7	20	6	AR167024	AR167024 Sequence
C 249	13	72.2 227164	2	AC103418	Rattus no	322	12	66.7	20	6	AR167027	AR167027 Sequence
250	13	72.2 229438	2	AC107408	Rattus no	323	12	66.7	20	6	E08298	E08298 Sequence of
C 251	13	72.2 229604	2	AC130102	Rattus no	324	12	66.7	20	6	E08299	E08299 Sequence of
C 252	13	72.2 230760	2	AC073714	Mus muscu	325	12	66.7	20	6	E08300	E08300 Sequence of
253	13	72.2 233796	2	AC130568	Rattus no	326	12	66.7	20	6	E08301	E08301 Sequence of
254	13	72.2 234079	2	AC099074	Rattus no	327	12	66.7	20	6	E44258	E44258 Oligo-DNA s
C 255	13	72.2 235182	2	AC099082	Rattus no	328	12	66.7	20	6	E44259	E44259 Oligo-DNA s
C 256	13	72.2 235888	2	AC096391	Rattus no	329	12	66.7	20	6	E44260	E44260 Oligo-DNA s
257	13	72.2 237346	2	AC120688	Rattus no	330	12	66.7	20	6	AR210676	AR210676 Sequence
258	13	72.2 237855	2	AC136663	Rattus no	331	12	66.7	20	6	AR210677	AR210677 Sequence
259	13	72.2 238135	2	AC102968	Rattus no	332	12	66.7	20	6	AR210678	AR210678 Sequence
260	13	72.2 238976	2	AC106187	Rattus no	333	12	66.7	20	6	AR210679	AR210679 Sequence
261	13	72.2 240200	2	AC116206	Rattus no	C 334	12	66.7	20	6	AR210682	AR210682 Sequence
C 262	13	72.2 240783	2	AC025587	Mus muscu	C 335	12	66.7	20	6	AR349613	AR349613 Sequence
263	13	72.2 241909	2	AC127399	Rattus no	C 336	12	66.7	20	6	AX555049	AX555049 Sequence
C 264	13	72.2 243122	2	AC134020	Rattus no	C 337	12	66.7	20	6	AX803655	AX803655 Sequence
C 265	13	72.2 243686	2	AC096430	Rattus no	338	12	66.7	20	6	AX803657	AX803657 Sequence
C 266	13	72.2 244105	2	AC098897	Rattus no	C 339	12	66.7	21	6	AX037298	AX037298 Sequence
C 267	13	72.2 246625	2	AC094293	Rattus no	C 340	12	66.7	21	6	AX037299	AX037299 Sequence
268	13	72.2 247141	2	AC129710	Rattus no	C 341	12	66.7	21	6	AX037300	AX037300 Sequence
C 269	13	72.2 247654	2	AC122658	Rattus no	C 342	12	66.7	21	6	AX037301	AX037301 Sequence
C 270	13	72.2 248880	2	AC111302	Rattus no	C 343	12	66.7	22	6	CO827605	CO827605 Sequence
271	13	72.2 249811	2	AC094988	Rattus no	C 344	12	66.7	22	6	KR349602	KR349602 Sequence
272	13	72.2 249967	2	AC128272	Rattus no	C 345	12	66.7	22	6	AX370745	AX370745 Sequence
C 273	13	72.2 250169	2	AC126583	Rattus no	C 346	12	66.7	22	6	AX556786	AX556786 Sequence
C 274	13	72.2 251856	2	AC146256	pan. txcg1	347	12	66.7	24	6	AR061891	AR061891 Sequence
C 275	13	72.2 253525	2	AC107349	Rattus no	348	12	66.7	24	6	AX803685	AX803685 Sequence
276	13	72.2 253746	2	AC135747	Rattus no	349	12	66.7	24	6	AX803692	AX803692 Sequence
C 277	13	72.2 254280	2	AC131372	Rattus no	350	12	66.7	24	6	AX803693	AX803693 Sequence
278	13	72.2 254839	2	AC103176	Rattus no	351	12	66.7	24	6	AX803694	AX803694 Sequence
279	13	72.2 255447	2	AC096032	Rattus no	352	12	66.7	24	6	AX803695	AX803695 Sequence
C 280	13	72.2 255598	2	AC107340	Rattus no	353	12	66.7	24	6	AX803696	AX803696 Sequence
C 281	13	72.2 256059	2	AC098893	Rattus no	354	12	66.7	24	6	AX803697	AX803697 Sequence
282	13	72.2 259921	2	AC114206	Rattus no	355	12	66.7	24	6	AX803698	AX803698 Sequence
283	13	72.2 261110	2	AC122626	Rattus no	356	12	66.7	24	6	AX803699	AX803699 Sequence
C 284	13	72.2 265566	2	AC123187	Rattus no	357	12	66.7	24	6	AX803700	AX803700 Sequence
C 285	13	72.2 266609	2	AC116237	Rattus no	358	12	66.7	24	6	AX803701	AX803701 Sequence
286	13	72.2 268694	2	AC095697	Rattus no	359	12	66.7	24	6	AX803702	AX803702 Sequence
C 287	13	72.2 270962	2	AC149067	Mus muscu	360	12	66.7	24	6	AX803703	AX803703 Sequence
288	13	72.2 283789	2	AC110840	Rattus no	C 361	12	66.7	25	6	AR349603	AR349603 Sequence
289	13	72.2 292715	2	AC098382	Rattus no	C 362	12	66.7	25	6	AR349611	AR349611 Sequence
290	13	72.2 295057	2	AC106987	Rattus no	C 363	12	66.7	26	6	AR167081	AR167081 Sequence
291	13	72.2 336873	2	AC073666	Mus muscu	364	12	66.7	26	6	BD135777	BD135777 Method of
292	13	72.2 346597	2	AC134498	Rattus no	C 365	12	66.7	26	6	E08297	E08297 5' noncodin
C 293	12	66.7 12	6	BD194958	Method of	C 366	12	66.7	26	6	AR210736	AR210736 Sequence
C 294	12	66.7 12	6	AR349607	Sequence	367	12	66.7	27	6	AX037234	AX037234 Sequence
C 295	12	66.7 12	6	AX003945	Sequence	368	12	66.7	27	6	AX037235	AX037235 Sequence
C 296	12	66.7 12	6	AX021569	Sequence	369	12	66.7	27	6	AX037236	AX037236 Sequence
C 297	12	66.7 12	6	AX803684	Sequence	370	12	66.7	27	6	AX037237	AX037237 Sequence
C 298	12	66.7 14	6	E08296	Sequence	371	12	66.7	27	6	AX037238	AX037238 Sequence
C 299	12	66.7 14	6	AR210735	Sequence	372	12	66.7	27	6	AX037239	AX037239 Sequence
300	12	66.7 16	6	AR234385	Sequence	373	12	66.7	27	6	AX037240	AX037240 Sequence
301	12	66.7 18	6	AX803676	Sequence	374	12	66.7	27	6	AX037241	AX037241 Sequence
302	12	66.7 18	6	AX803677	Sequence	375	12	66.7	27	6	AX037242	AX037242 Sequence
303	12	66.7 18	6	AX803678	Sequence	376	12	66.7	27	6	AX037243	AX037243 Sequence
304	12	66.7 18	6	AX803679	Sequence	377	12	66.7	27	6	AX037244	AX037244 Sequence
305	12	66.7 18	6	AX803680	Sequence	378	12	66.7	27	6	AX037245	AX037245 Sequence
306	12	66.7 18	6	AX803681	Sequence	379	12	66.7	27	6	AX037246	AX037246 Sequence
307	12	66.7 18	6	AX803682	Sequence	380	12	66.7	27	6	AX037247	AX037247 Sequence
308	12	66.7 18	6	AX803683	Sequence	381	12	66.7	27	6	AX037248	AX037248 Sequence
309	12	66.7 18	6	AX803684	Sequence	382	12	66.7	27	6	AX037249	AX037249 Sequence
310	12	66.7 18	6	AX803687	Sequence	383	12	66.7	27	6	AX037250	AX037250 Sequence
311	12	66.7 18	6	AX803688	Sequence	384	12	66.7	27	6	AX037251	AX037251 Sequence

385	12	66.7	27	6	AX037252	AX037252 Sequence	458	12	66.7	61	6	AX979339	AX979339 Sequence
386	12	66.7	27	6	AX037253	AX037253 Sequence	459	12	66.7	61	6	BD114198	BD114198 EST and e
387	12	66.7	27	6	AX037254	AX037254 Sequence	460	12	66.7	110	14	AY690640	AY690640 Hepatitis
388	12	66.7	27	6	AX037255	AX037255 Sequence	461	12	66.7	110	14	AY690641	AY690641 Hepatitis
389	12	66.7	27	6	AX037256	AX037256 Sequence	462	12	66.7	110	14	AY690642	AY690642 Hepatitis
390	12	66.7	27	6	AX037257	AX037257 Sequence	463	12	66.7	110	14	AY690643	AY690643 Hepatitis
391	12	66.7	27	6	AX037258	AX037258 Sequence	464	12	66.7	110	14	AY690644	AY690644 Hepatitis
392	12	66.7	27	6	AX037259	AX037259 Sequence	465	12	66.7	110	14	AY690645	AY690645 Hepatitis
393	12	66.7	27	6	AX037260	AX037260 Sequence	466	12	66.7	110	14	AY690646	AY690646 Hepatitis
394	12	66.7	27	6	AX037261	AX037261 Sequence	467	12	66.7	110	14	AY690647	AY690647 Hepatitis
395	12	66.7	27	6	AX037262	AX037262 Sequence	468	12	66.7	110	14	AY690648	AY690648 Hepatitis
396	12	66.7	27	6	AX037263	AX037263 Sequence	469	12	66.7	110	14	AY690649	AY690649 Hepatitis
397	12	66.7	27	6	AX037264	AX037264 Sequence	470	12	66.7	110	14	AY690650	AY690650 Hepatitis
398	12	66.7	27	6	AX037265	AX037265 Sequence	471	12	66.7	110	14	AY690651	AY690651 Hepatitis
399	12	66.7	27	6	AX037266	AX037266 Sequence	472	12	66.7	110	14	AY690652	AY690652 Hepatitis
400	12	66.7	27	6	AX037267	AX037267 Sequence	473	12	66.7	110	14	AY690653	AY690653 Hepatitis
401	12	66.7	27	6	AX037268	AX037268 Sequence	474	12	66.7	110	14	AY690654	AY690654 Hepatitis
402	12	66.7	27	6	AX037269	AX037269 Sequence	475	12	66.7	110	14	AY690655	AY690655 Hepatitis
403	12	66.7	27	6	AX037270	AX037270 Sequence	476	12	66.7	116	14	HPCCHA12	HPCCHA12
404	12	66.7	27	6	AX037271	AX037271 Sequence	477	12	66.7	121	11	G31188	G31188
405	12	66.7	27	6	AX037272	AX037272 Sequence	478	12	66.7	123	14	HPCUT6CLN	HPCUT6CLN
406	12	66.7	27	6	AX037273	AX037273 Sequence	479	12	66.7	125	14	HPCCHA10	HPCCHA10
407	12	66.7	27	6	AX037274	AX037274 Sequence	480	12	66.7	128	14	AY336151	AY336151
408	12	66.7	27	6	AX037275	AX037275 Sequence	481	12	66.7	137	14	HPCUT55CLN	HPCUT55CLN
409	12	66.7	27	6	AX037276	AX037276 Sequence	482	12	66.7	138	6	E10300	E10300
410	12	66.7	27	6	AX037277	AX037277 Sequence	483	12	66.7	140	6	E10301	E10301
411	12	66.7	27	6	AX037278	AX037278 Sequence	484	12	66.7	142	14	S72378	S72378 ('5' region)
412	12	66.7	27	6	AX037279	AX037279 Sequence	485	12	66.7	149	14	HPCCB13	HPCCB13
413	12	66.7	27	6	AX037280	AX037280 Sequence	486	12	66.7	149	14	HPCCB16	HPCCB16
414	12	66.7	27	6	AX037281	AX037281 Sequence	487	12	66.7	149	14	HPCCB18	HPCCB18
415	12	66.7	27	6	AX037282	AX037282 Sequence	488	12	66.7	149	14	HPCCB2	HPCCB2
416	12	66.7	27	6	AX037283	AX037283 Sequence	489	12	66.7	149	14	HPCCB8	HPCCB8
417	12	66.7	27	6	AX037284	AX037284 Sequence	490	12	66.7	151	14	AY145960	AY145960
418	12	66.7	27	6	AX037285	AX037285 Sequence	491	12	66.7	155	6	AR095003	AR095003 Sequence
419	12	66.7	27	6	AX037286	AX037286 Sequence	492	12	66.7	155	14	HCU56523	HCU56523
420	12	66.7	27	6	AX037287	AX037287 Sequence	493	12	66.7	155	14	HCU56524	HCU56524
421	12	66.7	27	6	AX037288	AX037288 Sequence	494	12	66.7	155	14	HCU56525	HCU56525
422	12	66.7	27	6	AX037289	AX037289 Sequence	495	12	66.7	155	14	HCU56529	HCU56529
423	12	66.7	27	6	AX037290	AX037290 Sequence	496	12	66.7	155	14	HCU56532	HCU56532
424	12	66.7	27	6	AX037291	AX037291 Sequence	497	12	66.7	155	14	HCU56531	HCU56531
425	12	66.7	27	6	AX037292	AX037292 Sequence	498	12	66.7	155	14	HCU56537	HCU56537
426	12	66.7	27	6	AX037293	AX037293 Sequence	499	12	66.7	155	14	HCU56539	HCU56539
427	12	66.7	27	6	AX037294	AX037294 Sequence	500	12	66.7	155	14	HCU56542	HCU56542
428	12	66.7	27	6	AX037295	AX037295 Sequence	501	12	66.7	155	14	HCU56543	HCU56543
429	12	66.7	27	6	AX037296	AX037296 Sequence	502	12	66.7	155	14	HCU56536	HCU56536
430	12	66.7	27	6	AX037297	AX037297 Sequence	503	12	66.7	155	14	HCU56538	HCU56538
431	12	66.7	27	6	AX528763	AX528763 Sequence	504	12	66.7	155	14	HCU56537	HCU56537
432	12	66.7	27	6	AX528764	AX528764 Sequence	505	12	66.7	155	14	HCU56538	HCU56538
433	12	66.7	28	6	BD135776	BD135776 Method of	506	12	66.7	155	14	HCU56540	HCU56540
434	12	66.7	30	6	BD142100	BD142100 A method	507	12	66.7	155	14	HCU56541	HCU56541
435	12	66.7	30	6	BD157778	BD157778 Method of	508	12	66.7	155	14	HCU56542	HCU56542
436	12	66.7	39	6	AR127648	AR127648 Sequence	509	12	66.7	155	14	HCU56543	HCU56543
437	12	66.7	39	6	BD183019	BD183019 New funct	510	12	66.7	155	14	HCU56544	HCU56544
438	12	66.7	39	6	BD183019	BD183019 New funct	511	12	66.7	155	14	HCU56545	HCU56545
439	12	66.7	45	6	CQ759592	CQ759592 Sequence	512	12	66.7	155	14	HCU56546	HCU56546
440	12	66.7	46	6	AR398612	AR398612 Sequence	513	12	66.7	155	14	HCU56547	HCU56547
441	12	66.7	47	6	AR290862	AR290862 Sequence	514	12	66.7	155	14	HCU56548	HCU56548
442	12	66.7	48	6	BD138671	BD138671 Specific	515	12	66.7	155	14	HCU56549	HCU56549
443	12	66.7	48	6	BD138672	BD138672 Specific	516	12	66.7	155	14	HCU56550	HCU56550
444	12	66.7	48	6	AX003946	AX003946 Sequence	517	12	66.7	155	14	HCU56551	HCU56551
445	12	66.7	48	6	AX003947	AX003947 Sequence	518	12	66.7	155	14	HCU56552	HCU56552
446	12	66.7	48	6	AX021565	AX021565 Sequence	519	12	66.7	155	14	HCU56553	HCU56553
447	12	66.7	48	6	AX021566	AX021566 Sequence	520	12	66.7	155	14	HCU56554	HCU56554
448	12	66.7	48	6	AX021567	AX021567 Sequence	521	12	66.7	155	14	HCU56555	HCU56555
449	12	66.7	48	6	AX021575	AX021575 Sequence	522	12	66.7	155	14	HCU56556	HCU56556
450	12	66.7	48	6	AX021576	AX021576 Sequence	523	12	66.7	155	14	HCU56557	HCU56557
451	12	66.7	48	6	AX021631	AX021631 Sequence	524	12	66.7	155	14	HCU56558	HCU56558
452	12	66.7	50	6	BD006786	BD006786 Method fo	525	12	66.7	156	14	AY145906	AY145906
453	12	66.7	50	6	BD092003	BD092003 Potential	526	12	66.7	156	14	HCU56561	HCU56561
454	12	66.7	51	6	CQ007090	CQ007090 Sequence	527	12	66.7	156	14	HCU56562	HCU56562
455	12	66.7	51	6	CQ007443	CQ007443 Sequence	528	12	66.7	156	14	HPCCHALL	HPCCHALL
456	12	66.7	61	6	AR418645	AR418645 Sequence	529	12	66.7	157	14	HPCCHNCRAX	HPCCHNCRAX
457	12	66.7	61	6	AR418645	AR418645 Sequence	530	12	66.7	157	14	HPCCHNCRAX	HPCCHNCRAX

C 531	12	66.7	159	14	AF506625	AF506625 Hepatitis	C 604	12	66.7	176	14	AY145904	AY145904 Hepatitis
C 532	12	66.7	160	14	AY145915	AY145915 Hepatitis	C 605	12	66.7	176	14	AY145905	AY145905 Hepatitis
C 533	12	66.7	160	14	AY146043	AY146043 Hepatitis	C 606	12	66.7	176	14	AY145925	AY145925 Hepatitis
C 534	12	66.7	161	10	S45855	S45855 macrophage	C 607	12	66.7	176	14	AY145947	AY145947 Hepatitis
C 535	12	66.7	161	14	AY145979	AY145979 Hepatitis	C 608	12	66.7	176	14	HCV6329	HCV6329 Hepatitis
C 536	12	66.7	161	14	AY145995	AY145995 Hepatitis	C 609	12	66.7	176	14	HPC58CRAC	HPC58CRAC Hepatitis
C 537	12	66.7	161	14	AY146018	AY146018 Hepatitis	C 610	12	66.7	176	14	HPCUT34CTLN	HPCUT34CTLN Hepatitis
C 538	12	66.7	162	14	AY145983	AY145983 Hepatitis	C 611	12	66.7	176	14	HPCUT34CTLN	HPCUT34CTLN Hepatitis
C 539	12	66.7	162	14	AY145985	AY145985 Hepatitis	C 612	12	66.7	176	14	HPCUT34CTLN	HPCUT34CTLN Hepatitis
C 540	12	66.7	162	14	AY145989	AY145989 Hepatitis	C 613	12	66.7	177	6	A39089	A39089 Sequence 61
C 541	12	66.7	163	14	AF506690	AF506690 Hepatitis	C 614	12	66.7	177	6	A39095	A39095 Sequence 67
C 542	12	66.7	163	14	AY145986	AY145986 Hepatitis	C 615	12	66.7	177	6	A39096	A39096 Sequence 68
C 543	12	66.7	163	14	AY145991	AY145991 Hepatitis	C 616	12	66.7	177	6	A39097	A39097 Sequence 69
C 544	12	66.7	163	14	AY146016	AY146016 Hepatitis	C 617	12	66.7	177	6	A39098	A39098 Sequence 70
C 545	12	66.7	163	14	HPCUT8CLN	HPCUT8CLN	C 618	12	66.7	177	6	A39100	A39100 Sequence 72
C 546	12	66.7	164	14	AY145908	AY145908 Hepatitis	C 619	12	66.7	177	6	A39101	A39101 Sequence 73
C 547	12	66.7	165	14	AY145918	AY145918 Hepatitis	C 620	12	66.7	177	6	A39102	A39102 Sequence 74
C 548	12	66.7	165	14	AY145929	AY145929 Hepatitis	C 621	12	66.7	177	6	A39103	A39103 Sequence 75
C 549	12	66.7	165	14	AY145954	AY145954 Hepatitis	C 622	12	66.7	177	6	A39104	A39104 Sequence 76
C 550	12	66.7	165	14	AY145961	AY145961 Hepatitis	C 623	12	66.7	177	6	A39105	A39105 Sequence 77
C 551	12	66.7	165	14	AY146002	AY146002 Hepatitis	C 624	12	66.7	177	6	A39106	A39106 Sequence 78
C 552	12	66.7	165	14	AY146035	AY146035 Hepatitis	C 625	12	66.7	177	6	A39107	A39107 Sequence 79
C 553	12	66.7	165	14	AY146036	AY146036 Hepatitis	C 626	12	66.7	177	6	A39108	A39108 Sequence 80
C 554	12	66.7	165	14	AY146039	AY146039 Hepatitis	C 627	12	66.7	177	6	AR063423	AR063423 Sequence
C 555	12	66.7	166	14	AY146029	AY146029 Hepatitis	C 628	12	66.7	177	6	AR063429	AR063429 Sequence
C 556	12	66.7	166	14	AY146048	AY146048 Hepatitis	C 629	12	66.7	177	6	AR063430	AR063430 Sequence
C 557	12	66.7	167	14	AY145942	AY145942 Hepatitis	C 630	12	66.7	177	6	AR063431	AR063431 Sequence
C 558	12	66.7	167	14	AY146017	AY146017 Hepatitis	C 631	12	66.7	177	6	AR063432	AR063432 Sequence
C 559	12	66.7	167	14	AY146065	AY146065 Hepatitis	C 632	12	66.7	177	6	AR063434	AR063434 Sequence
C 560	12	66.7	167	14	AY146066	AY146066 Hepatitis	C 633	12	66.7	177	6	AR063435	AR063435 Sequence
C 561	12	66.7	169	14	AY145988	AY145988 Hepatitis	C 634	12	66.7	177	6	AR063436	AR063436 Sequence
C 562	12	66.7	169	14	AY146013	AY146013 Hepatitis	C 635	12	66.7	177	6	AR063437	AR063437 Sequence
C 563	12	66.7	169	14	AY146033	AY146033 Hepatitis	C 636	12	66.7	177	6	AR063438	AR063438 Sequence
C 564	12	66.7	170	14	AY145910	AY145910 Hepatitis	C 637	12	66.7	177	6	AR063439	AR063439 Sequence
C 565	12	66.7	170	14	AY145952	AY145952 Hepatitis	C 638	12	66.7	177	6	AR063440	AR063440 Sequence
C 566	12	66.7	170	14	AY146041	AY146041 Hepatitis	C 639	12	66.7	177	6	AR063441	AR063441 Sequence
C 567	12	66.7	170	14	AY146044	AY146044 Hepatitis	C 640	12	66.7	177	6	AR063442	AR063442 Sequence
C 568	12	66.7	171	14	AF506640	AF506640 Hepatitis	C 641	12	66.7	177	6	AR123614	AR123614 Sequence
C 569	12	66.7	171	14	AF506646	AF506646 Hepatitis	C 642	12	66.7	177	6	AR123620	AR123620 Sequence
C 570	12	66.7	171	14	AF506650	AF506650 Hepatitis	C 643	12	66.7	177	6	AR123621	AR123621 Sequence
C 571	12	66.7	171	14	AF506665	AF506665 Hepatitis	C 644	12	66.7	177	6	AR123622	AR123622 Sequence
C 572	12	66.7	171	14	AF506668	AF506668 Hepatitis	C 645	12	66.7	177	6	AR123623	AR123623 Sequence
C 573	12	66.7	171	14	AF506675	AF506675 Hepatitis	C 646	12	66.7	177	6	AR123625	AR123625 Sequence
C 574	12	66.7	171	14	AF506691	AF506691 Hepatitis	C 647	12	66.7	177	6	AR123626	AR123626 Sequence
C 575	12	66.7	171	14	AY145919	AY145919 Hepatitis	C 648	12	66.7	177	6	AR123627	AR123627 Sequence
C 576	12	66.7	171	14	AY145921	AY145921 Hepatitis	C 649	12	66.7	177	6	AR123628	AR123628 Sequence
C 577	12	66.7	171	14	AY145923	AY145923 Hepatitis	C 650	12	66.7	177	6	AR123629	AR123629 Sequence
C 578	12	66.7	171	14	AY145941	AY145941 Hepatitis	C 651	12	66.7	177	6	AR123630	AR123630 Sequence
C 579	12	66.7	171	14	AY146063	AY146063 Hepatitis	C 652	12	66.7	177	6	AR123631	AR123631 Sequence
C 580	12	66.7	172	14	AF506660	AF506660 Hepatitis	C 653	12	66.7	177	6	AR123632	AR123632 Sequence
C 581	12	66.7	172	14	AY146019	AY146019 Hepatitis	C 654	12	66.7	177	6	AR123633	AR123633 Sequence
C 582	12	66.7	172	14	AY146020	AY146020 Hepatitis	C 655	12	66.7	177	6	AR123635	AR123635 Sequence
C 583	12	66.7	172	14	AY146023	AY146023 Hepatitis	C 656	12	66.7	177	6	AR123636	AR123636 Sequence
C 584	12	66.7	172	14	AY146032	AY146032 Hepatitis	C 657	12	66.7	177	6	AR267361	AR267361 Sequence
C 585	12	66.7	172	14	AY146034	AY146034 Hepatitis	C 658	12	66.7	177	6	AR267363	AR267363 Sequence
C 586	12	66.7	173	14	AF506676	AF506676 Hepatitis	C 659	12	66.7	177	6	AR267364	AR267364 Sequence
C 587	12	66.7	173	14	AY145949	AY145949 Hepatitis	C 660	12	66.7	177	6	AR267366	AR267366 Sequence
C 588	12	66.7	174	14	AF506673	AF506673 Hepatitis	C 661	12	66.7	177	6	AR267367	AR267367 Sequence
C 589	12	66.7	174	14	AF506685	AF506685 Hepatitis	C 662	12	66.7	177	6	AR267368	AR267368 Sequence
C 590	12	66.7	174	14	AF506692	AF506692 Hepatitis	C 663	12	66.7	177	6	AR267369	AR267369 Sequence
C 591	12	66.7	174	14	AF506693	AF506693 Hepatitis	C 664	12	66.7	177	6	AR267370	AR267370 Sequence
C 592	12	66.7	174	14	AY145917	AY145917 Hepatitis	C 665	12	66.7	177	6	AR267371	AR267371 Sequence
C 593	12	66.7	174	14	AY145946	AY145946 Hepatitis	C 666	12	66.7	177	6	AR267372	AR267372 Sequence
C 594	12	66.7	174	14	AY146047	AY146047 Hepatitis	C 667	12	66.7	177	6	AR267373	AR267373 Sequence
C 595	12	66.7	174	14	AY146061	AY146061 Hepatitis	C 668	12	66.7	177	6	AR267374	AR267374 Sequence
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## ALIGNMENTS

RESULT 1  
LOCUS AX803675 18 bp DNA linear PAT 24-NOV-2003  
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ACCESSION AX803675  
VERSION AX803675.1 GI:38502217  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
HYPHON: INC. (US)

1 Frank, B.L., Goodchild, J., Hamlin, H.A., Kulkarni, R.E.,  
Roberts, P.C., Roberts, N.A., Walther, D.M. and Wolfe, J.L.  
Oligonucleotides specific for Hepatitis C Virus  
Patent: EP 1331267-A 38 30-JUL-2003;  
HYPHON: INC. (US)

FEATURES  
source 1.18  
location/Qualifiers  
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/db\_xref="taxon:32644"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 0.35;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGGTCCTCGAGNNNNNN 18

RESULT 2  
LOCUS AX803704 24 bp DNA linear PAT 24-NOV-2003  
DEFINITION Sequence 67 from Patent EP1331267.

ACCESSION AX803704  
VERSION AX803704.1 GI:38502246  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
HYPHON: INC. (US)

## ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 24;  
Best Local Similarity 88.9%; Pred. No. 0.34;  
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DEFINITION Homo sapiens chromosome 15 clone RP11-33819 map 15, LOW-PASS  
SEQUENCE SAMPLING.  
ACCESSION AC026845  
VERSION AC026845.3 GI:7677910  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
HYPHON: INC. (US)

1 Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 15, clone RP11-33819  
Unpublished  
2 (bases 1 to 65130)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Bassten, V., Beda, F.,  
Boguslavsky, L., Bouckhagalter, E., Brown, A., Burkett, G.,  
Campopiano, A., Castle, A., Chepelev, Y., Colangelo, M., Collins, S.,  
Collins, A., Cooke, P., DeArnell, K., Dewar, K., Diaz, J.S.,  
Dodge, S., Donnelly, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,  
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hagos, B., Heath, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,  
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lechoczy, J.,  
Levine, R., Liu, C., Liu, G., Locke, R., MacDonald, P., Margulis, N.,  
McCarthy, M., McEwan, P., McKernan, K., McPherson, R.,  
Meidum, J., Menes, L., Milova, T., Miranda, C., Miura, J.,  
Murphy, T., Naylor, D., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,  
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tamas, J.,  
Tessier, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,  
Vasiliou, H., Viel, R., Vo, A., Wilson, B., Wu, K., Wyman, D., Ye, W.J.,  
Young, G., Zaitoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (24-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 2, 2000 this sequence version replaced gi:7549706.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html



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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 18785
Center clone name: 338_I_9

* NOTE: This record contains 76 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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4247 4246: gap of 100 bp
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5115 5114: gap of 100 bp
5869 5868: contig of 754 bp in length
5969 5968: gap of 100 bp
6725 6724: contig of 756 bp in length
6825 6824: gap of 100 bp
7582 7581: contig of 757 bp in length
7682 7681: gap of 100 bp
8435 8434: contig of 753 bp in length
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9298 9297: contig of 763 bp in length
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12829 12828: gap of 100 bp
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*      55526      55625: gap of 100 bp
*      55626      56395: contig of 770 bp in length
*      56396      56495: gap of 100 bp
*      56496      57254: contig of 759 bp in length
*      57255      57354: gap of 100 bp
*      57355      58130: contig of 776 bp in length
*      58131      58230: gap of 100 bp
*      58231      59030: contig of 800 bp in length

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Best Local Similarity 87.5%: Pred. No. 5.2;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db      2404      GGTCTGTGAGNNNNNN 2419

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VERSION      CR354556.4      GI:4573955
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ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
      Cypriniformes; Cyprinidae; Danio.
      1 (bases 1 to 132013)
McLay, K.
Direct Submission
Submitted (22-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 24, 2004 this sequence version replaced gi:45581026.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: ZK100J22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 127952 bases at least Q40
Consensus quality: 129001 bases at least Q30
Insert size: 131013; sum-of-contigs
Insert size: 140547; 0.9% error; agarose-fp
Quality coverage: 9.49x in Q20 bases; sum-of-contigs Quality
Coverage: 9.02x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1      11176: contig of 11176 bp in length
*      11177      11276: gap of 100 bp
*      11277      27584: contig of 16308 bp in length
*      27585      27684: gap of 100 bp
*      27685      47675: contig of 19991 bp in length
*      47676      47775: gap of 100 bp

```

```

*      47776      72579: contig of 24804 bp in length
*      72580      72679: gap of 100 bp
*      72680      79964: contig of 7285 bp in length
*      79965      80064: gap of 100 bp
*      80065      82655: contig of 2601 bp in length
*      82656      82765: gap of 100 bp
*      82766      93308: contig of 10543 bp in length
*      93309      93408: gap of 100 bp
*      93409      98627: contig of 5219 bp in length
*      98628      98727: gap of 100 bp
*      98728      117865: contig of 19137 bp in length
*      117865      117964: gap of 100 bp
*      117965      129528: contig of 11564 bp in length
*      129529      129628: gap of 100 bp
*      129629      132013: contig of 2385 bp in length.

FEATURES
source
1..132013
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-100J22"
/clone_1b="Daniokey"
1..11176
/note="assembly fragment:00588
fragment chain:1"
11277..27584
/note="assembly fragment:01160
fragment chain:1"
27685..47675
/note="assembly fragment:00850
fragment chain:1"
47776..72579
/note="assembly fragment:01925
fragment chain:1"
72680..79964
/note="assembly fragment:00217
fragment chain:1"
80065..82665
/note="assembly fragment:00041
fragment chain:1"
82766..93308
/note="assembly fragment:00318
fragment chain:2"
93409..98627
/note="assembly fragment:00149
fragment chain:2"
98728..117864
/note="assembly fragment:01528
fragment chain:2"
117965..129528
/note="assembly fragment:00428
fragment chain:2"
129629..132013
/note="assembly fragment:00052.0"

ORIGIN
Query Match      88.9%: Score 16; DB 2; Length 132013;
Best Local Similarity 87.5%: Pred. No. 5.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3      GGUCCUGAGAGNNNNNN 18
Db      27694      GGTCTGTGAGNNNNNN 27679

RESULT 5
AC074014/c      132597 bp      DNA      linear      HTG 10-JUL-2000
LOCUS      Homo sapiens chromosome 10 clone RP11-113N2, *** SEQUENCING IN
DEFINITION      PROGRESS ***, 49 unordered pieces.
ACCESSION      AC074014
VERSION      AC074014.1      GI:8990970
KEYWORDS      HTG; HTGS_PHASE1.

```

SOURCE  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 132597)  
JOURNAL The sequence of Homo sapiens clone  
REFERENCE 2 (bases 1 to 132597)  
AUTHORS Waterston, R. H.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
Project information -----  
Center project name: H\_NH0113N02  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 49 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1005: contig of 1005 bp in length  
1006 1105: gap of unknown length  
1106 2565: contig of 1460 bp in length  
2566 2665: gap of unknown length  
2666 4049: contig of 1384 bp in length  
4050 4149: gap of unknown length  
4150 5338: contig of 1189 bp in length  
5339 5438: gap of unknown length  
5439 6956: contig of 1518 bp in length  
6957 7056: gap of unknown length  
7057 8352: contig of 1295 bp in length  
8353 8451: gap of unknown length  
8452 10097: contig of 1646 bp in length  
10098 10197: gap of unknown length  
10198 11921: contig of 1724 bp in length  
11922 12021: gap of unknown length  
12022 13539: contig of 1518 bp in length  
13540 13639: gap of unknown length  
13640 15191: contig of 1552 bp in length  
15192 15291: gap of unknown length  
15292 16374: contig of 1083 bp in length  
16375 16474: gap of unknown length  
16475 17665: contig of 1191 bp in length  
17666 17765: gap of unknown length  
17766 19279: contig of 1514 bp in length  
19280 19379: gap of unknown length  
19380 21165: contig of 1786 bp in length  
21166 21265: gap of unknown length  
21266 23667: contig of 2402 bp in length  
23668 23767: gap of unknown length  
23768 25010: contig of 1243 bp in length  
25011 25110: gap of unknown length  
25111 26546: contig of 1436 bp in length  
26547 26646: gap of unknown length  
26647 28807: contig of 2161 bp in length  
28808 28907: gap of unknown length  
28908 30678: contig of 1771 bp in length  
30679 30778: gap of unknown length  
30779 32558: contig of 1780 bp in length  
32559 32658: gap of unknown length  
32659 35293: contig of 2635 bp in length  
35294 35393: gap of unknown length  
35394 37213: contig of 1820 bp in length

37214 37313: gap of unknown length  
37314 38852: contig of 1539 bp in length  
38853 38952: gap of unknown length  
38953 40925: contig of 1973 bp in length  
40926 41025: gap of unknown length  
41026 43907: contig of 2882 bp in length  
43908 44007: gap of unknown length  
44008 45759: contig of 1752 bp in length  
45760 45859: gap of unknown length  
45860 48247: contig of 2388 bp in length  
48248 48347: gap of unknown length  
48348 50917: contig of 2570 bp in length  
50918 51017: gap of unknown length  
51018 54604: contig of 3587 bp in length  
54605 54704: gap of unknown length  
54705 57091: contig of 2387 bp in length  
57092 57191: gap of unknown length  
57192 59589: contig of 2398 bp in length  
59590 59689: gap of unknown length  
59690 62419: contig of 2730 bp in length  
62420 62519: gap of unknown length  
62520 63834: contig of 1315 bp in length  
63835 63934: gap of unknown length  
63935 65827: contig of 1893 bp in length  
65828 65927: gap of unknown length  
65928 67980: contig of 2053 bp in length  
67981 68080: gap of unknown length  
68081 70135: contig of 2055 bp in length  
70136 70235: gap of unknown length  
70236 73759: contig of 3524 bp in length  
73760 73859: gap of unknown length  
73860 77360: contig of 3501 bp in length  
77361 77460: gap of unknown length  
77461 80240: contig of 2780 bp in length  
80241 80340: gap of unknown length  
80341 83980: contig of 3640 bp in length  
83981 84080: gap of unknown length  
84081 88936: contig of 4856 bp in length  
88937 89036: gap of unknown length  
89037 93965: contig of 4929 bp in length  
93966 94065: gap of unknown length  
94066 99061: contig of 4996 bp in length  
99062 99161: gap of unknown length  
99162 103192: contig of 4031 bp in length  
103193 103292: gap of unknown length  
103293 108582: contig of 5290 bp in length  
108583 108682: gap of unknown length  
108683 114011: contig of 5329 bp in length  
114012 114111: gap of unknown length  
114112 119936: contig of 5825 bp in length  
119937 120036: gap of unknown length  
120037 126621: contig of 6585 bp in length  
126622 126721: gap of unknown length  
126722 126722 132597: contig of 5876 bp in length.

## FEATURES

source  
1..132597  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="10"  
/clone="RP11-113N2"

## ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 132597;  
Best local Similarity 87.5%; Pred. No. 5.1;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

## QY

3 GGUCUGGAGNNNNN 18

## DB

10207 GGTCCTGAGNNNNN 10192

## RESULT 6

LOCUS	BX927307/c				
DEFINITION	Danio rerio clone DKEY-93M12, *** SEQUENCING IN PROGRESS ***, 8				
ACCESSION	BX927307	155605 bp	DNA	linear	HTG 29-JAN-2004
VERSION	BX927307.1	GI:41392964			
KEYWORDS	HTG; HTGS PHASE1.				
SOURCE	Danio rerio (zebrafish)				
ORGANISM	Danio rerio				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. 1 (bases 1 to 155605) McLay, K.				
AUTHORS	Submitted (29-JUN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zf1sh-help@sanger.ac.uk Clonerequests@clonerequests.sanger.ac.uk				
TITLE	Genome Center				
JOURNAL	Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: zf1sh-help@sanger.ac.uk				
COMMENT	Project Information ----- Center project name: zk93M12 ----- Summary Statistics Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 152630 bases at least Q40 Consensus quality: 153155 bases at least Q40 Consensus quality: 153593 bases at least Q20 Insert size: 154905; sum-of-contigs Insert size: 175125; 3.3% error; agarose-gel Quality coverage: 11.48x in Q20 bases; sum-of-contigs Quality coverage: 10.25x in Q20 bases; agarose-gel ----- NOTE: This is a 'working draft' sequence. It currently * consists of 8 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. 1 1 36395: contig of 36395 bp in length 36396 36495: gap of 100 bp 36496 45440: contig of 8945 bp in length 45441 45540: gap of 100 bp 45541 73268: contig of 27728 bp in length 73269 73367: gap of 100 bp 73368 78367: contig of 4999 bp in length 78368 78467: gap of 100 bp 78468 95723: contig of 17256 bp in length 95724 95823: gap of 100 bp 95824 98390: contig of 2567 bp in length 98391 98490: gap of 100 bp 98491 104560: contig of 6070 bp in length 104561 104661: gap of 100 bp 104661 155605: contig of 50945 bp in length. Location/Qualifiers 1. 155605 /organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" /clone="DKEY-93M12" /clone_lib="DanioKey" 1. 36395 /note="assembly_frgment:01036 frgment_chain:1" 36496 . 45440 /note="assembly_frgment:00150 frgment_chain:1" 45541 . 73268				

```

/note="assembly_fragment:00527
fragment_chain:1"
misc_feature
73369..78367
/note="assembly_fragment:00037
fragment_chain:1"
78468..95723
/note="assembly_fragment:00309
fragment_chain:1"
95824..98390
/note="assembly_fragment:00024"
98491..104560
/note="assembly_fragment:00082.0"
104661..155605
/note="assembly_fragment:01671"

ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 155605;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      3  GGUCCUGAGAGNNNNNN 18
      |||:|||||
Db      45550  GGTCCTGAGAGNNNNN 45535

RESULT 7
LOCUS      CR752651      162408 bp      DNA      linear      HTG 26-AUG-2004
DEFINITION      Danio rerio clone CH211-167J6, WORKING DRAFT SEQUENCE, 11 unordered
ACCESSION      CR752651
VERSION      CR752651.2  GI:51571682
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 162408)
Burton, J.
Direct Submission
Submitted (24-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
fish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Aug 26, 2004 this sequence version replaced gi:51534192.

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: ZC167J6
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 158163 bases at least Q40
Consensus quality: 159103 bases at least Q30
Consensus quality: 159748 bases at least Q20
Insert size: 161308; sum-of-contigs
Insert size: 160976; 2.4% error; agarose-fp
Quality coverage: 6.33x in Q20 bases; sum-of-contigs Quality
coverage: 7.91x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 20585: contig of 20585 bp in length
* 20586 20685: gap of 100 bp

```

\* 20686 34543: contig of 13858 bp in length  
\* 34544 34643: gap of 100 bp  
\* 34644 62759: contig of 2816 bp in length  
\* 62760 62859: gap of 100 bp  
\* 126983 127082: contig of 64123 bp in length  
\* 127083 130122: contig of 3040 bp in length  
\* 130123 130222: gap of 100 bp  
\* 130223 132710: contig of 2488 bp in length  
\* 132711 132893: gap of 183 bp  
\* 132894 132897: contig of 4 bp in length  
\* 132898 149121: contig of 16124 bp in length  
\* 149122 149221: gap of 100 bp  
\* 149222 151297: contig of 2076 bp in length  
\* 151298 151397: gap of 100 bp  
\* 151398 155131: contig of 3734 bp in length  
\* 155132 155231: gap of 100 bp  
\* 155232 162408: contig of 7177 bp in length.  
\* Location/Qualifiers

FEATURES  
Source 1.162408  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="CH211-16706"  
/clone\_lib="CHORI-211"  
1.20565  
/note="assembly\_fragment:00681"  
fragment\_chain:1  
20686..34543  
/note="assembly\_fragment:00297"  
fragment\_chain:1  
clone\_end:77  
vector\_side:left  
34644..62759  
/note="assembly\_fragment:00951"  
fragment\_chain:1  
62860..126982  
/note="assembly\_fragment:01369"  
fragment\_chain:1  
127083..130122  
/note="assembly\_fragment:00187"  
fragment\_chain:1  
130223..132897  
/note="assembly\_fragment:00173"  
fragment\_chain:1  
132998..149121  
/note="assembly\_fragment:00485"  
fragment\_chain:1  
clone\_end:86  
vector\_side:right  
149222..151297  
/note="assembly\_fragment:00130"  
151398..155131  
/note="assembly\_fragment:00162"  
155232..162408  
/note="assembly\_fragment:00210"

ORIGIN  
Query Match 88.9%; Score 16; DB 2; Length 162408;  
Best Local Similarity 87.5%; Pred. No. 5.1;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 3 GGUCCTGAGAGNNNNNN 18  
Db 130113 GGTCCTGAGAGNNNNNN 130128

RESULT 8  
CR774197/c CR774197 166622 bp DNA linear HTG 16-SEP-2004  
LOCUS Danio rerio clone DKEX-279J3, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 5  
DEFINITION unordered pieces.

ACCESSION CR774197  
VERSION CR774197.1 GI:52213982  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 166622)  
REFERENCE  
AUTHORS McClay, K.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk  
COMMENT  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: ZK279J3  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 164818 bases at least Q40  
Consensus quality: 165177 bases at least Q30  
Consensus quality: 165623 bases at least Q20  
Insert size: 166222; sum-of-contigs  
Insert size: 169536; 2.7% error; agarose-fp  
Quality coverage: 7.81x in Q20 bases; sum-of-contigs Quality coverage: 7.73x in Q20 bases; agarose-fp

\*\*\*\*\* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. \* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. \*  
1 13522: contig of 13522 bp in length  
\* 13523 13622: gap of 100 bp  
\* 13623 90740: contig of 77118 bp in length  
\* 90741 90840: gap of 100 bp  
\* 90841 132601: contig of 41761 bp in length  
\* 132602 132701: gap of 100 bp  
\* 132702 139994: contig of 7293 bp in length  
\* 139995 140094: gap of 100 bp  
\* 140095 166622: contig of 26528 bp in length.  
Location/Qualifiers

FEATURES  
Source 1.166622  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-279J3"  
/clone\_lib="DanioKey"  
1.13522  
/note="assembly\_fragment:00072"  
fragment\_chain:1  
13623..90740  
/note="assembly\_fragment:00972"  
fragment\_chain:1  
90841..132601  
/note="assembly\_fragment:00561"  
fragment\_chain:1  
132702..139994  
/note="assembly\_fragment:00019"  
140095..166622  
/note="assembly\_fragment:00207.0"

ORIGIN  
Query Match 88.9%; Score 16; DB 2; Length 166622;  
Best Local Similarity 87.5%; Pred. No. 5.1;

```

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 GGUCCUGAGANNNNNN 18
Db 90850 GGTCTCGAGANNNNNN 90835

RESULT 9
CR812468/c 172578 bp DNA linear HTG 27-SEP-2004
LOCUS Danio rerio clone CH211-252P18, WORKING DRAFT SEQUENCE, 9 unordered
DEFINITION pieces.
ACCESSION CR812468.2 GI:52748667
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Danio rerio (zebrafish)
SOURCE Danio rerio
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 172578)

REFERENCE
AUTHORS Burton,J.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf5ish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Sep 27, 2004 this sequence version replaced gi:52694424.

COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf5ish-help@sanger.ac.uk
----- Project Information
Center project name: zc252P18
----- Summary Statistics
Assembly program: XGAP; version 4.5
Chemistry: Dye-terminator; 10% of reads
Consensus quality: 169202 bases at least Q40
Consensus quality: 169775 bases at least Q30
Consensus quality: 170291 bases at least Q20
Insert size: 171778; sum-of-contigs
Insert size: 177356; 3.4% error; agarose-fp
Quality coverage: 7.52x in Q20 bases; sum-of-contigs Quality
coverage: 7.28x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 3745: contig of 3745 bp in length
* 3746 3845: gap of 100 bp
* 3846 7408: contig of 3563 bp in length
* 7409 7508: gap of 100 bp
* 7509 16760: contig of 9252 bp in length
* 16761 16860: gap of 100 bp
* 16861 34627: contig of 1767 bp in length
* 34628 34727: gap of 100 bp
* 34728 58287: contig of 23560 bp in length
* 58288 58387: gap of 100 bp
* 58388 87381: contig of 28994 bp in length
* 87382 87481: gap of 100 bp
* 87482 108899: contig of 21418 bp in length
* 108900 108999: gap of 100 bp
* 109000 160080: contig of 51081 bp in length
* 160081 160180: gap of 100 bp
* 160181 172578: contig of 12398 bp in length.
*
* Location/Qualifiers
* 1..172578
* /organism="Danio rerio"

```

```

/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-252P18"
/clone_1b="CHORI-211"
1..3745
/note="assembly_fragment:00055
clone_end:SP6
vector_side:left"
3846..7408
/note="assembly_fragment:00024
fragment_chain:1"
7509..16760
/note="assembly_fragment:00091
fragment_chain:1"
16861..34627
/note="assembly_fragment:00369
fragment_chain:1"
34728..58287
/note="assembly_fragment:00801
fragment_chain:1"
58388..87381
/note="assembly_fragment:01078
fragment_chain:1"
87482..108899
/note="assembly_fragment:00562
fragment_chain:1"
109000..160080
/note="assembly_fragment:01434
fragment_chain:1"
160181..172578
/note="assembly_fragment:00188
fragment_chain:1
clone_end:77
vector_side:right"

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 172578;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 GGUCCUGAGANNNNNN 18
Db 160190 GGTCTCGAGANNNNNN 160175.

RESULT 10
BX927353/c 177849 bp DNA linear HTG 30-MAR-2004
LOCUS Danio rerio clone CH211-83P14, *** SEQUENCING IN PROGRESS ***
DEFINITION unordered pieces.
ACCESSION BX927353.3 GI:46016460
VERSION BX927353.3
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 177849)
Sims,S.
Direct Submission
Submitted (29-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf5ish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Apr 1, 2004 this sequence version replaced gi:45822741.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf5ish-help@sanger.ac.uk
----- Project Information
Center project name: zc83P14
----- Summary Statistics

```

Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 172770 bases at least Q40  
Consensus quality: 173502 bases at least Q30  
Consensus quality: 174263 bases at least Q20  
Insert size: 176549; sum-of-consigs  
Insert size: 192086; 9.2% error; agarose-fp  
Quality coverage: 6.80x in Q20 bases; sum-of-consigs Quality  
Coverage: 6.48x in Q20 bases; agarose-fp

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 14 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 12893: contig of 12893 bp in length  
\* 12894 12893: gap of 100 bp  
\* 12994 23124: contig of 10131 bp in length  
\* 23125 23124: gap of 100 bp  
\* 23225 30967: contig of 7743 bp in length  
\* 30968 31067: gap of 100 bp  
\* 31068 47274: contig of 16307 bp in length  
\* 47275 47374: gap of 100 bp  
\* 47375 69050: contig of 21676 bp in length  
\* 69051 69150: gap of 100 bp  
\* 69151 71771: contig of 2621 bp in length  
\* 71772 71872: gap of 100 bp  
\* 71872 113609: contig of 41738 bp in length  
\* 113610 113710: gap of 100 bp  
\* 113710 116503: contig of 2794 bp in length  
\* 116504 116603: gap of 100 bp  
\* 116604 143811: contig of 27208 bp in length  
\* 143812 143911: gap of 100 bp  
\* 143912 146264: contig of 2353 bp in length  
\* 146265 146364: gap of 100 bp  
\* 146365 150965: contig of 4601 bp in length  
\* 150966 151065: gap of 100 bp  
\* 151066 153687: contig of 2622 bp in length  
\* 153688 153787: gap of 100 bp  
\* 153788 158079: contig of 4292 bp in length  
\* 158080 158179: gap of 100 bp  
\* 158180 177849: contig of 19670 bp in length.

FEATURES  
Source  
1. 177849  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone\_id="CH211-83F14"  
/clone\_id="CHORI-211"  
1. 12893  
/note="assembly fragment: 00524  
fragment chain:1"  
clone\_end:SP6  
vector\_side:left"  
12994. 23124  
/note="assembly fragment: 00395  
fragment chain:1"  
23225. 30967  
/note="assembly fragment: 00295  
fragment chain:1"  
31068. 47274  
/note="assembly fragment: 00699  
fragment chain:2"  
47375. 69050  
/note="assembly fragment: 00947  
fragment chain:2"  
69151. 71771  
/note="assembly fragment: 00121  
fragment chain:2"  
71872. 113609

misc\_feature /note="assembly fragment: 01900  
fragment chain:2"  
113710. 116503  
/note="assembly fragment: 00098  
fragment chain:2"  
116604. 143811  
/note="assembly fragment: 01503  
fragment chain:2"  
143912. 146264  
/note="assembly fragment: 00076  
fragment chain:2"  
146365. 150965  
/note="assembly fragment: 00231  
fragment chain:3"  
151066. 153687  
/note="assembly fragment: 00144  
fragment chain:3"  
153788. 158079  
/note="assembly fragment: 00178  
fragment chain:3"  
158180. 177849  
/note="assembly fragment: 01212  
clone\_end:T7  
vector\_side:right"

misc\_feature  
misc\_feature  
misc\_feature  
misc\_feature  
misc\_feature

ORIGIN  
Query Match 88.9%; Score 16; DB 2; Length 177849;  
Best Local Similarity 87.5%; Pred. No. 5.1;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 3 GCUCUGAGNNNNN 18  
Db 71881 GGTCTGAGNNNNN 71866

RESULT 11  
CR752654  
LOCUS 178025 bp DNA linear HTG 26-AUG-2004  
DEFINITION Danio rerio clone DKEX-168C17, WORKING DRAFT SEQUENCE, 17 unordered  
pieces.  
ACCESSION CR752654 GI:51571685  
VERSION CR752654.2  
HG: HTGS PHASE1: HTGS DRAFT.  
KEYWORDS  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 178025)

REFERENCE  
AUTHORS Burton, J.  
TITLE Direct Submission  
JOURNAL Submitted (24-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
fish-help@sanger.ac.uk; clone requests: clonequest@sanger.ac.uk  
On Aug 26, 2004 this sequence version replaced gi:51534195.

COMMENT  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: ZK168C17  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 172534 bases at least Q40  
Consensus quality: 173763 bases at least Q30  
Consensus quality: 174582 bases at least Q20  
Insert size: 176425; sum-of-consigs  
Insert size: 154806; 2.0% error; agarose-fp  
Quality coverage: 4.54x in Q20 bases; sum-of-consigs Quality  
coverage: 5.39x in Q20 bases; agarose-fp  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 17 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

```

1 3834: contig of 3834 bp in length
3835 3934: gap of 100 bp
3935 16304: contig of 12370 bp in length
16305 16404: gap of 100 bp
16405 20173: contig of 3769 bp in length
20174 20273: gap of 100 bp
20274 27022: contig of 6749 bp in length
27023 27122: gap of 100 bp
27123 34543: contig of 7421 bp in length
34544 34643: gap of 100 bp
34644 46503: contig of 11860 bp in length
46504 46603: gap of 100 bp
46604 58667: contig of 12064 bp in length
58668 58767: gap of 100 bp
58768 63238: contig of 4471 bp in length
63239 63339: gap of 100 bp
63340 73750: contig of 10412 bp in length
73751 73851: gap of 100 bp
73852 92011: contig of 18061 bp in length
92012 92011: gap of 100 bp
92012 114018: contig of 22007 bp in length
114019 114118: gap of 100 bp
114119 120729: contig of 6611 bp in length
120730 120829: gap of 100 bp
120830 129601: contig of 8772 bp in length
129602 129701: gap of 100 bp
129702 136172: contig of 6471 bp in length
136173 136272: gap of 100 bp
136273 138394: contig of 2122 bp in length
138395 138495: gap of 100 bp
138496 157132: contig of 18638 bp in length
157133 157232: gap of 100 bp
157233 178025: contig of 20793 bp in length.
Location/Qualifiers
1. 178025

```

```

FEATURES
    source
        1. 178025
            /organism="Danio rerio"
            /mol_type="genomic DNA"
            /db_xref="taxon:7955"
            /clone="DKF1-166C17"
            /clone_lib="DantolKey"
            1. 3834
                /note="assembly fragment:00043"
                fragment_chain:1"
            3935..16304
                /note="assembly fragment:00687"
                fragment_chain:1"
            16405..20173
                /note="assembly fragment:00122"
                fragment_chain:1"
            20274..27022
                /note="assembly fragment:00241"
                fragment_chain:1"
            27123..34543
                /note="assembly fragment:00152"
                fragment_chain:1"
            34644..46503
                /note="assembly fragment:00423"
                fragment_chain:1"
            46604..58667
                /note="assembly fragment:00510"
                fragment_chain:1"
            58768..63238
                /note="assembly fragment:00068"
                fragment_chain:1"
            63339..73750

```

```

misc_feature /note="assembly fragment:00597"
              fragment_chain:2"
              73851..91911
              /note="assembly fragment:00926"
              fragment_chain:2"
              92012..114018
              /note="assembly fragment:01225"
              fragment_chain:2"
              114119..120729
              /note="assembly fragment:00196"
              fragment_chain:2"
              120830..129601
              /note="assembly fragment:00344"
              fragment_chain:2"
              129702..136172
              /note="assembly fragment:00291"
              fragment_chain:2"
              136273..138394
              /note="assembly fragment:00093.0"
              138495..157132
              /note="assembly fragment:00794"
              157233..178025
              /note="assembly fragment:01064"

```

```

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 178025;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 3 GGUCUGGAGNNNNN 18
Db 157123 GGTCGAGNNNNN 157138

```

```

RESULT 12
AC133391/c 184628 bp DNA linear HTG 27-NOV-2002
LOCUS
DEFINITION
Danio rerio clone CH211-3467 strain Tue, WORKING DRAFT SEQUENCE, 8
ordered pieces.
AC133391
AC133391.2 GI:25698912
HTG; HTGS PHASE2; HTGS DRAFT.

```

```

KEYWORDS
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteichthys;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 184628)

```

```

REFERENCE
AUTHORS
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,
Laric, P., Lee, L.H., S.-O., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Marques, E.H., Mastello, C., Mascheri, B., McDowell, J.,
Paguirigan, C., Pearson, R., Portnov, M.E., Prasad, A.,
Redix-Dugue, N., Schandier, K., Schaefer, M.G., Sison, C.,
Stancipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,
Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
NISC Comparative Sequencing Initiative
2 (bases 1 to 184628)
Unpublished

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
TITLE
JOURNAL
Submitted (27-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovenmont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 184628)
Green, E.D.
Direct Submission

```

```

COMMENT
Submitted (27-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovenmont Circle, Gaithersburg, MD 20877, USA
On Nov 27, 2002 this sequence version replaced gi:22779506.
-----
Center: NIH Intramural Sequencing Center

```





```

* 32792 57260: contig of 24469 bp in length
* 57261 57360: gap of 100 bp
* 57361 63085: contig of 5725 bp in length
* 63086 63185: gap of 100 bp
* 63186 137034: contig of 73849 bp in length
* 137035 137134: gap of 100 bp
* 137135 164138: contig of 27004 bp in length
* 164139 164238: gap of 100 bp
* 164239 170118: contig of 5880 bp in length
* 170119 170218: gap of 100 bp
* 170219 177353: contig of 7135 bp in length
* 177354 177454: gap of 100 bp
* 177455 189909: contig of 12456 bp in length.

FEATURES
SOURCE
  1..189909
    /organism="Danio rerio"
    /mol_type="genomic DNA"
    /db_xref="taxon:7955"
    /clone="DKEX-262A18"
    /clone_lib="DanioKey"
  1..14842
    /note="assembly_fragment:00491"
    /fragment_chain:"1"
  14843..22644
    /note="assembly_fragment:00108"
    /fragment_chain:"1"
  22745..32691
    /note="assembly_fragment:00675"
    /fragment_chain:"1"
  32792..57260
    /note="assembly_fragment:01254"
    /fragment_chain:"1"
  57361..63085
    /note="assembly_fragment:00187"
    /fragment_chain:"2"
  63186..137034
    /note="assembly_fragment:01656"
    /fragment_chain:"2"
  137135..164138
    /note="assembly_fragment:00868"
    /fragment_chain:"2"
  164239..170118
    /note="assembly_fragment:00064"
    /fragment_chain:"2"
  170219..177353
    /note="assembly_fragment:00268.0"
    /fragment_chain:"2"
  177454..189909
    /note="assembly_fragment:00351"

ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 189909;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3  GGUCCUGAGANNNNNN 18
Db      14833  GGTCCTGAGANNNNNN 14848

RESULT 14
CR376763/c 198047 bp DNA linear HTG 03-APR-2004
DEFINITION Danio rerio clone CH211-10L22, *** SEQUENCING IN PROGRESS ***, 14
unordered pieces.
ACCESSION CR376763
VERSION CR376763.4 GI:46194657
KEYWORDS HTG; HTGS; PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 198047)
AUTHORS McIay,K.

```

```

TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (01-APR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk
On Apr 3, 2004 this sequence version replaced gi:46019467.

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zc10L22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 192805 bases at least Q40
Consensus quality: 193672 bases at least Q30
Consensus quality: 194568 bases at least Q20
Insert size: 196747; sum-of-contigs
Insert size: 201230; 9.6% error; agarose-fp
Quality coverage: 7.13x in Q20 bases; sum-of-contigs Quality
coverage: 7.02x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 3382: contig of 3382 bp in length
3383 3482: gap of 100 bp
3483 21388: contig of 17906 bp in length
21389 21488: gap of 100 bp
21489 37498: contig of 16010 bp in length
37499 37598: gap of 100 bp
37599 67786: contig of 30188 bp in length
67787 67886: gap of 100 bp
67887 71536: contig of 3650 bp in length
71537 71636: gap of 100 bp
71637 80081: contig of 8445 bp in length
80082 80181: gap of 100 bp
80182 82322: contig of 2141 bp in length
82323 82422: gap of 100 bp
82423 106063: contig of 23641 bp in length
106064 106163: gap of 100 bp
106164 109599: contig of 3436 bp in length
109600 109699: gap of 100 bp
109700 113444: contig of 3745 bp in length
113445 113544: gap of 100 bp
113545 143985: contig of 30441 bp in length
143986 144085: gap of 100 bp
144086 164108: contig of 20023 bp in length
164109 164208: gap of 100 bp
164209 169935: contig of 5727 bp in length
169936 170035: gap of 100 bp
170036 198047: contig of 28012 bp in length.

FEATURES
SOURCE
  1..198047
    /organism="Danio rerio"
    /mol_type="genomic DNA"
    /db_xref="taxon:7955"
    /clone="CH211-10L22"
    /clone_lib="CHORI-211"
  1..3382
    /note="assembly_fragment:00160"
    /fragment_chain:"1"
  3483..21388
    /note="assembly_fragment:00723"
    /fragment_chain:"1"
  21489..37498
    /note="assembly_fragment:00356"

```

Query Match	88.9%	Score 16	DB 2	Length 198047
Best Local Similarity	87.5%	Pred. No. 5		
Matches 14	Conservative 2	Mismatches 0	Indels 0	Gaps 0

RESULT 15	LOCUS	DEFINITION
BX901895/c	213402 bp	DNA linear HTG 31-JAN-2008
BX901895		DnaO retro clone CH211-218C11, WORKING DRAFT SEQUENCE, 15

LOCUS	213402 bp	DNA	linear	HTG 31-JAN-2004
DEFINITION	Dn1o rer1o clone CH211-218C11, WORKING DRAFT SEQUENCE, 15			
ACCESSION	unordered pieces.			
VERSION	BK901895			
KEYWORDS	BK901895.4 GI:41529663			
SOURCE	HTG; HTGS; PHASE1; HTGS DRAFT; HTGS_FULPROP.			
ORGANISM	Dn1o rer1o (zebrafish)			
	Dn1o rer1o			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 213402)	Burton, J	Direct Submission	
		Submitted (30-JAN-2004)	Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zish-help@sanger.ac.uk	
			clone requests: clonequest@sanger.ac.uk	
			On Jan 31, 2004 this sequence version replaced gi:41411281.	

```

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----
Project Information
Center project name: ZC218C11
-----
Summary Statistics

```

```

Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 207086 bases at least Q40
Consensus quality: 208069 bases at least Q30
Consensus quality: 209254 bases at least Q20
Insert size: 212002; sum-of-contigs
Insert size: 217067; 3.2% error; agarose-fp
Quality coverage: 11.46x in Q20 bases; sum-of-contigs Quality
coverage: 11.33x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

56095	contig of 56095 bp in length
56096	gap of 100 bp
56196	91877: contig of 35662 bp in length
91878	91977: gap of 100 bp
91978	120593: contig of 28616 bp in length
120594	120693: gap of 100 bp
120694	127251: contig of 6656 bp in length
127352	127451: gap of 100 bp
127452	133708: contig of 6257 bp in length
133709	133808: gap of 100 bp
133809	137225: contig of 3467 bp in length
137226	137375: gap of 100 bp
137376	143536: contig of 6161 bp in length
143537	143536: gap of 100 bp
143637	149179: contig of 5543 bp in length
149180	149219: gap of 100 bp
149280	153535: contig of 4246 bp in length
153536	153625: gap of 100 bp
153626	175190: contig of 21565 bp in length
175191	175290: gap of 100 bp
175291	186583: contig of 11233 bp in length
186584	186683: gap of 100 bp
186684	192410: contig of 5727 bp in length
192411	192510: gap of 100 bp
192511	196007: contig of 3497 bp in length
196008	196107: gap of 100 bp
196108	209446: contig of 13339 bp in length
209447	209546: gap of 100 bp
209547	213402: contig of 3856 bp in length

```

USERS
source
location/Qualifiers
1..2133402
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-218C11"
/clone_1kb="CHORI-211"
1..56095
/note="assembly fragment:03265
fragment_chain:1"
misc_feature
56196..91877
/note="assembly fragment:02468
fragment_chain:1"
91978..120593
/note="assembly fragment:01885
fragment_chain:1"
120694..127351
/note="assembly fragment:00484
fragment_chain:1"
127452..133708
/note="assembly fragment:00625
fragment_chain:1"
133809..133775
/note="assembly fragment:00001"
133736..143536
/note="assembly fragment:00376"

```

```

misc_feature 143637..149179
                /note="assembly_fragment:00977"
misc_feature 149280..153525
                /note="assembly_fragment:00193
                fragment_chain:2"
misc_feature 153626..175190
                /note="assembly_fragment:01442
                fragment_chain:2"
misc_feature 175291..186593
                /note="assembly_fragment:00773
                fragment_chain:2"
misc_feature 186684..192410
                /note="assembly_fragment:00279
                fragment_chain:2"
misc_feature 192511..196007
                /note="assembly_fragment:00046
                fragment_chain:2"
misc_feature 196108..209446
                /note="assembly_fragment:01162
                fragment_chain:2"
misc_feature 209547..213402
                /note="assembly_fragment:00115
                fragment_chain:2
                clone_end:SP6
                vector_side:right"

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 213402;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUCGAGAGNNNNNN 18
Db 127461 GGTCTCGAGNNNNNN 127446

RESULT 16
LOCUS BX927073 215185 bp DNA linear HTG 18-FEB-2004
DEFINITION Danio rerio clone DKXP-78C2, *** SEQUENCING IN PROGRESS ***; 7
unordered pieces.
ACCESSION BX927073
VERSION BX927073.3 GI:42592534
KEYWORDS HTGS PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 215185)
McLay, K.
Direct Submission
Submitted (16-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 17, 2004 this sequence version replaced gi:41016204.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: ZK078C2
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 211838 bases at least Q40
Consensus quality: 212487 bases at least Q30
Consensus quality: 213129 bases at least Q20
Insert size: 214585; sum-of-contigs
Insert size: 219324; 2.6% error; agarose-fp
Quality coverage: 8.00x in Q20 bases; sum-of-contigs Quality
coverage: 7.92x in Q20 bases; agarose-fp

```

```

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 3729: contig of 3729 bp in length
* 3730 3829: gap of 100 bp
* 3830 26383: contig of 22554 bp in length
* 26384 26483: gap of 100 bp
* 26484 33119: contig of 6636 bp in length
* 33120 33219: gap of 100 bp
* 33220 110818: contig of 77599 bp in length
* 110819 110918: gap of 100 bp
* 110919 127149: contig of 16231 bp in length
* 127150 127249: gap of 100 bp
* 127250 154645: contig of 27396 bp in length
* 154646 215185: gap of 100 bp
* 154746 154746: gap of 100 bp
* 154746 215185: contig of 60440 bp in length.
*
FEATURES
source 1..215185
        /organism="Danio rerio"
        /mol_type="genomic DNA"
        /db_xref="taxon:7955"
        /clone="DKXP-78C2"
        /clone_1b="DanioKeyplot"
        1..3729
        /note="assembly_fragment:00023
        fragment_chain:1"
        3830..26383
        /note="assembly_fragment:00331
        fragment_chain:1"
        26484..33119
        /note="assembly_fragment:00064
        fragment_chain:2"
        33220..110818
        /note="assembly_fragment:01713
        fragment_chain:2"
        110919..127149
        /note="assembly_fragment:00146"
        127250..154645
        /note="assembly_fragment:00622.0"
        154746..215185
        /note="assembly_fragment:00949"

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 215185;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUCGAGAGNNNNNN 18
Db 3720 GGTCTCGAGNNNNNN 3735

RESULT 17
LOCUS CR388047 221924 bp DNA linear HTG 20-AUG-2004
DEFINITION Danio rerio clone DKXP-244D13, WORKING DRAFT SEQUENCE, 13 unordered
pieces.
ACCESSION CR388047
VERSION CR388047.4 GI:51491001
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 221924)
Sims, S.

```

TITLE  
JOURNAL

Direct Submission  
Submitted (18-ANG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk  
On Aug 20, 2004 this sequence version replaced g1:51470662.

COMMENT  
Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
Project Information  
Center project name: zK244D13  
Summary Statistics  
Assembly program: XGAP4, version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 217655 bases at least Q40  
Consensus quality: 218961 bases at least Q30  
Consensus quality: 219692 bases at least Q20  
Insert size: 220724; sum-of-contigs  
Insert size: 220298; 0.4% error; agarose-fp  
Quality coverage: 6.50x in Q20 bases; sum-of-contigs Quality coverage: 6.61x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 8096: contig of 8096 bp in length  
8097 8196: gap of 100 bp  
8197 12272: contig of 4076 bp in length  
12273 12372: gap of 100 bp  
12373 25914: contig of 13542 bp in length  
25915 26014: gap of 100 bp  
26015 34581: contig of 8567 bp in length  
34582 34681: gap of 100 bp  
34682 41378: contig of 6697 bp in length  
41379 41479: gap of 100 bp  
41479 70308: contig of 28830 bp in length  
70309 70409: gap of 100 bp  
70409 78606: contig of 8198 bp in length  
78607 78706: gap of 100 bp  
78707 91797: contig of 13091 bp in length  
91798 91897: gap of 100 bp  
91898 97614: contig of 5717 bp in length  
97615 97714: gap of 100 bp  
97715 107223: contig of 9509 bp in length  
107224 107323: gap of 100 bp  
107324 124557: contig of 17234 bp in length  
124558 124657: gap of 100 bp  
124658 148614: contig of 23957 bp in length  
148615 148714: gap of 100 bp  
148715 221924: contig of 73210 bp in length.

FEATURES  
source  
1. .221924  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKFZ-244D13"  
/clone\_idb="DantoKey"  
1. .8096  
/note="assembly fragment:00448  
fragment chain:1"  
8197 .12272  
/note="assembly fragment:00056  
fragment chain:1"  
12373 .25914  
/note="assembly fragment:00694  
fragment chain:1"  
26015 .34581  
misc\_feature

misc\_feature  
/note="assembly fragment:00348  
fragment chain:1"  
34682 .41378  
/note="assembly fragment:00103  
fragment chain:2"  
41479 .70308  
/note="assembly fragment:01223  
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70409 .78606  
/note="assembly fragment:00153  
fragment chain:2"  
78707 .91797  
/note="assembly fragment:00566  
fragment chain:3"  
91898 .97614  
/note="assembly fragment:00016  
fragment chain:3"  
97715 .107223  
/note="assembly fragment:00250  
fragment chain:3"  
107324 .124557  
/note="assembly fragment:00826  
fragment chain:4"  
124658 .148614  
/note="assembly fragment:00984  
fragment chain:4"  
148715 .221924  
/note="assembly fragment:01540.0"

ORIGIN  
Query Match 88.9%; Score 16; DB 2; Length 221924;  
Best Local Similarity 87.5%; Pred. No. 5;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGUCGCGAGNNNNNN 18  
Db 97605 GGTCTCGAGNNNNNN 97620

RESULT 18  
AC068379  
LOCUS  
Homo sapiens chromosome 3 clone RP11-537116 map 3, LOW-PASS  
DEFINITION  
SEQUENCE SAMPLING.  
AC068379  
AC068379.4 GI:10945763  
VERSION  
HTG; HTGS PHASE0.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 222876)  
Birren,B., Linton,L., Nussbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Baerlein,V., Beda,F., Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G., Campione,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatae,A., Klein,J., LaRoque,K., Lamazara,R., Lander,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Margulis,N., McCarthy,M., McEwan,P., McGurk,A., McKeirnan,K., McPherson,R., Meldrum,J., Menesh,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,T., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

TITLE  
JOURNAL  
COMMENT

Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,T.,  
Teeffaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,D.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,U., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Oct 22, 2000 this sequence version replaced gi:10305231.  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WtBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information  
Center project name: L10217

Center clone name: 537\_I\_16

NOTE: This record contains 278 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 728: contig of 728 bp in length  
\* 729 828: gap of 100 bp  
\* 829 1559: contig of 731 bp in length  
\* 1560 2382: contig of 723 bp in length  
\* 2383 2482: gap of 100 bp  
\* 2483 3231: contig of 749 bp in length  
\* 3232 3331: gap of 100 bp  
\* 3332 4056: contig of 725 bp in length  
\* 4057 4156: gap of 100 bp  
\* 4157 4881: contig of 725 bp in length  
\* 4882 4981: gap of 100 bp  
\* 4982 5714: contig of 733 bp in length  
\* 5715 5814: gap of 100 bp  
\* 5815 6526: contig of 712 bp in length  
\* 6527 7343: gap of 100 bp  
\* 7344 7443: contig of 717 bp in length  
\* 7444 8173: contig of 730 bp in length  
\* 8174 8273: gap of 100 bp  
\* 8274 8980: contig of 707 bp in length  
\* 8981 9080: gap of 100 bp  
\* 9081 9788: contig of 708 bp in length  
\* 9789 9888: gap of 100 bp  
\* 9889 10620: contig of 732 bp in length  
\* 10621 11471: contig of 751 bp in length  
\* 11472 11571: gap of 100 bp  
\* 11572 12317: contig of 746 bp in length  
\* 12318 12417: gap of 100 bp  
\* 12419 13148: contig of 731 bp in length  
\* 13149 13248: gap of 100 bp  
\* 13249 13973: contig of 725 bp in length  
\* 13974 14073: gap of 100 bp  
\* 14074 14812: contig of 735 bp in length  
\* 14813 14912: gap of 100 bp  
\* 14913 15633: contig of 721 bp in length  
\* 15634 15733: gap of 100 bp  
\* 15734 16475: contig of 742 bp in length  
\* 16476 17284: gap of 100 bp  
\* 17285 17384: contig of 703 bp in length  
\* 17384: gap of 100 bp

17385 18078: contig of 694 bp in length  
\* 18079 18178: gap of 100 bp  
\* 18179 18888: contig of 710 bp in length  
\* 18889 18988: gap of 100 bp  
\* 18989 19732: contig of 744 bp in length  
\* 19733 19832: gap of 100 bp  
\* 19833 20559: contig of 727 bp in length  
\* 20560 20659: gap of 100 bp  
\* 20660 21391: contig of 732 bp in length  
\* 21392 21491: gap of 100 bp  
\* 21492 22218: contig of 727 bp in length  
\* 22219 22318: gap of 100 bp  
\* 22319 23037: contig of 715 bp in length  
\* 23038 23137: gap of 100 bp  
\* 23138 23846: contig of 709 bp in length  
\* 23847 23946: gap of 100 bp  
\* 23947 24668: contig of 722 bp in length  
\* 24669 24768: gap of 100 bp  
\* 24769 25500: contig of 732 bp in length  
\* 25501 25600: gap of 100 bp  
\* 25601 26321: contig of 721 bp in length  
\* 26322 26421: gap of 100 bp  
\* 26422 27131: contig of 710 bp in length  
\* 27132 27231: gap of 100 bp  
\* 27232 27952: contig of 721 bp in length  
\* 27953 28052: gap of 100 bp  
\* 28053 28736: contig of 684 bp in length  
\* 28737 28836: gap of 100 bp  
\* 28837 29582: contig of 746 bp in length  
\* 29583 29682: gap of 100 bp  
\* 29683 30397: contig of 715 bp in length  
\* 30398 30497: gap of 100 bp  
\* 30498 31242: contig of 745 bp in length  
\* 31243 31342: gap of 100 bp  
\* 31343 32069: contig of 727 bp in length  
\* 32070 32169: gap of 100 bp  
\* 32170 32889: contig of 720 bp in length  
\* 32890 32989: gap of 100 bp  
\* 32990 33723: contig of 734 bp in length  
\* 33724 33823: gap of 100 bp  
\* 33824 34523: contig of 700 bp in length  
\* 34524 35342: gap of 100 bp  
\* 35343 35442: contig of 713 bp in length  
\* 35443 36172: gap of 100 bp  
\* 36173 36272: contig of 730 bp in length  
\* 36273 36988: contig of 716 bp in length  
\* 36989 37080: gap of 100 bp  
\* 37081 37820: contig of 732 bp in length  
\* 37821 37920: gap of 100 bp  
\* 37921 38636: contig of 716 bp in length  
\* 38637 38736: gap of 100 bp  
\* 38737 39455: contig of 719 bp in length  
\* 39456 39555: gap of 100 bp  
\* 39556 40249: contig of 694 bp in length  
\* 40250 40349: gap of 100 bp  
\* 40350 41074: contig of 725 bp in length  
\* 41075 41174: gap of 100 bp  
\* 41175 41907: contig of 733 bp in length  
\* 41908 42007: gap of 100 bp  
\* 42009 42726: contig of 719 bp in length  
\* 42727 42826: gap of 100 bp  
\* 42827 43579: contig of 753 bp in length  
\* 43580 43679: gap of 100 bp  
\* 43680 44374: contig of 635 bp in length  
\* 44375 44474: gap of 100 bp  
\* 44475 45180: contig of 706 bp in length  
\* 45181 45280: gap of 100 bp  
\* 45281 45979: contig of 693 bp in length  
\* 45980 46079: gap of 100 bp  
\* 46080 46821: contig of 742 bp in length  
\* 46822 46921: gap of 100 bp  
\* 46922 47645: contig of 724 bp in length

```

* 47745: gap of 100 bp
* 47746 48465: contig of 720 bp in length
* 48466 48565: gap of 100 bp
* 48566 49289: contig of 724 bp in length
* 49290 49389: gap of 100 bp
* 49390 50107: contig of 718 bp in length
* 50108 50207: gap of 100 bp
* 50208 50925: contig of 718 bp in length
* 50926 51025: gap of 100 bp
* 51026 51736: contig of 711 bp in length
* 51737 51836: gap of 100 bp
* 51837 52543: contig of 707 bp in length
* 52544 52643: gap of 100 bp
* 52644 53346: contig of 703 bp in length
* 53347 53446: gap of 100 bp
* 53447 54192: contig of 746 bp in length
* 54193 54292: gap of 100 bp
* 54293 55014: contig of 722 bp in length
* 55015 55114: gap of 100 bp
* 55115 55824: contig of 710 bp in length
* 55825 55924: gap of 100 bp
* 55925 56531: contig of 727 bp in length

Query Match      88.9%; Score 16; DB 2; Length 222876;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GGUCCTGGAGNNNNNN 18
Db      61571 GGTCCTGGAGNNNNNN 61586

RESULT 19
LOCUS      BX927188      228022 bp      DNA      linear      HTG 10-OCT-2004
DEFINITION Dario rerio clone DKEX-264N13, WORKING DRAFT SEQUENCE, 9 unordered
            pieces.
ACCESSION  BX927188.4 GI:41630180
VERSION    HTG_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS   Dario rerio (zebrafish)
SOURCE     Dario rerio
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
            Cypriniformes; Cyprinidae; Danio.
            1 (bases 1 to 228022)
            McLaren, S.
REFERENCE  Submitted (08-OCT-2004) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            zfish-help@sanger.ac.uk Clone requests: clonesrequest@sanger.ac.uk
            On Feb 2, 2004 this sequence version replaced gi:41322817.
            ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: zfish-help@sanger.ac.uk
            ----- Project Information
            Center project name: zK264N13
            ----- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: dye-terminator; 100% of reads
            Consensus quality: 225138 bases at least Q40
            Consensus quality: 225502 bases at least Q30
            Consensus quality: 225841 bases at least Q20
            Insert size: 227222; sum-of-contigs
            Insert size: 221727; 4.7% error; agarose-fp
            Quality coverage: 8.04x in Q20 bases; sum-of-contigs Quality
            coverage: 8.28x in Q20 bases; agarose-fp
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 9 contigs. The true order of the pieces
            * is not known and their order in this sequence record is

```

```

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 16758: contig of 16758 bp in length
* 16759 16858: gap of 100 bp
* 16859 20882: contig of 4024 bp in length
* 20883 20982: gap of 100 bp
* 20983 75976: contig of 5494 bp in length
* 75977 76076: gap of 100 bp
* 76077 82135: contig of 6059 bp in length
* 82136 82235: gap of 100 bp
* 82236 85336: contig of 7301 bp in length
* 85337 89637: gap of 100 bp
* 89638 101310: contig of 11674 bp in length
* 101311 101410: gap of 100 bp
* 101411 120443: contig of 19033 bp in length
* 120444 120544: gap of 100 bp
* 120545 168465: contig of 47923 bp in length
* 168467 168566: gap of 100 bp
* 168567 228022: contig of 59456 bp in length.

FEATURES
    source
        1..228022
            /organism="Dario rerio"
            /mol_type="genomic DNA"
            /db_xref="taxon:7955"
            /clone="DKEX-264N13"
            /clone_id="DarioKey"
            1..16758
                /note="assembly fragment:00363
                fragment chain:1"
            16859..20882
                /note="assembly fragment:00009
                fragment chain:1"
            20983..75976
                /note="assembly fragment:02092
                fragment chain:1"
            76077..82135
                /note="assembly fragment:00052
                fragment chain:1"
            82236..89637
                /note="assembly fragment:00113
                fragment chain:2"
            89637..101310
                /note="assembly fragment:00225
                fragment chain:2"
            101411..120443
                /note="assembly fragment:00552
                fragment chain:2"
            120544..168466
                /note="assembly fragment:00801.0"
            168567..228022
                /note="assembly fragment:01365"

ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 222876;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GGUCCTGGAGNNNNNN 18
Db      168457 GGTCCTGGAGNNNNNN 168472

RESULT 20
LOCUS      CR394526      256581 bp      DNA      linear      HTG 23-SEP-2004
DEFINITION Dario rerio clone DKEX-161J15, *** SEQUENCING IN PROGRESS ***. 27
            unordered pieces.
ACCESSION  CR394526
VERSION    CR394526.3 GI:52626694
KEYWORDS   HTG; HTGS_PHASE1.

```

SOURCE  
ORGANISM  
Dario rerio (zebrafish)  
Dario rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Osteichthyes;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 256581)  
Sims, S.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Submitted (22-SEP-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Sep 23, 2004 this sequence version replaced gi:52546046.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: zK161J15  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 247852 bases at least Q40  
Consensus quality: 249576 bases at least Q30  
Consensus quality: 250950 bases at least Q20  
Insert size: 253981; sum-of-contigs  
Quality coverage: 6.48x in Q20 bases; sum-of-contigs Quality  
coverage: 7.43x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 27 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
3691: contig of 3691 bp in length  
3692 3791: gap of 100 bp  
3792 7092: contig of 3301 bp in length  
7093 7192: gap of 100 bp  
7193 9583: contig of 2391 bp in length  
9584 9683: gap of 100 bp  
9684 34302: contig of 24619 bp in length  
34303 50724: gap of 100 bp  
50725 50824: contig of 16322 bp in length  
50825 60657: gap of 100 bp  
60658 60757: contig of 9833 bp in length  
60758 78706: gap of 100 bp  
78707 78806: contig of 17949 bp in length  
78807 85342: gap of 100 bp  
85343 85442: contig of 6536 bp in length  
85443 88417: gap of 100 bp  
88418 88517: contig of 2975 bp in length  
88519 110986: gap of 100 bp  
110987 110987: contig of 22469 bp in length  
110988 153767: gap of 100 bp  
153768 153866: contig of 42680 bp in length  
153867 157321: gap of 100 bp  
157322 157421: contig of 3455 bp in length  
157422 162377: gap of 100 bp  
162378 162477: contig of 4956 bp in length  
162478 177129: gap of 100 bp  
177130 177229: contig of 14652 bp in length  
177230 180400: gap of 100 bp  
180401 180500: contig of 3171 bp in length  
180501 180501: gap of 100 bp  
180502 182753: contig of 2253 bp in length  
182754 182853: gap of 100 bp  
182854 187045: contig of 4192 bp in length  
187046 187145: gap of 100 bp  
187146 189392: contig of 2247 bp in length  
189393

FEATURES  
Source  
1. 256581  
/organism="Dario rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone\_lib="DKEX-161J15"  
/clone\_lib="DanioKey"  
1. 3691  
/note="assembly\_fragment:00537  
fragment\_chain:1"  
/note="assembly\_fragment:00493  
fragment\_chain:1"  
3792. 7092  
/note="assembly\_fragment:00970  
fragment\_chain:2"  
60758. 78706  
/note="assembly\_fragment:01890  
fragment\_chain:2"  
78807. 85342  
/note="assembly\_fragment:00719  
fragment\_chain:2"  
85443. 88417  
/note="assembly\_fragment:00311  
fragment\_chain:2"  
88518. 110986  
/note="assembly\_fragment:02875  
fragment\_chain:2"  
110987. 153766  
/note="assembly\_fragment:03755  
fragment\_chain:3"  
153867. 157321  
/note="assembly\_fragment:00450  
fragment\_chain:3"  
157422. 162377  
/note="assembly\_fragment:00651  
fragment\_chain:3"  
162478. 177129  
/note="assembly\_fragment:01349  
fragment\_chain:3"  
177230. 180400  
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DEFINITION Sequence 10 from Patent WO20059357.  
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VERSION AX528761.1 GI:25172816  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Pedersen,M.L.  
TITLE Assay and kit for analyzing gene expression  
JOURNAL Patent: WO 02059357-A 10 01-AUG-2002;  
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LOCUS AX528762 29 bp DNA linear PAT 21-NOV-2002  
DEFINITION Sequence 11 from Patent WO20059357.  
ACCESSION AX528762

VERSION AX528762.1 GI:25172817  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Pedersen,M.L.  
TITLE Assay and kit for analyzing gene expression  
JOURNAL Patent: WO 02059357-A 11 01-AUG-2002;  
FEATURES  
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/note="synthetic construct"  
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Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
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LOCUS AC129972 62373 bp DNA linear HTG 16-AUG-2002  
DEFINITION Felis catus clone RP86-320J5, LOM-PASS SEQUENCE SAMPLING.  
ACCESSION AC129972  
VERSION AC129972.1 GI:22267645  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Felis catus (cat)  
ORGANISM Felis catus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
REFERENCE 1 (bases 1 to 62373)  
AUTHORS Birren,B., Nusbaum,C. and Lander,E.  
TITLE Felis catus, clone RP86-320J5  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 62373)  
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barnes,N., Bastien,V., Bloom,T., Bognuslavsky,L., Bouhglalter,B.,  
Camarata,J., Chang,J., Chazaro,B., Choquet,Y., Collymore,A.,  
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Roman,J., Roy,A., Schauer,S., Schuppback,R., Seaman,S., Severy,P.,  
Smith,C., Spencer,B., Stange-Thoman,N., Stojanovic,N., Talamae,J.,  
Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
Zembek,L., Zimmer,A. and Zody,M.  
DIRECT SUBMISSION  
Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WtBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L24474

Center clone name: 320\_J\_5

NOTE: This record contains 77 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

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2327 2426: gap of 100 bp  
2427 3127: contig of 701 bp in length  
3128 3227: gap of 100 bp  
3228 3969: contig of 742 bp in length  
3970 4069: gap of 100 bp  
4070 4784: contig of 715 bp in length  
4785 4885: gap of 100 bp  
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5684 6412: contig of 729 bp in length  
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6513 7215: contig of 703 bp in length  
7216 7315: gap of 100 bp  
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8024 8123: gap of 100 bp  
8124 8854: contig of 731 bp in length  
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19388 19487: gap of 100 bp  
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20208 20307: gap of 100 bp  
20309 21031: contig of 724 bp in length  
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51964 52773: contig of 710 bp in length  
52774 52773: gap of 100 bp  
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53500 54300: contig of 701 bp in length

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*	54400	contig of 709 bp in length
*	54401	contig of 709 bp in length
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*	55310	contig of 698 bp in length
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*	56007	gap of 100 bp
*	56008	gap of 100 bp
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*	56735	gap of 100 bp
*	56832	gap of 100 bp
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*	57543	gap of 100 bp

Query Match	83.3%	Score 15;	DB 2;	Length 62373;
Best Local Similarity	86.7%	Pred. No. 23;		
Matches 13; Conservative	2;	Mismatches 0;	Indels 0;	Gaps 0;

QY 4 GUCCUGGAGNNNNN 18

Db 50263 GTCCTGGAGNNNNN 50277

RESULT 24	LOCUS	DEFINITION
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AC101265	Mus musculus clone RP2-101A12, LOW-PASS SEQUENCE SAMPLING.	HTG 23-NOV-2001

VERSION AC101265.1 GI:17060040

**SOURCE**      **Mus musculus** (house mouse)

10

REFERENCE 1 (bases 1 to 72483)

TITLE Mus musculus, clone RP23-101A12

BOOKNAME	unpublished
REFERENCE	2 (bates 1 to 72483)

## ADDITIONS

TITLE	Direct Submission
JOURNAL	Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	All repeats were identified using RepeatMasker:

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: W1RR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L16315  
 Center clone name: 101\_A\_12  
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 NOTE: This record contains 87 individual

* sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allow overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.		
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44286	45014:	contig of 729 bp	in length
45015	45114:	gap of 100 bp	
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45958	46656:	contig of 739 bp	in length
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51691	51790:	gap of 100 bp	
51791	52517:	contig of 727 bp	in length
52518	52617:	gap of 100 bp	
52618	53339:	contig of 722 bp	in length
53340	53440:	gap of 100 bp	
53440	54185:	contig of 726 bp	in length
54166	54265:	gap of 100 bp	
54266	55017:	contig of 752 bp	in length
55018	55117:	gap of 100 bp	
55118	55841:	contig of 724 bp	in length
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55942	56657:	contig of 716 bp	in length
56658	56757:	gap of 100 bp	

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      *      56758      57482: contig of 725 bp in length
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Query Match
Best Local Similarity 83.3%; Score 15; DB 2; Length 72483;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

      OY      4      GUCCUGAGNNNNNN 18
      Db      16635 GTCTTGAGNNNNNN 16649
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RESULT 25
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WPCOMMENT
Sequence split into 5 fragments LOCUS AC115635 Accesssion AC115635
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AC115635_1         100001      210000
AC115635_2         200001      310000
AC115635_3         300001      410000
AC115635_4         400001      484720
Continuation 75 of 5) of AC115635 from base 400001 (AC115635 Rattus norvegicus clone CH7

Query Match
Best Local Similarity 86.7%; Score 15; DB 2; Length 84720;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

      OY      4      GUCCUGAGNNNNNN 18
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Sequence	split into 4 fragments	LOCUS	AC097780	Accession	AC097780
Fragment Name	Begin	End			
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AC097780_1	100001	210000			
AC097780_2	200001	310000			
AC097780_3	300001	362708			
LOCUS	AC097780	362708 bp	DNA	linear	HTG 26-SEP-2002
DEFINITION	Rattus norvegicus clone CH230-39A11, *** SEQUENCING IN PROGRESS				
ACCESSION	AC097780				
VERSION	AC097780.5 GI:23322019				
KEYWORDS	HTG; HTGS_PHASE1.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 362708) Muzny, D., Marle, F., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alshrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Gante, R., Garcia, A., Garner, T., Garza, M., Gebregergs, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,				
AUTHORS					

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* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*      147743      147843: gap of unknown length
*      147843      161886: contig of 14044 bp in length
*      161887      161986: gap of unknown length
*      161987      173563: contig of 11577 bp in length
*      173564      173663: gap of unknown length
*      173664      180705: contig of 7042 bp in length
*      180706      180805: gap of unknown length
*      180806      306402: contig of 125597 bp in length
*      306403      306502: gap of unknown length
*      306503      317763: contig of 11261 bp in length
*      317764      317863: gap of unknown length
*      317864      319488: contig of 1625 bp in length
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*      319589      321206: contig of 1618 bp in length
*      321207      321306: gap of unknown length
*      321307      322705: contig of 1399 bp in length
*      322706      322805: gap of unknown length
*      322806      325171: contig of 2266 bp in length
*      325172      325271: gap of unknown length
*      325272      326695: contig of 1424 bp in length
*      326696      326795: gap of unknown length
*      326796      328719: contig of 1924 bp in length
*      328720      328819: gap of unknown length
*      328820      334149: contig of 5330 bp in length
*      334150      334249: gap of unknown length
*      334250      337024: contig of 2775 bp in length
*      337025      337125: gap of unknown length
*      337125      340982: contig of 3858 bp in length
*      340983      341082: gap of unknown length
*      341083      344519: contig of 3437 bp in length
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*      344620      353148: contig of 8529 bp in length
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Query Match	83.3%	Score 15;	DB 2;	Length 150670;
Best Local Similarity	86.7%	Pred. No. 23;		
Matches 13; Conservative	2;	Mismatches 0;	Indels 0;	Gaps 0

Cy 4 GUCCUGAGNNNNN 18  
 Db 128508 GTCTGAGAGNNNNN 128522  
 RESULT 28  
 AC105679/c  
 LOCUS  
 DEFINITION  
 Rattus norvegicus clone CH230-266N24, \*\*\* SEQUENCING IN PROGRESS  
 \*\*\* 4 unordered pieces.  
 AC105679  
 AC105679.3 GI:23603083  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
 Rattus norvegicus (Norway rat)  
 SOURCE  
 ORGANISM  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 161787)  
 REFERENCE  
 AUTHORS  
 Muzny, D., Marz, M., Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J.,  
 Allen, C., Allen, H., Albrooke, S., Amin, A., Angiano, D.,  
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 TITLE  
 JOURNAL  
 Unpublished  
 2 (bases 1 to 161787)  
 REFERENCE  
 AUTHORS  
 Worley, K. C.

TITLE  
 JOURNAL  
 Direct Submission  
 Submitted (09-JAN-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 161787)  
 REFERENCE  
 AUTHORS  
 Rat Genome Sequencing Consortium.  
 TITLE  
 JOURNAL  
 Submitted (11-OCT-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Oct 9, 2002 this sequence version replaced gi:21736578.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
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 by sized gaps filled with Ns to the estimated size. The sequence  
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 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
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 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GNM0  
 Center clone name: CH230-266N24  
 ----- Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 135243 bases at least Q40  
 Consensus quality: 138805 bases at least Q30  
 Consensus quality: 141344 bases at least Q20  
 Estimated insert size: 147765; sum-of-contigs estimation  
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
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TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
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 JOURNAL  
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 JOURNAL  
 COMMENT

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,  
 Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,  
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 Weinstock, G., and Gibbs, R. A.

Direct Submission  
 Unpublished  
 2 (bases 1 to 222685)  
 Morley, K. C.  
 Direct Submission  
 Submitted (06-AUG-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 222685)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (20-NOV-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Nov 20, 2002 this sequence version replaced gi:23267477.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs should be indicated in the feature  
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 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information -----  
 Center project name: KBZU  
 Center clone name: CH230-163G18  
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 Assembly program: Phrap; version 0.990329  
 Consensus quality: 186066 bases at least Q40  
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 Consensus quality: 192829 bases at least Q20  
 Estimated insert size: 195607; sum-of-contigs estimation

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Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Gendank_draft_data.html) .
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                    146881..147979
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Beech Local Similarity 86.7%; Pred. No. 22;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy       4 GUCCUGAGANNNNN 18
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Db       180084 GTCTGTGAGNNNNN 180098
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LOCUS     ACI12325
DEFINITION Rattus norvegicus clone CH230-119B23, *** SEQUENCING IN PROGRESS
ACCESSION ACI12325
VERSION    ACI12325.4 GI:25006559
KEYWORDS  HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHD.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 235173)
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Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,

```

TITLE JOURNAL  
 REFERENCE  
 REFERENCE  
 AUTHORS  
 TITLE  
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 REFERENCE  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Frazer,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garra,M.,  
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 Puaao,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,  
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 Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,  
 Sanders,W., Severy,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,  
 Shetty,J., Shvartsbeyn,A., Slison,I., Siller,C.D., Smajls,D.,  
 Sneed,A., Sodergren,E., Song,X.-Z., Sorrell,E., Sosa,J.,  
 Steimle,M., Strong,R., Sutton,A., Stiney,A., Tabot,P., Taylor,C.,  
 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Uemari,K.,  
 Wang,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,  
 Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,  
 Williams,G., Willson,R., Wlecyk,R., Wooden,H., Worley,K.,  
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,  
 Yu,P., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von  
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
 Weinstock,G. and Gibbs,R.A.  
 Direct Submission  
 2 (bases 1 to 235173)  
 Worley,K.C.  
 Direct Submission  
 Submitted (21-FEB-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Nov 15, 2002 this sequence version replaced gi:23367822.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GOU5  
 Center clone name: CH230-119823  
 ----- Summary Statistics  
 Assembly program: Phrap, version 0.990329  
 Consensus quality: 196107 bases at least Q40

```

Consensus quality: 201820 bases at least Q30
Consensus quality: 205011 bases at least Q20
Estimated insert size: 193547; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 224145: contig of 224145 bp in length
* 224146 224245: gap of unknown length
* 224246 228440: contig of 4195 bp in length
* 228441 228540: gap of unknown length
* 228541 230920: contig of 2380 bp in length
* 230921 231020: gap of unknown length
* 231021 233289: contig of 1269 bp in length
* 233290 233389: gap of unknown length
* 233390 235173: contig of 2784 bp in length.
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*     1..235173
*         /organism="Rattus norvegicus"
*         /mol_type="genomic DNA"
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*         /clone="CH230-119B23"
*         12474..13929
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*                 /note="wgs_contig"
*                 165157..167210
*                     misc_feature
*                         /note="wgs_contig"
*                         184533..185625
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*                                 224246..225932
*                                     /note="wgs_contig"
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ORIGIN
Query Match 83.3%; Score 15; DB 2; Length 235173;
Best Local Similarity 86.7%; Pred. No. 22;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 4 GUCCUGAGAGNNNNN 18
|:|:|:|:|:|:|:|:|:|
Db 173271 GTCCCTGGAGNNNNN 173285

RESULT 32
LOCUS AX037200 27 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 112 from Patent WO00562923.
ACCESSION AX037200
VERSION AX037200.1 GI:11226625
KEYWORDS
SOURCE
ORGANISM
SOURCE synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Sibson, R.
TITLE Genetic analysis
JOURNAL Patent: WO 0056923-A 112 28-SEP-2000;
FEATURES
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)
source Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32650"
/note="replacement plasmid sequence"
ORIGIN
Query Match 77.8%; Score 14; DB 6; Length 27;

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Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGANNNNN 18  
:|||||  
Db 4 TCCTGAGANNNNN 17

RESULT 33  
AX037201 27 bp DNA linear PAT 16-NOV-2000

LOCUS AX037201  
DEFINITION Sequence 113 from Patent WO056923.  
ACCESSION AX037201  
VERSION AX037201.1 GI:11226626  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
Sibson,R.  
Genetic analysis  
Patent: WO 0056923-A 113 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1..27  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
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/note="replacement plasmid sequence"

FEATURES  
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1..27  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 UCCUGAGANNNNN 18  
:|||||  
Db 4 TCCTGAGANNNNN 17

RESULT 34  
AX037202 27 bp DNA linear PAT 16-NOV-2000

LOCUS AX037202  
DEFINITION Sequence 114 from Patent WO056923.  
ACCESSION AX037202  
VERSION AX037202.1 GI:11226627  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
Sibson,R.  
Genetic analysis  
Patent: WO 0056923-A 114 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1..27  
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/note="replacement plasmid sequence"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

FEATURES  
source  
1..27  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 UCCUGAGANNNNN 18  
:|||||  
Db -4 TCCTGAGANNNNN 17

RESULT 35

AX037203 27 bp DNA linear PAT 16-NOV-2000  
LOCUS AX037203  
DEFINITION Sequence 115 from Patent WO056923.  
ACCESSION AX037203  
VERSION AX037203.1 GI:11226628  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
Sibson,R.  
Genetic analysis  
Patent: WO 0056923-A 115 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
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/note="replacement plasmid sequence"

FEATURES  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGANNNNN 18  
:|||||  
Db 4 TCCTGAGANNNNN 17

RESULT 36  
AX037204 27 bp DNA linear PAT 16-NOV-2000

LOCUS AX037204  
DEFINITION Sequence 116 from Patent WO056923.  
ACCESSION AX037204  
VERSION AX037204.1 GI:11226629  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
Sibson,R.  
Genetic analysis  
Patent: WO 0056923-A 116 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1..27  
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/note="replacement plasmid sequence"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
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FEATURES  
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/note="replacement plasmid sequence"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGANNNNN 18  
:|||||  
Db 4 TCCTGAGANNNNN 17

RESULT 37  
AX037205 27 bp DNA linear PAT 16-NOV-2000

LOCUS AX037205  
DEFINITION Sequence 117 from Patent WO056923.  
ACCESSION AX037205  
VERSION AX037205.1 GI:11226630  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
Sibson,R.  
Genetic analysis  
Patent: WO 0056923-A 117 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1..27  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 117 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
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/note="replacement plasmid sequence"  
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Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18  
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4 TCCTGAGAGNNNNNN 17  
Db  
RESULT 38  
AX037206 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 118 from Patent WO0056923.  
ACCESSION AX037206  
VERSION AX037206.1 GI:11226631  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 118 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
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/note="replacement plasmid sequence"  
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Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
4 TCCTGAGAGNNNNNN 17  
Db  
RESULT 39  
AX037207 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 119 from Patent WO0056923.  
ACCESSION AX037207  
VERSION AX037207.1 GI:11226632  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 119 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
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/note="replacement plasmid sequence"

/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
4 TCCTGAGAGNNNNNN 17  
Db  
RESULT 40  
AX037208 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 120 from Patent WO0056923.  
ACCESSION AX037208  
VERSION AX037208.1 GI:11226633  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 120 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
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/note="replacement plasmid sequence"  
ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
4 TCCTGAGAGNNNNNN 17  
Db  
RESULT 41  
AX037209 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 121 from Patent WO0056923.  
ACCESSION AX037209  
VERSION AX037209.1 GI:11226634  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 121 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18

Db 4 TCCGTGAGANNNNNN 17

RESULT 42  
AX037210 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 122 from Patent WO0056923.  
ACCESSION AX037210  
VERSION AX037210.1 GI:11226635  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 122 28-SEP-2000;  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)

FEATURES  
source  
1. .27  
Location/Qualifiers  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGANNNNNN 18  
Db 4 TCCGTGAGANNNNNN 17

RESULT 43  
AX037211 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 123 from Patent WO0056923.  
ACCESSION AX037211  
VERSION AX037211.1 GI:11226636  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 123 28-SEP-2000;  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)

FEATURES  
source  
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Location/Qualifiers  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGANNNNNN 18  
Db 4 TCCGTGAGANNNNNN 17

RESULT 44  
AX037212 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 124 from Patent WO0056923.  
ACCESSION AX037212

VERSION AX037212.1 GI:11226637  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 124 28-SEP-2000;  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)

FEATURES  
source  
1. .27  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGANNNNNN 18  
Db 4 TCCGTGAGANNNNNN 17

RESULT 45  
AX037213 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 125 from Patent WO0056923.  
ACCESSION AX037213  
VERSION AX037213.1 GI:11226638  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 125 28-SEP-2000;  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)

FEATURES  
source  
1. .27  
Location/Qualifiers  
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/note="replacement plasmid sequence"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGANNNNNN 18  
Db 4 TCCGTGAGANNNNNN 17

RESULT 46  
AX037214 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 126 from Patent WO0056923.  
ACCESSION AX037214  
VERSION AX037214.1 GI:11226639  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 126 28-SEP-2000;

FEATURES  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
Source  
1. .27  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Db 5 UCCUGAGAGNNNNN 18  
4 TCCTGGAGAGNNNNN 17

RESULT 47  
LOCUS AX037215 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 127 from Patent WO0056923.  
ACCESSION AX037215  
VERSION AX037215.1 GI:11226640  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 127 28-SEP-2000;  
SIBSON,ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
Source  
1. .27  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Db 5 UCCUGAGAGNNNNN 18  
4 TCCTGGAGAGNNNNN 17

RESULT 48  
LOCUS AC100909 49799 bp DNA linear HTG 23-NOV-2001  
DEFINITION Mus musculus clone RP23-70124, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC100909  
VERSION AC100909.1 GI:17059683  
KEYWORDS HTG: HTGS PHASE0.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 49799)  
Birren,B., Linton,L., Nuebaum,C. and Lander,E.  
Mus musculus, clone RP23-70124  
Unpublished  
2 (bases 1 to 49799)  
Birren,B., Linton,L., Nuebaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Barina,N., Bastien,V., Boguslavsky,L., Bouhgalter,B.,  
Brown,A., Camarata,J., Campiano,A., Chang,J., Chazaro,B.,  
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
Cooke,P., Dearellano,K., Dewar,K., Diaz,U.S., Dodge,S., Faro,S.,  
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,  
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

TITLE  
JOURNAL  
COMMENT  
Hagoe,B., Headford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K.,  
Iamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,  
MacLaren,C., Macdonald,P., Major,J., Margolis,N., Matthews,C.,  
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,  
Meneses,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,  
Nordb,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,  
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
Raymond,C., Rella,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,  
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,  
Topham,K., Travers,M., Travis,N., Triggillo,D., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RW/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L14550  
Center clone name: 70\_I\_24  
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\* NOTE: This record contains 61 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
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\* 673 772: contig of 672 bp in length  
\* 773 772: gap of 100 bp  
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\* 2292 773: gap of 100 bp  
\* 2392 773: contig of 704 bp in length  
\* 3096 773: gap of 100 bp  
\* 3196 773: gap of 100 bp  
\* 3902 773: contig of 707 bp in length  
\* 3903 773: gap of 100 bp  
\* 4003 773: contig of 730 bp in length  
\* 4733 773: gap of 100 bp  
\* 4833 773: contig of 728 bp in length  
\* 5561 773: gap of 100 bp  
\* 5561 773: gap of 100 bp  
\* 6357 773: contig of 697 bp in length  
\* 6358 773: gap of 100 bp  
\* 6457 773: gap of 100 bp  
\* 6458 773: gap of 100 bp  
\* 7171 773: contig of 714 bp in length  
\* 7272 773: gap of 100 bp  
\* 8003 773: contig of 732 bp in length  
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\* 8918 773: gap of 100 bp  
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* 14619 15315: contig of 697 bp in length
* 15316 15415: gap of 100 bp
* 15416 16136: contig of 721 bp in length
* 16137 16236: gap of 100 bp
* 16237 16953: contig of 717 bp in length
* 16954 17053: gap of 100 bp
* 17054 17775: contig of 722 bp in length
* 17776 17875: gap of 100 bp
* 17876 18608: contig of 733 bp in length
* 18609 18708: gap of 100 bp
* 18709 19430: contig of 722 bp in length
* 19431 19530: gap of 100 bp
* 19531 20240: contig of 710 bp in length
* 20241 20340: gap of 100 bp
* 20341 21052: contig of 712 bp in length
* 21053 21152: gap of 100 bp
* 21153 21872: contig of 720 bp in length
* 21873 21972: gap of 100 bp
* 21973 22694: contig of 722 bp in length
* 22695 22794: gap of 100 bp
* 22795 23520: contig of 726 bp in length
* 23521 23620: gap of 100 bp
* 23621 24348: contig of 728 bp in length
* 24349 24448: gap of 100 bp
* 24449 25178: contig of 730 bp in length
* 25179 25278: gap of 100 bp
* 25279 25954: contig of 676 bp in length
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* 28383 28482: gap of 100 bp
* 28483 29191: contig of 709 bp in length
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* 29292 30008: contig of 717 bp in length
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* 30109 30828: contig of 720 bp in length
* 30829 30928: gap of 100 bp
* 30929 31656: contig of 728 bp in length
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* 33320 33419: gap of 100 bp
* 33420 34136: contig of 717 bp in length
* 34137 34236: gap of 100 bp
* 34237 34954: contig of 718 bp in length
* 34955 35054: gap of 100 bp
* 35055 35765: contig of 711 bp in length
* 35766 35865: gap of 100 bp
* 35866 36588: contig of 723 bp in length
* 36589 36688: gap of 100 bp
* 36689 37414: contig of 726 bp in length
* 37415 37514: gap of 100 bp
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* 38347 39063: contig of 717 bp in length
* 39064 39163: gap of 100 bp
* 39164 39862: contig of 699 bp in length
* 39863 39962: gap of 100 bp
* 39963 40680: contig of 718 bp in length
* 40681 40780: gap of 100 bp
* 40781 41486: contig of 706 bp in length
* 41487 41586: gap of 100 bp
* 41587 42310: contig of 724 bp in length
* 42311 42410: gap of 100 bp
* 42411 43135: contig of 725 bp in length

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* 44798 44897: gap of 100 bp
* 44898 45635: contig of 738 bp in length
* 45636 45735: gap of 100 bp
* 45736 46475: contig of 740 bp in length
* 46476 46575: gap of 100 bp
* 46576 47296: contig of 721 bp in length
* 47297 47396: gap of 100 bp
* 47397 48125: contig of 729 bp in length
* 48126 48225: gap of 100 bp
* 48226 48953: contig of 728 bp in length
* 48954 49053: gap of 100 bp
* 49054 49799: contig of 746 bp in length.

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-70124"
/clone_lib="RPCI-23 Female Mouse BAC"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 49799;
Best Local Similarity 85.7%; Pred. No. 1e+02; Mismatches 0; Gaps 0;
Matches 12; Conservative 2; Indels 0;

Oy 5 UCCUGAGAGNNNNN 18
Db 45628 TCCTGGAGNNNNN 45641

RESULT 49
AC100333
LOCUS 55662 bp DNA linear HTG 22-NOV-2001
DEFINITION Mus musculus clone RP23-126H4, LOW-PASS SEQUENCE SAMPLING.
AC100333
VERSION AC100333.1 GI:17047699
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 55662)
AUTHORS Birren,B., Linton,L., Nuebaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-126H4
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 55662)
AUTHORS Birren,B., Linton,L., Nuebaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barta,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Brown,A., Camarata,J., Campoliano,A., Chang,J., Chazarov,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., D'Arellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Grinde,S., Gord,S., Goyette,W., Graham,L., Grand-Pierre,N.,
Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Labrecque,K.,
Lamasares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., MacDonald,P., Major,J., Marguis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Mcpheeters,R., Meldrum,J.,
Meneses,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Olivier,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rossetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Teste,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission

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## JOURNAL

## COMMENT

Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www.seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L15120

Center clone name: 126\_H\_4

\* NOTE: This record contains 68 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 740: contig of 740 bp in length  
\* 741 840: gap of 100 bp  
\* 841 1580: contig of 740 bp in length  
\* 1581 1680: gap of 100 bp  
\* 1681 2386: contig of 706 bp in length  
\* 2387 2486: gap of 100 bp  
\* 2487 3189: contig of 703 bp in length  
\* 3190 3289: gap of 100 bp  
\* 3290 3396: contig of 707 bp in length  
\* 3397 4096: gap of 100 bp  
\* 4097 4829: contig of 733 bp in length  
\* 4830 4929: gap of 100 bp  
\* 4930 5658: contig of 729 bp in length  
\* 5659 5759: gap of 100 bp  
\* 5759 6497: contig of 739 bp in length  
\* 6498 6597: gap of 100 bp  
\* 6598 7326: contig of 729 bp in length  
\* 7327 7427 8125: contig of 699 bp in length  
\* 8126 8225: gap of 100 bp  
\* 8226 8939: contig of 714 bp in length  
\* 8940 9039: gap of 100 bp  
\* 9040 9747: contig of 708 bp in length  
\* 9748 9847: gap of 100 bp  
\* 9848 10564: contig of 717 bp in length  
\* 10565 10664: gap of 100 bp  
\* 10665 11396: contig of 732 bp in length  
\* 11397 11496: gap of 100 bp  
\* 11497 12177: contig of 681 bp in length  
\* 12178 12277: gap of 100 bp  
\* 12278 13011: contig of 734 bp in length  
\* 13012 13111: gap of 100 bp  
\* 13112 13854: contig of 743 bp in length  
\* 13855 13954: gap of 100 bp  
\* 13955 14689: contig of 735 bp in length  
\* 14690 14789: gap of 100 bp  
\* 14790 15484: contig of 695 bp in length  
\* 15485 15584: gap of 100 bp  
\* 15585 16282: contig of 698 bp in length  
\* 16283 16382: gap of 100 bp  
\* 16383 17083: contig of 701 bp in length  
\* 17084 17183: gap of 100 bp  
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\* 17884 17983: gap of 100 bp  
\* 17984 18713: contig of 730 bp in length  
\* 18714 18813: gap of 100 bp  
\* 18814 19552: contig of 739 bp in length  
\* 19553 19652: gap of 100 bp

19653 20349: contig of 697 bp in length  
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\* 21189 21288: gap of 100 bp  
\* 21289 22032: contig of 744 bp in length  
\* 22033 22132: gap of 100 bp  
\* 22133 22833: contig of 701 bp in length  
\* 22834 22933: gap of 100 bp  
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\* 23646 23745: gap of 100 bp  
\* 23746 24454: contig of 709 bp in length  
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\* 25381 26121: contig of 741 bp in length  
\* 26122 26221: gap of 100 bp  
\* 26222 26968: contig of 747 bp in length  
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\* 27912 28611: contig of 700 bp in length  
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\* 29462 29561: gap of 100 bp  
\* 29562 30303: contig of 742 bp in length  
\* 30304 30403: gap of 100 bp  
\* 30404 31117: contig of 714 bp in length  
\* 31118 31217: gap of 100 bp  
\* 31218 31936: contig of 719 bp in length  
\* 31937 32036: gap of 100 bp  
\* 32037 32758: contig of 722 bp in length  
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\* 32859 33583: contig of 725 bp in length  
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\* 49212 49953: contig of 742 bp in length



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\* 50758 50857: gap of 100 bp in length  
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\* 51594 51693: gap of 100 bp  
\* 51694 52396: contig of 703 bp in length  
\* 52397 52496: gap of 100 bp  
\* 52497 53205: contig of 709 bp in length  
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\* 54007 54106: gap of 100 bp  
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\* 54836 54935: gap of 100 bp  
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Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 11389 TCCTGAGAGNNNNN 11402

RESULT 50  
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DEFINITION Mus musculus clone RP23-127B24, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC100339  
VERSION AC100339.1 GI:17047705  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 59918)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Mus musculus, clone RP23-127B24  
Unpublished  
2 (bases 1 to 59918)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barna, N., Baetsen, V., Boguslavsky, L., Boungalter, B.,  
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Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,  
Ferrira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,  
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagoe, B., Heatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,  
Lamaze, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C.,  
McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J.,  
Menue, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,  
Oliver, J., Peterson, K., Phunhahang, P., Pierre, N., Pollard, V.,  
Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,  
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talama, J., Teefaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zaitoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 330 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A. F. A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WITR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L15132  
Center clone name: 127\_B\_24  
\* NOTE: This record contains 73 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
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\* 702 801: gap of 100 bp  
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\* 1617 2343: contig of 727 bp in length  
\* 2344 2443: gap of 100 bp  
\* 2443 3177: contig of 734 bp in length  
\* 3178 3277: gap of 100 bp  
\* 3278 4007: contig of 730 bp in length  
\* 4008 4107: gap of 100 bp  
\* 4108 4834: contig of 727 bp in length  
\* 4835 4935: gap of 100 bp  
\* 4935 5674: contig of 740 bp in length  
\* 5675 5774: gap of 100 bp  
\* 5775 6482: contig of 708 bp in length  
\* 6483 6582: gap of 100 bp  
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\* 7294 7393: gap of 100 bp  
\* 7394 8131: contig of 738 bp in length  
\* 8132 8231: gap of 100 bp  
\* 8232 8957: contig of 726 bp in length  
\* 8958 9057: gap of 100 bp  
\* 9058 9789: contig of 732 bp in length  
\* 9790 9889: gap of 100 bp  
\* 9890 10623: contig of 733 bp in length  
\* 10623 10722: gap of 100 bp  
\* 10723 11428: contig of 706 bp in length  
\* 11429 11528: gap of 100 bp  
\* 11529 12116: contig of 588 bp in length  
\* 12117 12216: gap of 100 bp  
\* 12217 12935: contig of 719 bp in length  
\* 12936 13035: gap of 100 bp  
\* 13036 13754: contig of 719 bp in length  
\* 13755 13854: gap of 100 bp  
\* 13855 14594: contig of 740 bp in length  
\* 14595 14694: gap of 100 bp  
\* 14695 15421: contig of 727 bp in length  
\* 15422 15521: gap of 100 bp  
\* 15522 16272: contig of 751 bp in length  
\* 16273 16372: gap of 100 bp  
\* 16373 17116: contig of 744 bp in length  
\* 17117 17216: gap of 100 bp  
\* 17217 17960: contig of 744 bp in length  
\* 17961 18060: gap of 100 bp  
\* 18061 18783: contig of 723 bp in length  
\* 18784 18883: gap of 100 bp  
\* 18884 19602: contig of 719 bp in length  
\* 19603 19702: gap of 100 bp  
\* 19703 20433: contig of 731 bp in length  
\* 20434 20533: gap of 100 bp  
\* 20534 21265: contig of 732 bp in length  
\* 21266 21365: gap of 100 bp  
\* 21366 22083: contig of 718 bp in length  
\* 22084 22183: gap of 100 bp  
\* 22184 22910: contig of 727 bp in length

```

* 22911 23010: gap of 100 bp
* 23011 23740: contig of 730 bp in length
* 23741 23840: gap of 100 bp
* 23841 24589: contig of 749 bp in length
* 24590 24689: gap of 100 bp
* 24690 25411: contig of 722 bp in length
* 25412 25511: gap of 100 bp
* 25512 26241: contig of 730 bp in length
* 26242 26341: gap of 100 bp
* 26342 26992: contig of 551 bp in length
* 26993 27717: gap of 100 bp
* 27717 27817: contig of 724 bp in length
* 27817 28535: contig of 720 bp in length
* 28537 28636: gap of 100 bp
* 28637 29352: contig of 715 bp in length
* 29352 30183: contig of 731 bp in length
* 30183 30283: gap of 100 bp
* 30283 31032: contig of 749 bp in length
* 31032 31132: gap of 100 bp
* 31132 31865: contig of 733 bp in length
* 31865 32700: contig of 736 bp in length
* 32701 32800: gap of 100 bp
* 32801 33537: contig of 737 bp in length
* 33538 33637: gap of 100 bp
* 33638 34375: contig of 738 bp in length
* 34376 34475: gap of 100 bp
* 34476 35215: contig of 740 bp in length
* 35216 35315: gap of 100 bp
* 35316 36035: contig of 720 bp in length
* 36036 36135: gap of 100 bp
* 36136 36859: contig of 724 bp in length
* 36860 37681: contig of 722 bp in length
* 37682 38521: gap of 100 bp
* 38522 38621: contig of 740 bp in length
* 38622 39346: gap of 100 bp
* 39347 39446: gap of 100 bp
* 39447 40183: contig of 737 bp in length
* 40184 40283: gap of 100 bp
* 40284 40990: contig of 707 bp in length
* 40991 41090: gap of 100 bp
* 41091 41830: contig of 740 bp in length
* 41831 41930: gap of 100 bp
* 41931 42669: contig of 739 bp in length
* 42670 42769: gap of 100 bp
* 42770 43503: contig of 734 bp in length
* 43504 43603: gap of 100 bp
* 43604 44317: contig of 714 bp in length
* 44318 44417: gap of 100 bp
* 44418 45132: contig of 715 bp in length
* 45133 45232: gap of 100 bp
* 45233 45954: contig of 722 bp in length
* 45955 46054: gap of 100 bp
* 46055 46768: contig of 714 bp in length
* 46769 46868: gap of 100 bp
* 46869 47613: contig of 745 bp in length
* 47614 47713: gap of 100 bp
* 47714 48455: contig of 742 bp in length
* 48456 48555: gap of 100 bp
* 48556 49289: contig of 734 bp in length
* 49290 49389: gap of 100 bp
* 49390 50129: contig of 740 bp in length
* 50130 50229: gap of 100 bp
* 50230 50969: contig of 740 bp in length
* 50970 51069: gap of 100 bp
* 51070 51800: contig of 731 bp in length
* 51801 51900: gap of 100 bp
* 51901 52622: contig of 722 bp in length
* 52623 52722: gap of 100 bp

```

```

Query Match      77.8%   Score 14; DB 2; Length 59918;
Best Local Similarity 85.7%   Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Cy      5 UCCUGAGGNNNNNN 18
Db      4827 TCCTGAGNNNNNN 4840

```

```

RESULT 51
LOCUS      AC125441
DEFINITION Mus musculus clone RP24-487N17, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC125441
VERSION     AC125441.1 GI:21591995
KEYWORDS   HTG; HTGS PHASE0.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

REFERENCE   1 (bases 1 to 62676)
AUTHORS     Birren, B., Nussbaum, C. and Lander, E.
TITLE       Mus musculus, clone RP24-487N17
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 62676)
AUTHORS     Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
            Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
            Camarata, U., Chang, J., Charazro, B., Choepel, T., Collymore, A.,
            Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J.S., Dodge, S.,
            Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
            Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagob, B.,
            Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
            Karlas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K.,
            Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C.,
            McCarthy, M., Meldrum, J., Menues, L., Mihova, T., Mlenga, V.,
            Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
            O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
            Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
            Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
            Smith, C., Spencer, B., Strange-Rhoman, N., Stojanovic, N., Talamas, J.,
            Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
            Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
            Zemek, L., Zimmer, A. and Zody, M.

```

```

TITLE       Direct Submission
JOURNAL     Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26703
Center clone name: 487_N_17

```

```

* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely

```

```
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 712: contig of 712 bp in length
* 713 812: gap of 100 bp
* 813 1582: contig of 770 bp in length
* 1583 1682: gap of 100 bp
* 1683 2455: contig of 773 bp in length
* 2456 2555: gap of 100 bp
* 2556 3265: contig of 711 bp in length
* 3267 3365: gap of 100 bp
* 3367 4088: contig of 722 bp in length
* 4089 4188: gap of 100 bp
* 4189 4919: contig of 731 bp in length
* 4920 5019: gap of 100 bp
* 5020 5775: contig of 756 bp in length
* 5776 5875: gap of 100 bp
* 5876 6639: contig of 764 bp in length
* 6640 6739: gap of 100 bp
* 6740 7502: contig of 763 bp in length
* 7503 7602: gap of 100 bp
* 7603 8356: contig of 754 bp in length
* 8357 8456: gap of 100 bp
* 8457 9194: contig of 738 bp in length
* 9195 9294: gap of 100 bp
* 9295 10048: contig of 754 bp in length
* 10049 10148: gap of 100 bp
* 10149 10876: contig of 728 bp in length
* 10877 10976: gap of 100 bp
* 10977 11744: contig of 768 bp in length
* 11745 11844: gap of 100 bp
* 11845 12609: contig of 765 bp in length
* 12610 12709: gap of 100 bp
* 12710 13425: contig of 716 bp in length
* 13426 13525: gap of 100 bp
* 13526 14296: contig of 771 bp in length
* 14297 14396: gap of 100 bp
* 14397 15143: contig of 747 bp in length
* 15144 15243: gap of 100 bp
* 15243 15970: contig of 727 bp in length
* 15971 16070: gap of 100 bp
* 16071 16811: contig of 741 bp in length
* 16812 16911: gap of 100 bp
* 16912 17636: contig of 725 bp in length
* 17637 17736: gap of 100 bp
* 17737 18489: contig of 753 bp in length
* 18490 18589: gap of 100 bp
* 18590 19347: contig of 758 bp in length
* 19348 19447: gap of 100 bp
* 19448 20212: contig of 765 bp in length
* 20213 20312: gap of 100 bp
* 20313 21021: contig of 709 bp in length
* 21022 21121: gap of 100 bp
* 21122 21890: contig of 769 bp in length
* 21891 21990: gap of 100 bp
* 21991 22718: contig of 728 bp in length
* 22719 22818: gap of 100 bp
* 22819 23553: contig of 735 bp in length
* 23554 23653: gap of 100 bp
* 23654 24397: contig of 744 bp in length
* 24398 24497: gap of 100 bp
* 24498 25256: contig of 759 bp in length
* 25257 25356: gap of 100 bp
* 25357 26104: contig of 748 bp in length
* 26105 26204: gap of 100 bp
* 26205 26965: contig of 761 bp in length
* 26966 27065: gap of 100 bp
* 27066 27818: contig of 753 bp in length
* 27819 27918: gap of 100 bp
*
* 27919 28681: contig of 763 bp in length
* 28682 28781: gap of 100 bp
* 28782 29492: contig of 711 bp in length
* 29493 29592: gap of 100 bp
* 29593 30353: contig of 761 bp in length
* 30354 30453: gap of 100 bp
* 30454 31230: contig of 777 bp in length
* 31231 31330: gap of 100 bp
* 31331 32081: contig of 751 bp in length
* 32082 32181: gap of 100 bp
* 32182 32897: contig of 716 bp in length
* 32898 32997: gap of 100 bp
* 32999 33718: contig of 721 bp in length
* 33719 33818: gap of 100 bp
* 33819 34565: contig of 747 bp in length
* 34566 34665: gap of 100 bp
* 34666 35410: contig of 745 bp in length
* 35411 35510: gap of 100 bp
* 35511 36277: contig of 767 bp in length
* 36278 36377: gap of 100 bp
* 36378 37130: contig of 753 bp in length
* 37131 37230: gap of 100 bp
* 37231 37997: contig of 767 bp in length
* 37998 38097: gap of 100 bp
* 38098 38863: contig of 766 bp in length
* 38864 38963: gap of 100 bp
* 38964 39719: contig of 756 bp in length
* 39720 39819: gap of 100 bp
* 39820 40572: contig of 753 bp in length
* 40573 40672: gap of 100 bp
* 40673 41416: contig of 744 bp in length
* 41417 41516: gap of 100 bp
* 41517 42238: contig of 722 bp in length
* 42239 42338: gap of 100 bp
* 42340 43072: contig of 734 bp in length
* 43073 43172: gap of 100 bp
* 43173 43923: contig of 751 bp in length
* 43924 44023: gap of 100 bp
* 44024 44785: contig of 762 bp in length
* 44786 44885: gap of 100 bp
* 44886 45637: contig of 752 bp in length
* 45638 45737: gap of 100 bp
* 45738 46490: contig of 753 bp in length
* 46491 46590: gap of 100 bp
* 46591 47355: contig of 765 bp in length
* 47356 47455: gap of 100 bp
* 47456 48219: contig of 764 bp in length
* 48220 48319: gap of 100 bp
* 48320 49027: contig of 708 bp in length
* 49028 49127: gap of 100 bp
* 49128 49885: contig of 758 bp in length
* 49886 49985: gap of 100 bp
* 49986 50743: contig of 758 bp in length
* 50744 50843: gap of 100 bp
* 50844 51597: contig of 754 bp in length
* 51598 51697: gap of 100 bp
* 51698 52398: contig of 701 bp in length
* 52399 52498: gap of 100 bp
* 52499 53237: contig of 739 bp in length
* 53238 53337: gap of 100 bp
* 53338 54097: contig of 760 bp in length
* 54098 54197: gap of 100 bp
* 54198 54952: contig of 755 bp in length
* 54953 55052: gap of 100 bp
* 55053 55818: contig of 766 bp in length
* 55819 55918: gap of 100 bp
* 55919 56683: contig of 765 bp in length
* 56684 56783: gap of 100 bp
* 56784 57512: contig of 729 bp in length
* 57513 57612: gap of 100 bp
* 57613 58380: contig of 768 bp in length
* 58381 58480: gap of 100 bp
* 58481 59236: contig of 756 bp in length
```

```

*      59237      59336: gap of 100 bp
*      59337      60090: contig of 754 bp in length
*      60091      60190: gap of 100 bp

Query Match      77.8%; Score 14; DB 2; Length 62676;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy      5 UCCUGAGANNNNNN 18
      :||:|||||
Db      50735 TCCTGAGANNNNNN 50748

RESULT 52
LOCUS AC062003
DEFINITION Homo sapiens chromosome 11 clone RP11-132H5 map 11, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC062003
VERSION AC062003.1 GI:7630742
KEYWORDS HTG; HTGS_PHASED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 64345)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barra,N., Bastien,V., Beda,F.,
Boguslavsky,L., Bouckigalter,B., Brown,A., Burkett,G.,
Campilano,A., Casale,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,D.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galaan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karataas,A.,
Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehocsky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Margulis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisan,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
Submitted (21-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L9886
Center Clone name: 132_H_5

```

```

* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
697 696: contig of 696 bp in length
797 796: gap of 100 bp
1501 1500: contig of 704 bp in length
1601 1600: gap of 100 bp
2298 2298: contig of 698 bp in length
2399 2398: gap of 100 bp
3099 3099: contig of 701 bp in length
3199 3199: gap of 100 bp
3200 3200: gap of 100 bp
3907 3907: contig of 708 bp in length
3908 4007: gap of 100 bp
4008 4683: contig of 676 bp in length
4684 4783: gap of 100 bp
4784 5495: contig of 712 bp in length
5496 5595: gap of 100 bp
5596 6303: contig of 708 bp in length
6304 6403: gap of 100 bp
6404 7109: contig of 706 bp in length
7110 7209: gap of 100 bp
7210 7917: contig of 708 bp in length
7918 8017: gap of 100 bp
8018 8720: contig of 703 bp in length
8721 8820: gap of 100 bp
8821 9522: contig of 702 bp in length
9523 9622: gap of 100 bp
9623 10322: contig of 700 bp in length
10323 10422: gap of 100 bp
10423 11149: contig of 727 bp in length
11150 11249: gap of 100 bp
11250 11962: contig of 713 bp in length
11963 12062: gap of 100 bp
12063 12767: contig of 705 bp in length
12768 12867: gap of 100 bp
12868 13575: contig of 708 bp in length
13576 13675: gap of 100 bp
13676 14364: contig of 689 bp in length
14365 14464: gap of 100 bp
14465 15167: contig of 703 bp in length
15168 15267: gap of 100 bp
15268 15968: contig of 701 bp in length
15969 16068: gap of 100 bp
16069 16771: contig of 703 bp in length
16771 16871: gap of 100 bp
16872 17567: contig of 696 bp in length
17568 18372: gap of 100 bp
18373 18472: gap of 100 bp
18473 19172: contig of 700 bp in length
19173 19272: gap of 100 bp
19273 19993: contig of 721 bp in length
19993 20093: gap of 100 bp
20094 20813: contig of 720 bp in length
20814 20913: gap of 100 bp
20914 21626: contig of 713 bp in length
21627 21726: gap of 100 bp
21727 22425: contig of 699 bp in length
22426 22525: gap of 100 bp
22526 23319: contig of 694 bp in length
23319 23319: gap of 100 bp
23320 24037: contig of 718 bp in length
24038 24137: gap of 100 bp
24138 24853: contig of 716 bp in length
24854 24953: gap of 100 bp
24954 25669: contig of 716 bp in length
25670 25770: gap of 100 bp
25770 26479: contig of 710 bp in length
26479 26579: gap of 100 bp
26580 27282: contig of 703 bp in length
27283 27382: gap of 100 bp
27383 28102: contig of 720 bp in length

```

\* NOTE: This record contains 80 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.

Query Match	Similarity	Score	DB	Length
Best Local	Best Local	Pred. No.	1e-02	64345
Matches	12; Conservative	2; Mismatches	0; Indels	0; Gaps
*	28103	28202: gap of 100 bp	in length	
*	28203	28912: contig of 710 bp	in length	
*	28203	29012: gap of 100 bp	in length	
*	28913	29739: contig of 727 bp	in length	
*	29013	29839: gap of 100 bp	in length	
*	29740	29839: gap of 100 bp	in length	
*	29840	30552: contig of 713 bp	in length	
*	30553	30652: gap of 100 bp	in length	
*	30653	31339: contig of 687 bp	in length	
*	31340	31449: gap of 100 bp	in length	
*	31440	32115: contig of 676 bp	in length	
*	32116	32215: gap of 100 bp	in length	
*	32216	32917: contig of 702 bp	in length	
*	32918	33017: gap of 100 bp	in length	
*	33018	33728: contig of 711 bp	in length	
*	33729	33828: gap of 100 bp	in length	
*	33829	34540: contig of 712 bp	in length	
*	34541	34640: gap of 100 bp	in length	
*	34641	35349: contig of 709 bp	in length	
*	35350	35449: gap of 100 bp	in length	
*	35450	36170: contig of 721 bp	in length	
*	36171	36270: gap of 100 bp	in length	
*	36271	36980: contig of 710 bp	in length	
*	36981	37080: gap of 100 bp	in length	
*	37081	37809: contig of 729 bp	in length	
*	37810	37909: gap of 100 bp	in length	
*	37910	38612: contig of 703 bp	in length	
*	38613	38712: gap of 100 bp	in length	
*	38713	39412: contig of 700 bp	in length	
*	39413	39512: gap of 100 bp	in length	
*	39513	40207: contig of 695 bp	in length	
*	40208	40307: gap of 100 bp	in length	
*	40308	41001: contig of 694 bp	in length	
*	41002	41101: gap of 100 bp	in length	
*	41102	41812: contig of 711 bp	in length	
*	41813	41912: gap of 100 bp	in length	
*	41913	42613: contig of 701 bp	in length	
*	42614	42713: gap of 100 bp	in length	
*	42714	43421: contig of 708 bp	in length	
*	43422	43521: gap of 100 bp	in length	
*	43522	44236: contig of 715 bp	in length	
*	44237	44336: gap of 100 bp	in length	
*	44337	45045: contig of 709 bp	in length	
*	45046	45145: gap of 100 bp	in length	
*	45146	45811: contig of 686 bp	in length	
*	45812	45931: gap of 100 bp	in length	
*	45932	46638: contig of 707 bp	in length	
*	46639	46738: gap of 100 bp	in length	
*	46739	47452: contig of 714 bp	in length	
*	47453	47552: gap of 100 bp	in length	
*	47553	48261: contig of 709 bp	in length	
*	48262	48361: gap of 100 bp	in length	
*	48362	49059: contig of 698 bp	in length	
*	49060	49159: gap of 100 bp	in length	
*	49160	49862: contig of 703 bp	in length	
*	49863	49962: gap of 100 bp	in length	
*	49963	50667: contig of 705 bp	in length	
*	50668	50767: gap of 100 bp	in length	
*	50768	51462: contig of 695 bp	in length	
*	51463	51562: gap of 100 bp	in length	
*	51563	52280: contig of 718 bp	in length	
*	52281	52380: gap of 100 bp	in length	
*	52381	53094: contig of 714 bp	in length	
*	53095	53194: gap of 100 bp	in length	
*	53195	53865: contig of 671 bp	in length	
*	53866	53965: gap of 100 bp	in length	
*	53966	54663: contig of 698 bp	in length	
*	54664	54763: gap of 100 bp	in length	
*	54764	55470: contig of 707 bp	in length	
*	55471	55570: gap of 100 bp	in length	

```

0Y      5 UCCUGAGGANNNNN 18
Db      49052 TCCTGGAGANNNNN 49065

RESULT 53
AC025214          65174 bp   DNA       linear    HTG 07-MAR-2000
LOCUS AC025214
DEFINITION Homo sapiens chromosome 1 clone RP11-25B7 map 1, LOW-PASS SEQUENCE
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 65174)
AUTHORS Birren, B., Linton, L., Nussbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 1, clone RP11-25B7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 65174)
AUTHORS Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barre, N., Bastien, V., Beda, F.,
Bogdanavskiy, L., Boukhalter, B., Brown, A., Burkett, G.,
Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Glade, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karstae, A.,
Klein, J., Larocque, K., Lamazares, R., Landers, T., Lenoczky, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Margulis, N.,
McCarthy, M., McEwan, P., McGuck, T., McKernan, K., McPeeters, R.,
Meldrum, J., Menus, L., Mihov, T., Miranda, C., Mieng, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tessier, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainou, J., Zimmer, A. and Zody, M.
COMMENT Direct Submission
Submitted (07-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7950
Center clone name: 25_B_7
-----
* NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
689: contig of 689 bp in length
690
789: gap of 100 bp
790
1486: contig of 697 bp in length

```

1487 1586: gap of 100 bp  
1587 2280: contig of 694 bp in length  
2281 2380: gap of 100 bp  
2381 3071: contig of 691 bp in length  
3072 3171: gap of 100 bp  
3172 3865: contig of 695 bp in length  
3867 3965: gap of 100 bp  
3967 4664: contig of 698 bp in length  
4665 4764: gap of 100 bp  
4765 5467: contig of 703 bp in length  
5468 5567: gap of 100 bp  
5568 6263: contig of 696 bp in length  
6264 6363: gap of 100 bp  
6364 7084: contig of 721 bp in length  
7085 7184: gap of 100 bp  
7185 7841: contig of 657 bp in length  
7842 7941: gap of 100 bp  
7942 8638: contig of 697 bp in length  
8639 8738: gap of 100 bp  
8739 9431: contig of 693 bp in length  
9432 9531: gap of 100 bp  
9532 10235: contig of 704 bp in length  
10236 10335: gap of 100 bp  
10336 11052: contig of 717 bp in length  
11053 11152: gap of 100 bp  
11153 11855: contig of 703 bp in length  
11856 11955: gap of 100 bp  
11956 12666: contig of 711 bp in length  
12667 12766: gap of 100 bp  
12767 13465: contig of 699 bp in length  
13466 13565: gap of 100 bp  
13566 14265: contig of 700 bp in length  
14266 14365: gap of 100 bp  
14366 15069: contig of 704 bp in length  
15070 15169: gap of 100 bp  
15170 15857: contig of 688 bp in length  
15858 15957: gap of 100 bp  
15959 16643: contig of 686 bp in length  
16644 16743: gap of 100 bp  
16744 17437: contig of 694 bp in length  
17438 17537: gap of 100 bp  
17538 18221: contig of 684 bp in length  
18222 18321: gap of 100 bp  
18322 19004: contig of 683 bp in length  
19005 19104: gap of 100 bp  
19105 19819: contig of 715 bp in length  
19820 19919: gap of 100 bp  
19920 20604: contig of 685 bp in length  
20605 20704: gap of 100 bp  
20705 21403: contig of 699 bp in length  
21404 21503: gap of 100 bp  
21504 22200: contig of 697 bp in length  
22201 22300: gap of 100 bp  
22301 23007: contig of 707 bp in length  
23008 23107: gap of 100 bp  
23108 23805: contig of 698 bp in length  
23806 23905: gap of 100 bp  
23906 24597: contig of 692 bp in length  
24598 24697: gap of 100 bp  
24698 25394: contig of 697 bp in length  
25395 25494: gap of 100 bp  
25495 26178: contig of 684 bp in length  
26179 26278: gap of 100 bp  
26279 26970: contig of 692 bp in length  
26971 27070: gap of 100 bp  
27071 27783: contig of 713 bp in length  
27784 27883: gap of 100 bp  
27884 28583: contig of 700 bp in length  
28584 29408: contig of 725 bp in length  
29409 29508: gap of 100 bp  
29509 30221: contig of 713 bp in length  
30222 30321: gap of 100 bp

30322 31022: contig of 701 bp in length  
31023 31122: gap of 100 bp  
31123 31808: contig of 686 bp in length  
31809 31908: gap of 100 bp  
31909 32583: contig of 675 bp in length  
32584 32683: gap of 100 bp  
32684 33371: contig of 688 bp in length  
33372 33471: gap of 100 bp  
33472 34163: contig of 692 bp in length  
34164 34263: gap of 100 bp  
34264 34933: contig of 670 bp in length  
34934 35033: gap of 100 bp  
35034 35680: contig of 647 bp in length  
35681 35780: gap of 100 bp  
35781 36484: contig of 704 bp in length  
36485 36584: gap of 100 bp  
36585 37306: contig of 722 bp in length  
37307 37406: gap of 100 bp  
37407 38105: contig of 699 bp in length  
38106 38205: gap of 100 bp  
38206 38897: contig of 692 bp in length  
38898 38997: gap of 100 bp  
38998 39694: contig of 697 bp in length  
39695 39794: gap of 100 bp  
39795 40492: contig of 698 bp in length  
40493 40592: gap of 100 bp  
40593 41279: contig of 687 bp in length  
41280 41379: gap of 100 bp  
41380 42055: contig of 676 bp in length  
42056 42155: gap of 100 bp  
42156 42850: contig of 695 bp in length  
42851 42950: gap of 100 bp  
42952 43552: contig of 702 bp in length  
43553 43752: gap of 100 bp  
43753 44467: contig of 715 bp in length  
44468 44567: gap of 100 bp  
44568 45268: contig of 701 bp in length  
45269 45368: gap of 100 bp  
45369 46078: contig of 710 bp in length  
46079 46178: gap of 100 bp  
46179 46860: contig of 682 bp in length  
46861 46960: gap of 100 bp  
46961 47663: contig of 703 bp in length  
47664 47763: gap of 100 bp  
47764 48430: contig of 667 bp in length  
48431 48530: gap of 100 bp  
48531 49221: contig of 691 bp in length  
49222 49321: gap of 100 bp  
49322 50016: contig of 695 bp in length  
50017 50116: gap of 100 bp  
50117 50830: contig of 714 bp in length  
50831 50930: gap of 100 bp  
50931 51612: contig of 682 bp in length  
51613 51712: gap of 100 bp  
51713 52400: contig of 688 bp in length  
52401 52500: gap of 100 bp  
52501 53310: contig of 710 bp in length  
53310 53310: gap of 100 bp  
53311 53996: contig of 686 bp in length  
53997 54096: gap of 100 bp  
54097 54810: contig of 714 bp in length  
54811 54910: gap of 100 bp

Query Match 77.8%; Score 14; DB 2; Length 65174;  
Best Local Similarity 85.7%; Pred. No. 1e+02; 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 0; Indels 0;

Qy 5 UCCUGAGNNNNNN 18  
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Db 47656 TCCTGAGNNNNNN 47669

RESULT 54

AC100485  
 LOCUS AC100485 66795 bp DNA linear HTG 30-JUL-2002  
 DEFINITION Mus musculus clone RP23-142A10, LOW-PASS SEQUENCE SAMPLING.  
 ACCESSION AC100485  
 VERSION AC100485.2 GI:22004531  
 KEYWORDS HTG; HTGS PHASE0.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 66795)  
 AUTHORS Birren, B., Nusbaum, C. and Lander, E.  
 TITLE Mus musculus, clone RP23-142A10  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 66795)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Baetien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M., McKean, P., McKernan, K., McNeeters, R., Melidim, J., Menueu, L., Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Nobdu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santoe, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 DIRECT SUBMISSION  
 JOURNAL Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REFERENCE 3 (bases 1 to 66795)  
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Melidim, J., Menueu, L., Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Nobdu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 DIRECT SUBMISSION  
 JOURNAL Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 COMMENT On Jul 30, 2002 this sequence version replaced g1:17047851.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/MIT Center for Genome Research  
 Center code: WIDR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L15450

Center clone name: 142\_A\_10  
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 \* NOTE: This record contains 86 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.  
 \* 1  
 \* 664 663: contig of 663 bp in length  
 \* 764 763: gap of 100 bp  
 \* 1438 1437: contig of 674 bp in length  
 \* 1538 1537: gap of 100 bp  
 \* 2213 2212: contig of 675 bp in length  
 \* 2213 2212: gap of 100 bp  
 \* 2313 2297: contig of 685 bp in length  
 \* 2998 3097: gap of 100 bp  
 \* 3098 3784: contig of 687 bp in length  
 \* 3785 3884: gap of 100 bp  
 \* 3885 4574: contig of 690 bp in length  
 \* 4575 4674: gap of 100 bp  
 \* 4675 5350: contig of 676 bp in length  
 \* 5351 5450: gap of 100 bp  
 \* 5451 6104: contig of 654 bp in length  
 \* 6105 6204: gap of 100 bp  
 \* 6205 6874: contig of 670 bp in length  
 \* 6875 6974: gap of 100 bp  
 \* 6975 7655: contig of 681 bp in length  
 \* 7656 7735: gap of 100 bp  
 \* 7736 8432: contig of 677 bp in length  
 \* 8433 8532: gap of 100 bp  
 \* 8533 9208: contig of 676 bp in length  
 \* 9209 9308: gap of 100 bp  
 \* 9309 9982: contig of 674 bp in length  
 \* 9983 10082: gap of 100 bp  
 \* 10083 10754: contig of 672 bp in length  
 \* 10755 10854: gap of 100 bp  
 \* 10855 11535: contig of 681 bp in length  
 \* 11536 11635: gap of 100 bp  
 \* 11636 12322: contig of 687 bp in length  
 \* 12323 12422: gap of 100 bp  
 \* 12423 13114: contig of 692 bp in length  
 \* 13115 13214: gap of 100 bp  
 \* 13215 13894: contig of 680 bp in length  
 \* 13895 13994: gap of 100 bp  
 \* 13995 14655: contig of 661 bp in length  
 \* 14656 14755: gap of 100 bp  
 \* 14756 15418: contig of 663 bp in length  
 \* 15419 15518: gap of 100 bp  
 \* 15519 16196: contig of 678 bp in length  
 \* 16197 16296: gap of 100 bp  
 \* 16297 16969: contig of 673 bp in length  
 \* 16970 17069: gap of 100 bp  
 \* 17070 17758: contig of 689 bp in length  
 \* 17759 17858: gap of 100 bp  
 \* 17859 18543: contig of 685 bp in length  
 \* 18544 18643: gap of 100 bp  
 \* 18644 19318: contig of 675 bp in length  
 \* 19319 19418: gap of 100 bp  
 \* 19419 20095: contig of 677 bp in length  
 \* 20096 20195: gap of 100 bp  
 \* 20196 20888: contig of 693 bp in length  
 \* 20889 20988: gap of 100 bp  
 \* 20989 21680: contig of 692 bp in length  
 \* 21681 21780: gap of 100 bp  
 \* 21781 22461: contig of 681 bp in length  
 \* 22462 22561: gap of 100 bp  
 \* 22562 23228: contig of 667 bp in length  
 \* 23229 23328: gap of 100 bp

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* 23339 24012: contig of 664 bp in length
* 24013 24112: gap of 100 bp
* 24113 24790: contig of 678 bp in length
* 24791 24891: gap of 100 bp
* 24891 25564: contig of 674 bp in length
* 25565 25664: gap of 100 bp
* 25665 26353: contig of 689 bp in length
* 26354 27116: gap of 100 bp
* 27117 27217: gap of 100 bp
* 27217 27891: contig of 674 bp in length
* 27891 28786: contig of 696 bp in length
* 28787 28786: gap of 100 bp
* 28787 29472: contig of 685 bp in length
* 29472 29571: gap of 100 bp
* 29571 30236: contig of 665 bp in length
* 30237 30336: gap of 100 bp
* 30337 31024: contig of 688 bp in length
* 31025 31124: gap of 100 bp
* 31125 31801: contig of 677 bp in length
* 31802 31901: gap of 100 bp
* 31902 32570: contig of 669 bp in length
* 32571 32670: gap of 100 bp
* 32671 33351: contig of 681 bp in length
* 33352 33451: gap of 100 bp
* 33452 34117: contig of 666 bp in length
* 34118 34217: gap of 100 bp
* 34218 34894: contig of 677 bp in length
* 34895 34994: gap of 100 bp
* 34995 35668: contig of 674 bp in length
* 35669 35768: gap of 100 bp
* 35769 36442: contig of 674 bp in length
* 36443 36542: gap of 100 bp
* 36543 37225: contig of 683 bp in length
* 37226 37325: gap of 100 bp
* 37326 37998: contig of 673 bp in length
* 37999 38098: gap of 100 bp
* 38099 38786: contig of 687 bp in length
* 38787 38885: gap of 100 bp
* 38886 39566: contig of 681 bp in length
* 39567 39666: gap of 100 bp
* 39667 40345: contig of 679 bp in length
* 40346 40445: gap of 100 bp
* 40446 41124: contig of 679 bp in length
* 41125 41225: gap of 100 bp
* 41226 41900: contig of 676 bp in length
* 41901 42000: gap of 100 bp
* 42001 42693: contig of 693 bp in length
* 42694 42793: gap of 100 bp
* 42794 43469: contig of 676 bp in length
* 43470 43569: gap of 100 bp
* 43570 44232: contig of 663 bp in length
* 44233 44332: gap of 100 bp
* 44333 45033: contig of 701 bp in length

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Query Match 77.8%; Score 14; DB 2; Length 66795;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGANNNNNN 18  
 Db 44225 TCCTGAGANNNNNN 44238

RESULT 55  
 AC027792  
 LOCUS AC027792 Homo sapiens chromosome 17 clone RP11-222B7 map 17, LOW-PASS  
 DEFINITION  
 SEQUENCE SAMPLING.  
 AC027792  
 ACCESSION AC027792.1 GI:7382634  
 VERSION  
 KEYWORDS HTG; HTGS\_PHASE0.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 REFERENCE 1 (bases 1 to 67822)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 TITLE Homo sapiens chromosome 17, clone RP11-222B7  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 67822)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
 Anderson, S., Baldwin, J., Barua, N., Baetsen, V., Bede, F.,  
 Boguslavsky, L., Bouckgalter, J., Brown, A., Burkett, G.,  
 Campione, A., Castle, A., Choe, Y., Colangelo, M., Collins, S.,  
 Collymore, A., Cooke, P., DeRubeis, K., Dewar, K., Diaz, J.S.,  
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,  
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 Grand-pierre, N., Grant, G., Hages, B., Heath, A., Horton, L.,  
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 Klein, J., Larocque, K., Lamazares, R., Landers, T., Lenoczky, J.,  
 Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,  
 McCarthy, M., McEwan, P., McGuire, A., McKernan, K., McKeeters, R.,  
 Meldrum, J., Menus, L., Mihova, T., Miranda, C., Mianga, V., Morrow, J.,  
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,  
 Pisanu, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talmas, J.,  
 Testa, S., Theodore, J., Tizell, A., Travers, M., Trigg, J.,  
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
 Direct Submission

TITLE  
 JOURNAL  
 COMMENT  
 Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

Project Information

Center project name: L9026

Center clone name: 222\_B.7

NOTE: This record contains 76 individual  
 sequencing reads that have not been assembled into  
 contigs. Runs of N are used to separate the reads  
 and the order in which they appear is completely  
 arbitrary. Low-pass sequence sampling is useful for  
 identifying clones that may be gene-rich and allows  
 overlap relationships among clones to be deduced.  
 However, it should not be assumed that this clone  
 will be sequenced to completion. In the event that  
 the record is updated, the accession number will  
 be preserved.

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1 778: contig of 778 bp in length
779 878: gap of 100 bp
879 1676: contig of 798 bp in length
1677 1776: gap of 100 bp
1777 2564: contig of 788 bp in length
2565 2664: gap of 100 bp
2665 3450: contig of 786 bp in length
3451 3551: gap of 100 bp
3551 4345: contig of 795 bp in length
4346 4446: gap of 100 bp
4446 5232: contig of 787 bp in length
5233 6138: gap of 100 bp
6138 6238: contig of 806 bp in length
6239 7032: gap of 100 bp
7033 7132: contig of 794 bp in length
7133 7920: gap of 100 bp
7920: contig of 788 bp in length

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\* 7921 8020: gap of 100 bp  
\* 8021 8813: contig of 793 bp in length  
\* 8814 8913: gap of 100 bp  
\* 8914 9690: contig of 777 bp in length  
\* 9691 9790: gap of 100 bp  
\* 9791 10568: contig of 778 bp in length  
\* 10569 10668: gap of 100 bp  
\* 10669 11453: contig of 785 bp in length  
\* 11454 11553: gap of 100 bp  
\* 11554 12321: contig of 768 bp in length  
\* 12322 12421: gap of 100 bp  
\* 12421 13216: contig of 795 bp in length  
\* 13217 13316: gap of 100 bp  
\* 13317 14121: contig of 805 bp in length  
\* 14122 14221: gap of 100 bp  
\* 14222 14996: contig of 775 bp in length  
\* 14997 15096: gap of 100 bp  
\* 15097 15903: contig of 807 bp in length  
\* 15904 16004: gap of 100 bp  
\* 16004 16810: contig of 807 bp in length  
\* 16811 16910: gap of 100 bp  
\* 16911 17716: contig of 806 bp in length  
\* 17717 17816: gap of 100 bp  
\* 17817 18607: contig of 791 bp in length  
\* 18608 18707: gap of 100 bp  
\* 18708 19492: contig of 785 bp in length  
\* 19493 19592: gap of 100 bp  
\* 19593 20373: contig of 781 bp in length  
\* 20374 20473: gap of 100 bp  
\* 20474 21283: contig of 810 bp in length  
\* 21284 21383: gap of 100 bp  
\* 21384 22166: contig of 783 bp in length  
\* 22167 22266: gap of 100 bp  
\* 22267 23063: contig of 797 bp in length  
\* 23064 23163: gap of 100 bp  
\* 23164 23956: contig of 793 bp in length  
\* 23957 24056: gap of 100 bp  
\* 24057 24858: contig of 802 bp in length  
\* 24859 24958: gap of 100 bp  
\* 24959 25760: contig of 802 bp in length  
\* 25761 25860: gap of 100 bp  
\* 25861 26662: contig of 802 bp in length  
\* 26663 26763: gap of 100 bp  
\* 26763 27537: contig of 774 bp in length  
\* 27537 27636: gap of 100 bp  
\* 27637 28430: contig of 794 bp in length  
\* 28431 28530: gap of 100 bp  
\* 28531 29333: contig of 803 bp in length  
\* 29334 29433: gap of 100 bp  
\* 29434 30240: contig of 806 bp in length  
\* 30240 30339: gap of 100 bp  
\* 30340 31121: contig of 782 bp in length  
\* 31122 31221: gap of 100 bp  
\* 31222 32013: contig of 792 bp in length  
\* 32014 32113: gap of 100 bp  
\* 32114 32908: contig of 795 bp in length  
\* 32909 33008: gap of 100 bp  
\* 33009 33806: contig of 798 bp in length  
\* 33807 33906: gap of 100 bp  
\* 33907 34692: contig of 786 bp in length  
\* 34693 34792: gap of 100 bp  
\* 34793 35568: contig of 776 bp in length  
\* 35569 35668: gap of 100 bp  
\* 35669 36465: contig of 797 bp in length  
\* 36466 36566: gap of 100 bp  
\* 36567 37354: contig of 789 bp in length  
\* 37355 37454: gap of 100 bp  
\* 37455 38242: contig of 788 bp in length  
\* 38243 38342: gap of 100 bp  
\* 38343 39138: contig of 796 bp in length  
\* 39139 39238: gap of 100 bp  
\* 39239 40028: contig of 790 bp in length  
\* 40029 40128: gap of 100 bp

\* 40129 40909: contig of 781 bp in length  
\* 40910 41009: gap of 100 bp  
\* 41010 41826: contig of 817 bp in length  
\* 41827 41926: gap of 100 bp  
\* 41927 42720: contig of 794 bp in length  
\* 42721 42820: gap of 100 bp  
\* 42821 43631: contig of 811 bp in length  
\* 43632 43731: gap of 100 bp  
\* 43732 44532: contig of 801 bp in length  
\* 44533 44632: gap of 100 bp  
\* 44633 44545: contig of 819 bp in length  
\* 44546 45551: gap of 100 bp  
\* 45552 46335: contig of 784 bp in length  
\* 46336 46436: gap of 100 bp  
\* 46437 47247: contig of 811 bp in length  
\* 47248 47347: gap of 100 bp  
\* 47347 48126: contig of 780 bp in length  
\* 48127 48226: gap of 100 bp  
\* 48227 49003: contig of 777 bp in length  
\* 49004 49103: gap of 100 bp  
\* 49104 49900: contig of 797 bp in length  
\* 49901 50001: gap of 100 bp  
\* 50001 50779: contig of 779 bp in length  
\* 50780 50879: gap of 100 bp  
\* 50880 51676: contig of 797 bp in length  
\* 51677 51776: gap of 100 bp  
\* 51777 52552: contig of 776 bp in length  
\* 52553 52652: gap of 100 bp  
\* 52653 53450: contig of 798 bp in length  
\* 53451 53550: gap of 100 bp  
\* 53551 54352: contig of 802 bp in length  
\* 54353 54452: gap of 100 bp  
\* 54453 55253: contig of 803 bp in length  
\* 55254 55355: gap of 100 bp  
\* 55356 56151: contig of 796 bp in length  
\* 56152 56251: gap of 100 bp  
\* 56252 57033: contig of 782 bp in length  
\* 57034 57134: gap of 100 bp  
\* 57134 57925: contig of 792 bp in length  
\* 57926 58025: gap of 100 bp  
\* 58026 58857: contig of 832 bp in length  
\* 58858 58957: gap of 100 bp  
\* 58958 59748: contig of 791 bp in length  
\* 59749 59849: gap of 100 bp  
\* 59849 60650: contig of 802 bp in length  
\* 60651 60751: gap of 100 bp  
\* 60751 61555: contig of 804 bp in length  
\* 61555 61654: gap of 100 bp

Query Match 77.8%; Score 14; DB 2; Length 67822;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 UCCUGAGNNNNNN 18  
Db 33799 TCCTGGAGNNNNNN 33812

RESULT 56  
AC102023 73882 bp DNA linear HTG 23-NOV-2001  
LOCUS  
DEFINITION Mus musculus clone RP24-68N17, LOW-PASS SEQUENCE SAMPLING.  
AC102023  
ACCESSION  
VERSION AC102023.1 GI:17061109  
KEYWORDS HTG; HTGS PHASED.  
SOURCE  
MUS musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 73882)  
AUTHORS Birren,B., Linton,L., Nuebaum,C. and Lander,E.  
TITLE  
JOURNAL Mus musculus, clone RP24-68N17  
Unpublished

REFERENCE  
AUTHORS

2 (bases 1 to 73882)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Batra, N., Basteien, V., Boguslavsky, L., Bouckgalter, B.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Choepe, I., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooke, P., DeRellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,  
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,  
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
Jones, C., Kanat, A., Karatas, A., Kells, C., LaRocque, K.,  
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,  
McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Melidrin, J.,  
Menesh, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,  
Oliver, J., Peterson, K., Phunthang, P., Pierre, N., Pollard, V.,  
Raymond, C., Rella, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,  
Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talmas, J., Tesfaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L17890  
Center clone name: 68\_N\_17

\*\*\*\*\* NOTE: This record contains 88 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
747 746: contig of 746 bp in length  
847 846: gap of 100 bp  
1577 1576: contig of 730 bp in length  
1677 1676: gap of 100 bp  
2426 2425: contig of 749 bp in length  
2526 2525: gap of 100 bp  
3221 3221: contig of 696 bp in length  
3322 3321: gap of 100 bp  
4086 4085: contig of 764 bp in length  
4186 4185: gap of 100 bp  
4889 4889: contig of 704 bp in length  
4990 4989: gap of 100 bp  
5704 5704: contig of 715 bp in length  
5804 5804: gap of 100 bp  
5805 5805: contig of 774 bp in length  
6578 6578: gap of 100 bp  
6679 6679: gap of 100 bp  
7423 7423: contig of 745 bp in length  
7523 7523: gap of 100 bp  
8270 8270: contig of 747 bp in length  
8371 8370: gap of 100 bp  
9117 9117: contig of 747 bp in length  
9217 9217: gap of 100 bp  
9218 9218: contig of 709 bp in length  
9926 9926: gap of 100 bp

10027 10773: contig of 747 bp in length  
10774 10873: gap of 100 bp  
10874 11635: contig of 762 bp in length  
11636 11735: gap of 100 bp  
11736 12489: contig of 754 bp in length  
12490 12589: gap of 100 bp  
12590 13332: contig of 743 bp in length  
13333 13432: gap of 100 bp  
13433 14169: contig of 737 bp in length  
14170 14269: gap of 100 bp  
14270 15000: contig of 731 bp in length  
15000 15100: gap of 100 bp  
15101 15839: contig of 738 bp in length  
15839 15938: gap of 100 bp  
15939 16653: contig of 715 bp in length  
16654 16753: gap of 100 bp  
16754 17495: contig of 742 bp in length  
17496 17595: gap of 100 bp  
17596 18344: contig of 749 bp in length  
18345 18444: gap of 100 bp  
18445 19165: contig of 721 bp in length  
19166 19265: gap of 100 bp  
19266 20001: contig of 736 bp in length  
20002 20862: contig of 761 bp in length  
20863 20952: gap of 100 bp  
20963 21714: contig of 752 bp in length  
21715 22575: contig of 761 bp in length  
22576 22675: gap of 100 bp  
22676 23434: contig of 759 bp in length  
23435 23534: gap of 100 bp  
23535 24285: contig of 761 bp in length  
24286 24395: gap of 100 bp  
24396 25146: contig of 751 bp in length  
25147 25246: gap of 100 bp  
25247 25970: contig of 724 bp in length  
25971 26070: gap of 100 bp  
26071 26810: contig of 740 bp in length  
26811 26910: gap of 100 bp  
26910 27670: contig of 760 bp in length  
27671 27770: gap of 100 bp  
27771 28520: contig of 750 bp in length  
28521 28620: gap of 100 bp  
28621 29349: contig of 729 bp in length  
29350 29449: gap of 100 bp  
29450 30205: contig of 756 bp in length  
30206 30305: gap of 100 bp  
30306 31039: contig of 734 bp in length  
31039 31139: gap of 100 bp  
31140 31882: contig of 743 bp in length  
31883 31982: gap of 100 bp  
31983 32734: contig of 752 bp in length  
32735 32834: gap of 100 bp  
32835 33587: contig of 753 bp in length  
33588 33687: gap of 100 bp  
33688 34423: contig of 756 bp in length  
34424 34523: gap of 100 bp  
34524 35254: contig of 731 bp in length  
35255 35354: gap of 100 bp  
35355 36083: contig of 729 bp in length  
36084 36183: gap of 100 bp  
36184 36938: contig of 755 bp in length  
36939 37038: gap of 100 bp  
37039 37761: contig of 723 bp in length  
37762 38553: contig of 692 bp in length  
38554 38653: gap of 100 bp  
38654 39391: contig of 738 bp in length  
39392 39491: gap of 100 bp  
39492 40238: contig of 747 bp in length  
40239 40338: gap of 100 bp  
40339 41094: contig of 756 bp in length

```

* 41095 41194: gap of 100 bp
* 41195 41949: contig of 755 bp in length
* 41950 42049: gap of 100 bp
* 42050 42791: contig of 742 bp in length
* 42792 42891: gap of 100 bp
* 42892 43626: contig of 735 bp in length
* 43627 43726: gap of 100 bp
* 43727 44466: contig of 740 bp in length
* 44467 44566: gap of 100 bp
* 44567 45302: contig of 736 bp in length
* 45303 45402: gap of 100 bp
* 45403 46150: contig of 748 bp in length
* 46151 46250: gap of 100 bp
* 46251 47000: contig of 750 bp in length
* 47001 47100: gap of 100 bp
* 47101 47805: contig of 705 bp in length
* 47806 47905: gap of 100 bp
* 47906 48646: contig of 741 bp in length
* 48647 48746: gap of 100 bp
* 48747 49499: contig of 753 bp in length
* 49500 49599: gap of 100 bp
* 49600 50345: contig of 746 bp in length
* 50346 50445: gap of 100 bp
* 50446 51185: contig of 740 bp in length
* 51186 51285: gap of 100 bp
* 51286 52048: contig of 763 bp in length
* 52049 52148: gap of 100 bp
* 52149 52875: contig of 727 bp in length
* 52876 52975: gap of 100 bp
* 52976 53699: contig of 724 bp in length
* 53700 53799: gap of 100 bp
* 53800 54514: contig of 715 bp in length
* 54515 54614: gap of 100 bp
* 54615 55372: contig of 758 bp in length
* 55373 55472: gap of 100 bp
* 55473 56192: contig of 720 bp in length
* 56193 56292: gap of 100 bp
* 56293 57036: contig of 744 bp in length
* 57037 57136: gap of 100 bp
* 57137 57873: contig of 737 bp in length
* 57874 57973: gap of 100 bp

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```

Query Match      77.8%: Score 14; DB 2; Length 73882;
Best Local Similarity 85.7%: Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 UCCUGAGAGNNNNNN 18
   :||:|||||
Db 31032 TCCTGAGAGNNNNN 31045

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RESULT 57
AC021390      81233 bp   DNA      linear   HTG 13-JUL-2000
LOCUS Homo sapiens clone RP11-27N15, LOW-PASS SEQUENCE SAMPLING.
AC021390
AC021390.2 GI:9136426
VERSION HTG; HTGS_PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 81233)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-27N15
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 81233)
        Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
        Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
        Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G., Castle,A.,
        Choquel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
        D'Atellano,K., Dewar,K., Domino,M., Doyle,M., Fenesfor,J.,
        Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,

```

# JOURNAL COMMENT

```

Gardyna,S., Grant,G., Hages,B., Heford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Karttas,A., Klein,J.,
Landers,T., Lehoczy,D., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Margulis,N., McEwan,P., McGurt,A., McKernan,K.,
McSheeters,R., Meldrum,J., Menus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-JUN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705716.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W1BR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4723
Center clone name: 27_N_15
-----
* NOTE: This record contains 90 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
784 883: contig of 783 bp in length
884 1668: contig of 785 bp in length
1669 1768: gap of 100 bp
1769 2571: contig of 803 bp in length
2572 2671: gap of 100 bp
2672 3492: contig of 821 bp in length
3493 3592: gap of 100 bp
3593 4378: contig of 786 bp in length
4379 4478: gap of 100 bp
4479 5320: contig of 842 bp in length
5321 5420: gap of 100 bp
5421 6248: contig of 828 bp in length
6249 6348: gap of 100 bp
6349 7149: contig of 801 bp in length
7150 7249: gap of 100 bp
7250 8080: contig of 831 bp in length
8081 8180: gap of 100 bp
8181 8991: contig of 811 bp in length
8992 9091: gap of 100 bp
9091 9897: contig of 806 bp in length
9897 9997: gap of 100 bp
9998 10787: contig of 790 bp in length
10788 10887: gap of 100 bp
10888 11681: contig of 794 bp in length
11682 11781: gap of 100 bp
11782 12604: contig of 823 bp in length
12605 12704: gap of 100 bp
12705 13499: contig of 795 bp in length
13500 13599: gap of 100 bp
13600 14431: contig of 832 bp in length
14432 14531: gap of 100 bp
14532 15338: contig of 807 bp in length
15339 15438: gap of 100 bp
15439 16259: contig of 821 bp in length

```

```

* 16260 16359: gap of 100 bp
* 16360 17159: contig of 800 bp in length
* 17160 17259: gap of 100 bp
* 17260 18071: contig of 812 bp in length
* 18072 18171: gap of 100 bp
* 18172 18933: contig of 762 bp in length
* 18934 19033: gap of 100 bp
* 19034 19832: contig of 799 bp in length
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* 19933 20759: contig of 827 bp in length
* 20760 20860 21633: contig of 774 bp in length
* 20860 21733: gap of 100 bp
* 21634 22552: contig of 819 bp in length
* 22553 22653: gap of 100 bp
* 22653 23465: contig of 813 bp in length
* 23466 23565: gap of 100 bp
* 23566 24469: contig of 804 bp in length
* 24470 25295: gap of 100 bp
* 25296 25395: gap of 100 bp
* 25396 26214: contig of 819 bp in length
* 26215 26315: gap of 100 bp
* 26315 27132: contig of 817 bp in length
* 27132 27232: gap of 100 bp
* 27232 28055: contig of 824 bp in length
* 28056 28155: gap of 100 bp
* 28156 28961: contig of 806 bp in length
* 28962 29062 29622: contig of 561 bp in length
* 29623 30529: gap of 100 bp
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* 30630 31415: contig of 786 bp in length
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* 31516 32337: contig of 822 bp in length
* 32338 32437: gap of 100 bp
* 32438 33250: contig of 813 bp in length
* 33251 33350: gap of 100 bp
* 33351 34141: contig of 791 bp in length
* 34142 34241: gap of 100 bp
* 34242 35058: contig of 817 bp in length
* 35059 35158: gap of 100 bp
* 35159 35956: contig of 798 bp in length
* 35957 36056: gap of 100 bp
* 36057 36886: contig of 830 bp in length
* 36887 36986: gap of 100 bp
* 36987 37796: contig of 810 bp in length
* 37797 37896: gap of 100 bp
* 37897 38697 38796: gap of 800 bp in length
* 38697 39595: contig of 799 bp in length
* 39596 39695: gap of 100 bp
* 39696 40484: contig of 789 bp in length
* 40485 40584: gap of 100 bp
* 40585 41392: contig of 808 bp in length
* 41393 41493: gap of 100 bp
* 41493 42281: contig of 789 bp in length
* 42282 42381: gap of 100 bp
* 42382 43197: contig of 816 bp in length
* 43198 43297: gap of 100 bp
* 43298 44107: contig of 810 bp in length
* 44108 44207: gap of 100 bp
* 44208 44991: contig of 784 bp in length
* 44992 45091: gap of 100 bp
* 45092 45921: contig of 830 bp in length
* 45922 46021: gap of 100 bp
* 46022 46847: contig of 826 bp in length
* 46848 46947: gap of 100 bp
* 46948 47770: contig of 823 bp in length
* 47771 47870: gap of 100 bp
* 47871 48692: contig of 822 bp in length
* 48693 48792: gap of 100 bp

```

```

* 48793 49602: contig of 810 bp in length
* 49603 49702: gap of 100 bp
* 49703 50512: contig of 810 bp in length
* 50513 50612: gap of 100 bp
* 50613 51396: contig of 784 bp in length
* 51397 51496: gap of 100 bp
* 51497 52303: contig of 807 bp in length
* 52304 52403: gap of 100 bp
* 52404 53235: gap of 831 bp in length
* 53235 53335: gap of 100 bp
* 53335 54128 54237: gap of 793 bp in length
* 54128 54228 55034: gap of 100 bp
* 54228 55035 55134: gap of 100 bp
* 55035 55135 55927: contig of 793 bp in length
* 55135 55928 56027: gap of 100 bp
* 56028 56841: contig of 814 bp in length
* 56842 56941: gap of 100 bp
* 56942 57765: contig of 824 bp in length
* 57766 57865: gap of 100 bp
* 57866 58666: contig of 801 bp in length
* 58667 58766: gap of 100 bp
* 58767 59570: contig of 804 bp in length
* 59571 59671 60468: gap of 100 bp
* 59671 60468: contig of 798 bp in length
* 60469 60568: gap of 100 bp
* 60569 61348: contig of 780 bp in length
* 61349 61448: gap of 100 bp
* 61449 62272: contig of 824 bp in length
* 62273 62373 63167: contig of 795 bp in length
* 62373 63168 63267: gap of 100 bp
* 63168 63268 64080: contig of 813 bp in length
* 63268 64080: gap of 100 bp
* 64081 64180: gap of 100 bp

Query Match
Best Local Similarity 77.8%; Score 14; DB 2; Length 81233;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGNNNNNN 18
Db 11674 TCCTGAGNNNNNN 11687

RESULT 58
AC022890 83547 bp DNA linear HTG 24-AUG-2002
LOCUS Homo sapiens chromosome 6 clone RP11-516A8 map 6, LOW-PASS SEQUENCE
DEFINITION SAMPLING.
ACCESSION AC022890.2 GI:9160241
VERSION HTG; HTGS_PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 83547)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abramson,H., Allen,N.,
JOURNAL Unpublished
TITLE 2 (bases 1 to 83547)
REFERENCE 1 (bases 1 to 83547)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Unpublished
REFERENCE 1 (bases 1 to 83547)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abramson,H., Allen,N.,
Boguslavsky,L., Bouckling,A., Brown,A., Burkett,G., Bada,F.,
Chapel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Deaellano,K., Dewar,K., Domino,M., Doyle,M., Fencsator,J.,
Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardina,S., Grant,G., Hagoes,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Karatas,A., Klein,J.,
Lander,T., Lehotzky,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Maddison,P., Margulis,N., McEwan,P., McQuirk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,

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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
(bases 1 to 83547)

Bliren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Bouhgalter, B., Brown, A., Burkett, G., Campoliano, A., Castle, A., Choquel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margrie, N., McCarthy, M., McKean, P., McGuire, A., McKernan, K., McPheters, R., Melidim, J., Meneus, L., Minova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6922031.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L6230  
Center clone name: 516\_A\_8

\*\*\*\*\*  
\* NOTE: This record contains 88 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\*\*\*\*\*

1 847: contig of 847 bp in length  
848 947: gap of 100 bp  
948 1811: contig of 864 bp in length  
1812 1911: gap of 100 bp  
1912 2767: contig of 856 bp in length  
2768 2867: gap of 100 bp  
2868 3724: contig of 857 bp in length  
3725 3824: gap of 100 bp  
3825 4676: contig of 852 bp in length  
4677 4776: gap of 100 bp  
4777 5611: contig of 835 bp in length  
5612 5711: gap of 100 bp  
5712 6524: contig of 813 bp in length  
6525 7481: contig of 857 bp in length  
7482 7581: gap of 100 bp

\*\*\*\*\*

7582 8426: contig of 845 bp in length  
8427 8525: gap of 100 bp  
8527 9380: contig of 854 bp in length  
9381 9480: gap of 100 bp  
9481 10323: contig of 843 bp in length  
10324 10423: gap of 100 bp  
10424 11259: contig of 836 bp in length  
11260 11359: gap of 100 bp  
11360 12214: contig of 855 bp in length  
12215 12313: gap of 100 bp  
12315 13163: contig of 849 bp in length  
13164 13263: gap of 100 bp  
13264 14140: contig of 877 bp in length  
14141 14240: gap of 100 bp  
14241 15103: contig of 863 bp in length  
15104 15203: gap of 100 bp  
15204 16065: contig of 862 bp in length  
16066 16165: gap of 100 bp  
16166 17031: contig of 866 bp in length  
17032 17131: gap of 100 bp  
17132 17987: contig of 856 bp in length  
17988 18087: gap of 100 bp  
18088 18931: contig of 844 bp in length  
18932 19031: gap of 100 bp  
19032 19851: contig of 820 bp in length  
19852 19951: gap of 100 bp  
19952 20798: contig of 847 bp in length  
20799 20898: gap of 100 bp  
20899 21729: contig of 831 bp in length  
21730 21829: gap of 100 bp  
21830 22679: contig of 850 bp in length  
22679 22779: gap of 100 bp  
22779 23637: contig of 858 bp in length  
23638 23737: gap of 100 bp  
23738 24597: contig of 860 bp in length  
24598 24697: gap of 100 bp  
24698 25531: contig of 834 bp in length  
25532 25631: gap of 100 bp  
25632 26435: contig of 804 bp in length  
26436 26535: gap of 100 bp  
26536 27344: contig of 809 bp in length  
27345 27444: gap of 100 bp  
27445 28309: contig of 865 bp in length  
28310 28409: gap of 100 bp  
28410 29259: contig of 850 bp in length  
29260 29359: gap of 100 bp  
29360 30200: contig of 841 bp in length  
30201 30300: gap of 100 bp  
30301 31162: contig of 862 bp in length  
31163 31262: gap of 100 bp  
31263 32112: contig of 850 bp in length  
32113 32212: gap of 100 bp  
32213 33069: contig of 857 bp in length  
33070 33169: gap of 100 bp  
33170 34006: contig of 837 bp in length  
34007 34106: gap of 100 bp  
34107 34972: contig of 866 bp in length  
34973 35072: gap of 100 bp  
35073 35924: contig of 852 bp in length  
35925 36024: gap of 100 bp  
36025 36864: contig of 840 bp in length  
36865 36964: gap of 100 bp  
36965 37823: contig of 859 bp in length  
37824 37923: gap of 100 bp  
37924 38773: contig of 850 bp in length  
38774 38873: gap of 100 bp  
38874 39728: contig of 855 bp in length  
39729 39829: gap of 100 bp  
39829 40690: contig of 862 bp in length  
40691 40790: gap of 100 bp  
40791 41636: contig of 846 bp in length  
41637 41736: gap of 100 bp  
41737 42566: contig of 830 bp in length



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* 22158 22987: contig of 830 bp in length
* 22988 23087: gap of 100 bp
* 23088 23925: contig of 838 bp in length
* 23926 24025: gap of 100 bp
* 24026 24912: contig of 887 bp in length
* 24913 25012: gap of 100 bp
* 25013 25879: contig of 867 bp in length
* 25880 25979: gap of 100 bp
* 25980 26839: contig of 860 bp in length
* 26840 26939: gap of 100 bp
* 26940 27768: contig of 828 bp in length
* 27769 27868: gap of 100 bp
* 27869 28749: contig of 881 bp in length
* 28750 28849: gap of 100 bp
* 28850 29690: contig of 841 bp in length
* 29691 29790: gap of 100 bp
* 29791 30656: contig of 866 bp in length
* 30657 30756: gap of 100 bp
* 30757 31645: contig of 889 bp in length
* 31646 31745: gap of 100 bp
* 31746 32537: contig of 882 bp in length
* 32538 32737: gap of 100 bp
* 32738 33611: contig of 874 bp in length
* 33612 34563: contig of 852 bp in length
* 34564 35518: gap of 100 bp
* 35519 35618: gap of 100 bp
* 35619 36511: contig of 893 bp in length
* 36512 37487: contig of 876 bp in length
* 37488 37587: gap of 100 bp
* 37588 38427: contig of 839 bp in length
* 38427 38527: gap of 100 bp
* 38527 39372: contig of 846 bp in length
* 39373 39472: gap of 100 bp
* 39473 40331: contig of 859 bp in length
* 40332 40431: gap of 100 bp
* 40432 41243: contig of 832 bp in length
* 41244 41343: gap of 100 bp
* 41344 42165: contig of 822 bp in length
* 42166 42265: gap of 100 bp
* 42266 43103: contig of 838 bp in length
* 43104 43203: gap of 100 bp
* 43204 44032: contig of 829 bp in length
* 44033 44132: gap of 100 bp
* 44133 44989: contig of 857 bp in length
* 44990 45089: gap of 100 bp
* 45090 45967: contig of 878 bp in length
* 45968 46067: gap of 100 bp
* 46068 46924: contig of 857 bp in length
* 46925 47024: gap of 100 bp
* 47025 47868: contig of 844 bp in length
* 47869 47968: gap of 100 bp
* 47969 48846: contig of 878 bp in length
* 48847 48946: gap of 100 bp
* 48947 49814: contig of 868 bp in length
* 49815 49914: gap of 100 bp
* 49915 50765: contig of 851 bp in length
* 50766 50865: gap of 100 bp
* 50866 51729: contig of 864 bp in length
* 51730 51829: gap of 100 bp
* 51830 52708: contig of 879 bp in length
* 52709 52808: gap of 100 bp
* 52809 53684: contig of 876 bp in length
* 53685 53784: gap of 100 bp
* 53785 54646: contig of 862 bp in length
* 54647 54746: gap of 100 bp
* 54747 55641: contig of 895 bp in length
* 55642 55741: gap of 100 bp
* 55742 56601: contig of 860 bp in length
* 56602 57577: gap of 100 bp
* 57577: contig of 876 bp in length

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* 57578 57677: gap of 100 bp
* 57678 58550: contig of 873 bp in length
* 58551 58650: gap of 100 bp
* 58651 59526: contig of 876 bp in length
* 59527 59626: gap of 100 bp
* 59627 60500: contig of 874 bp in length
* 60501 60600: gap of 100 bp
* 60601 61448: contig of 848 bp in length
* 61449 61548: gap of 100 bp
* 61549 62398: contig of 850 bp in length
* 62399 62498: gap of 100 bp
* 62499 63363: contig of 865 bp in length
* 63364 63463: gap of 100 bp
* 63464 64326: contig of 863 bp in length
* 64327 64426: gap of 100 bp
* 64427 65285: contig of 859 bp in length
* 65286 65385: gap of 100 bp
* 65386 66245: contig of 860 bp in length
* 66246 66345: gap of 100 bp
* 66346 67188: contig of 843 bp in length

Query Match      77.8%; Score 14; DB 2; Length 85440;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy      5 UCCUGGAGNNNNN 18
Db      20162 TCCTGGAGNNNNN 20175

RESULT 60
AC138602
LOCUS      Mus musculus clone RP23-9113, LOW-PASS SEQUENCE SAMPLING.
DEFINITION
ACCESSION  AC138602
VERSION     AC138602.1 GI:27573472
KEYWORDS   HTG; HTGS PHASED.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 88940)
REFERENCE   Birren,B., Nusbaum,C. and Lander,E.
            Mus musculus, clone RP23-9113
            Unpublished
            2 (bases 1 to 88940)
REFERENCE   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barta,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., Deakrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Fairo,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hago,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karacas,A., Kells,C., Lander,T., Levine,R.,
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            Matthews,C., McCarthy,M., Meldrum,D., Menus,L., Minova,T.,
            Mienna,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
            Risse,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schnupack,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Talamas,J., Testaye,S., Theodore,J., Topham,K.,
            Travers,M., Vaseiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.
            Direct Submission
            Submitted (10-JAN-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            All repeats were identified using RepeatMasker:
            Smit,A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR

```

```
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center Project name: L22378
Center clone name: 91_I_3
-----
* NOTE: This record contains 83 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 976: contig of 976 bp in length
* 977 1076: gap of 100 bp
* 1077 2028: contig of 952 bp in length
* 2029 2128: gap of 100 bp
* 2129 3050: contig of 922 bp in length
* 3051 3150: gap of 100 bp
* 3151 4111: contig of 961 bp in length
* 4112 4211: gap of 100 bp
* 4212 5202: contig of 991 bp in length
* 5203 5302: gap of 100 bp
* 5303 6279: contig of 977 bp in length
* 6280 6379: gap of 100 bp
* 6380 7406: contig of 1027 bp in length
* 7407 8478: contig of 972 bp in length
* 8479 8578: gap of 100 bp
* 8579 9600: contig of 1022 bp in length
* 9601 9700: gap of 100 bp
* 9701 10655: contig of 955 bp in length
* 10656 11729: contig of 974 bp in length
* 11730 11828: gap of 100 bp
* 11830 12796: contig of 967 bp in length
* 12797 12896: gap of 100 bp
* 12897 13853: contig of 957 bp in length
* 13854 13953: gap of 100 bp
* 13954 14907: contig of 954 bp in length
* 14908 15007: gap of 100 bp
* 15008 15941: contig of 934 bp in length
* 15942 16041: gap of 100 bp
* 16042 17009: contig of 968 bp in length
* 17010 17109: gap of 100 bp
* 17110 18086: contig of 977 bp in length
* 18087 18186: gap of 100 bp
* 18187 19158: contig of 972 bp in length
* 19159 19258: gap of 100 bp
* 19259 20253: contig of 995 bp in length
* 20254 20353: gap of 100 bp
* 20354 21335: contig of 982 bp in length
* 21336 21435: gap of 100 bp
* 21436 22392: contig of 957 bp in length
* 22393 22492: gap of 100 bp
* 22493 23452: contig of 960 bp in length
* 23453 23552: gap of 100 bp
* 23553 24532: contig of 980 bp in length
* 24533 24632: gap of 100 bp
* 24633 25633: contig of 1001 bp in length
* 25634 25733: gap of 100 bp
* 25734 26729: contig of 996 bp in length
* 26730 26829: gap of 100 bp
* 26830 27804: contig of 975 bp in length
* 27805 27904: gap of 100 bp
* 27905 28888: contig of 984 bp in length
* 28889 28975: gap of 100 bp
* 28976 29975: contig of 987 bp in length
* 29976 30075: gap of 100 bp
*
* 30076 31045: contig of 970 bp in length
* 31046 31145: gap of 100 bp
* 31146 32118: contig of 973 bp in length
* 32119 32218: gap of 100 bp
* 32219 33219: contig of 933 bp in length
* 33219 33251: gap of 100 bp
* 33252 34237: contig of 986 bp in length
* 34238 34337: gap of 100 bp
* 34338 35324: contig of 987 bp in length
* 35325 35424: gap of 100 bp
* 35425 36413: contig of 989 bp in length
* 36414 36513: gap of 100 bp
* 36514 37512: contig of 999 bp in length
* 37513 37612: gap of 100 bp
* 37613 38602: contig of 990 bp in length
* 38603 38702: gap of 100 bp
* 38703 39704: contig of 1002 bp in length
* 39705 39804: gap of 100 bp
* 39805 40782: contig of 978 bp in length
* 40783 40882: gap of 100 bp
* 40883 41876: contig of 994 bp in length
* 41877 41976: gap of 100 bp
* 41977 42950: contig of 974 bp in length
* 42951 43050: gap of 100 bp
* 43051 44022: contig of 972 bp in length
* 44023 44122: gap of 100 bp
* 44123 45074: contig of 952 bp in length
* 45075 45174: gap of 100 bp
* 45175 46161: contig of 987 bp in length
* 46162 46261: gap of 100 bp
* 46262 47237: contig of 976 bp in length
* 47238 47338: gap of 100 bp
* 47339 48343: contig of 1006 bp in length
* 48344 48443: gap of 100 bp
* 48444 49414: contig of 971 bp in length
* 49415 49514: gap of 100 bp
* 49515 50516: contig of 1002 bp in length
* 50517 50617: gap of 100 bp
* 50618 51589: contig of 973 bp in length
* 51590 51689: gap of 100 bp
* 51690 52676: contig of 987 bp in length
* 52677 52776: gap of 100 bp
* 52777 53758: contig of 982 bp in length
* 53759 53858: gap of 100 bp
* 53859 54818: contig of 960 bp in length
* 54819 54918: gap of 100 bp
* 54919 55873: contig of 955 bp in length
* 55874 55973: gap of 100 bp
* 55974 56931: contig of 958 bp in length
* 56932 57031: gap of 100 bp
* 57032 57973: contig of 942 bp in length
* 57974 58073: gap of 100 bp
* 58074 59046: contig of 973 bp in length
* 59047 59146: gap of 100 bp
* 59147 60133: contig of 987 bp in length
* 60134 60233: gap of 100 bp
* 60234 61221: contig of 988 bp in length
* 61222 61321: gap of 100 bp
* 61322 62303: contig of 982 bp in length
* 62304 62403: gap of 100 bp
* 62404 63380: contig of 972 bp in length
* 63381 63480: gap of 100 bp
* 63481 64459: contig of 979 bp in length
* 64460 64559: gap of 100 bp
* 64560 65544: contig of 985 bp in length
* 65545 65644: gap of 100 bp
* 65645 66614: contig of 970 bp in length
* 66615 66714: gap of 100 bp
* 66715 67664: contig of 950 bp in length
* 67665 67764: gap of 100 bp
* 67765 68736: contig of 972 bp in length
* 68737 68836: gap of 100 bp
* 68837 69837: contig of 1001 bp in length
```



\* 69938 69937: gap of 100 bp  
\* 70938 70948: contig of 911 bp in length  
\* 70849 70948: gap of 100 bp  
\* 70949 71924: contig of 976 bp in length  
\* 71925 72024: gap of 100 bp  
\* 72025 72989: contig of 965 bp in length  
\* 72990 73089: gap of 100 bp  
\* 73090 74074: contig of 985 bp in length  
\* 74075 74174: gap of 100 bp  
\* 74175 75149: contig of 975 bp in length  
\* 75150 75249: gap of 100 bp  
\* 75250 76211: contig of 962 bp in length  
\* 76212 76311: gap of 100 bp

Query Match 77.8% Score 14; DB 2; Length 88940;  
Best Local Similarity 85.7% Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 5 UCCUGAGANNNNNN 18  
Db 86791 TCCTGAGANNNNNN 86804

#### RESULT 61

AC095920\_03

WPCOMMENT

Sequence split into 10 fragments LOCUS AC095920 Accession AC095920

Fragment Name	Begin	End
AC095920_00	1	110000
AC095920_01	100001	210000
AC095920_02	200001	310000
AC095920_03	300001	410000
AC095920_04	400001	510000
AC095920_05	500001	610000
AC095920_06	600001	710000
AC095920_07	700001	810000
AC095920_08	800001	910000
AC095920_09	900001	1005083

Continuation (4 of 10) of AC095920 From Base 300001 (AC095920 Rattus norvegicus clone CH

Query Match 77.8% Score 14; DB 2; Length 110000;  
Best Local Similarity 85.7% Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 UCCUGAGANNNNNN 18  
Db 85215 TCCTGAGANNNNNN 85228

#### RESULT 62

AC096315\_3

WPCOMMENT

Sequence split into 9 fragments LOCUS AC096315 Accession AC096315

Fragment Name	Begin	End
AC096315_0	1	110000
AC096315_1	100001	210000
AC096315_2	200001	310000
AC096315_3	300001	410000
AC096315_4	400001	510000
AC096315_5	500001	610000
AC096315_6	600001	710000
AC096315_7	700001	810000
AC096315_8	800001	848038

Continuation (4 of 9) of AC096315 From Base 300001 (AC096315 Rattus norvegicus clone CH2

Query Match 77.8% Score 14; DB 2; Length 110000;  
Best Local Similarity 85.7% Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 5 UCCUGAGANNNNNN 18  
Db 83645 TCCTGAGANNNNNN 83658

#### RESULT 63

AC112872\_0

WPCOMMENT

Sequence split into 5 fragments LOCUS AC112872 Accession AC112872

Fragment Name	Begin	End
AC112872_0	1	110000
AC112872_1	100001	210000
AC112872_2	200001	310000
AC112872_3	300001	410000
AC112872_4	400001	421172

LOCUS AC112872 421172 bp DNA linear HTG 11-OCT-2002  
DEFINITION Rattus norvegicus clone CH230-221D7, \*\*\* SEQUENCING IN PROGRESS  
\*\*\* 18 unordered pieces.

ACCESSION AC112872  
VERSION AC112872.6 GI:23817694  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

#### REFERENCE

AUTHORS

1 (bases 1 to 421172)  
Muzny,D.,Marle., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alibrooke,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
Biswal,R., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,  
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,  
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,  
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,  
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,  
Devila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,  
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,  
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,  
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falter,T., Fan,G.,  
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,  
Fraser,C.M., Gabris,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,  
Gedregoeigis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,  
Gubartine,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,  
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,  
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M.,  
Hollins,B., Howell,S., Hulik,S., Hume,J., Idlebird,D., Jackson,A.,  
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,  
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,  
Kowis,C., Kraft,C.L., Ledow,H., Levay,J., Lewis,L., Li,Z., Liu,J.,  
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,  
Lorenshewa,L., Louisedge,H., Lozada,R.J., Lu,X., Ma,J.,  
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,  
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,  
Mawhinney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,  
Milosavljevic,A., Miner,G., Ming,E., Montemayor,J., Moore,S.,  
Morgan,M., Morris,K., Morris,S., Mundasa,M., Murphy,N., Nair,L.,  
Narkervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,  
Nwokeneme,O., Okwunonu,G., Olarunpungson,A., Pal,S., Parks,K.,  
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,  
Pisnerak,S., Polindexter,A., Popovic,D., Primus,E., Pu,L., L.,  
Piazzi,M., Quirroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,  
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richard,S., Riggs,F.,  
Rivers,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,  
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,  
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smaiz,D.,  
Sneed,A., Sodergren,E., Song,X.-Z., Sotelle,R., Sosa,J.,  
Steinle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C.,  
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmami,K.,  
Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J.,  
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,  
Williams,G., Willison,R., Wlezyk,R., Wooden,H., Worley,K.,  
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,  
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von  
Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
Weinstock,G., and Gibbs,R.A.

TITLE

Direct Submission

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 421172)  
Worley, K.C.  
Direct Submission  
Submitted (25-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 421172)  
Rat Genome Sequencing Consortium.  
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Oct 11, 2002 this sequence version replaced gi:21743603.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GRWG  
Center clone name: CH230-231D7  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 302679 bases at least Q40  
Consensus quality: 309380 bases at least Q30  
Consensus quality: 313052 bases at least Q20  
Estimated insert size: 328717; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 18 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
5264: contig of 5264 bp in length  
5265  
5365: gap of unknown length  
5365  
23206: contig of 17842 bp in length  
23307  
23306: gap of unknown length  
23307  
51321: contig of 28015 bp in length  
51322  
51421: gap of unknown length  
51422  
68374: contig of 16953 bp in length  
68375  
68474: gap of unknown length  
68475  
73067: contig of 4593 bp in length  
73068  
73167: gap of unknown length  
73168  
259372: contig of 186205 bp in length  
259373  
259472: gap of unknown length  
259473  
267150: contig of 7678 bp in length  
267151  
267250: gap of unknown length  
267251  
308706: contig of 41456 bp in length  
308707  
308806: gap of unknown length  
341693: contig of 32887 bp in length  
341694  
341793: gap of unknown length  
341794  
379744: contig of 37951 bp in length  
379745  
379844: gap of unknown length

FEATURES  
source  
1. 421172  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-231D7"  
963. 1760  
/note="clone\_boundary  
site:ECORI  
end\_sequence:RWBOK16T"  
1678. 5264  
/note="wgs\_contig"  
23307. 26161  
/note="wgs\_contig"  
26212. 29344  
/note="wgs\_contig"  
71261. 73067  
/note="wgs\_contig"  
73168. 74530  
/note="wgs\_contig"  
259473. 261100  
/note="wgs\_contig"  
261928. 267150  
/note="wgs\_contig"  
308807. 310434  
/note="wgs\_contig"  
337486. 341693  
/note="wgs\_contig"  
341794. 345624  
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349912. 351036  
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ORIGIN  
Query Match 77.8%; Score 14; DB 2; Length 110000;  
Best Local Similarity 85.7%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 0;

QY 5 UCCUGAGNNNNNN 18  
:|||||  
Db 26154 TCCTGAGNNNNN 26167

RESULT 64  
AC025433/c 133614 bp DNA linear HTG 18-JUL-2000  
AC025433/c Homo sapiens chromosome 5 clone CTB-17D7, WORKING DRAFT SEQUENCE,  
20 ordered pieces.  
AC025433  
AC025433.4 GI:9256471  
VERSION  
HTG; HTGS PHASE2; HTGS\_DRAFT.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 133614)  
DOE Joint Genome Institute.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Sequencing of Human Chromosome 5  
Unpublished  
2 (bases 1 to 133614)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Jul 19, 2000 this sequence version replaced gi:7711806.

-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
-----

Project Information  
Center Project Name: 70811, H232  
Center clone name: CIT978SKB\_17D7  
-----

Summary Statistics  
Consensus quality: 117171 bases at least Q40  
Consensus quality: 127725 bases at least Q20  
Consensus quality: 130109 bases at least Q30  
Estimated insert size: 137000; pulse field gel estimation  
Estimated insert size: 132714; sum-of-contigs estimation  
Quality coverage: 4.57 in Q20 bases; pulse field gel estimation  
Quality coverage: 4.72 in Q20 bases; sum-of-contigs estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 20 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

1  
1671: contig of 1671 bp in length  
1672 1771: gap of unknown length  
1772 2774: contig of 1003 bp in length  
2775 2874: gap of unknown length  
2875 6617: contig of 3743 bp in length  
6618 6717: gap of unknown length  
6718 8135: contig of 1418 bp in length  
8136 8235: gap of unknown length  
8236 12447: contig of 4212 bp in length  
12448 12547: gap of unknown length  
12548 14359: contig of 1812 bp in length  
14360 14459: gap of unknown length  
14460 29085: contig of 14626 bp in length  
29086 29185: gap of unknown length  
29186 35376: contig of 6191 bp in length  
35377 35476: gap of unknown length  
35477 46481: contig of 11005 bp in length  
46482 46581: gap of unknown length  
46582 50727: contig of 4146 bp in length  
50728 50827: gap of unknown length  
50829 54905: contig of 4078 bp in length  
54906 55005: gap of unknown length  
55006 58540: contig of 3535 bp in length  
58541 58640: gap of unknown length  
58641 59894: contig of 1254 bp in length  
59895 59994: gap of unknown length  
59996 63699: contig of 3705 bp in length  
63700 63799: gap of unknown length  
63800 66138: contig of 2339 bp in length  
66139 66238: gap of unknown length  
66239 67963: contig of 1725 bp in length  
67964 68063: gap of unknown length  
68064 87222: contig of 19159 bp in length  
87223 87322: gap of unknown length  
87323 90431: contig of 3109 bp in length  
90432 90531: gap of unknown length  
90532 121085: contig of 30554 bp in length  
121086 121185: gap of unknown length  
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FEATURES  
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LOCATION/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="5"  
/clone="CTB-17D7"  
/clone\_lib="Caltech human BAC library B"

ORIGIN  
Query Match 77.8%; Score 14; DB 2; Length 133614;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGNNNNNN 18  
:|||||  
Db 35484 TCCTGAGNNNNNN 35471

RESULT 65  
AC023576  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AC023576 150695 bp DNA linear HTG 30-MAY-2000  
Homo sapiens chromosome 1 clone RP11-574J7 map 1, LOW-PASS SEQUENCE  
SMAPPING.  
AC023576  
HTG: HTGS\_PHASE0.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 150695)  
Homo sapiens chromosome 1, clone RP11-574J7  
Unpublished  
2 (bases 1 to 150695)  
Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barne, N., Bede, F., Boguslavsky, L.,  
Boukhalter, B., Brown, A., Burkett, G., Campiano, A., Cattle, A.,  
Choepe, Y., Collinge, M., Collins, S., Collamore, A., Cooke, P.,  
Darellano, K., Dewar, K., Dodge, S., Domingo, M., Doyle, M.,  
Fenster, J., Ferreira, P., FitzHugh, M., Forrest, C., Gage, D.,  
Galaan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hago, B., Heaford, A., Horton, L.,  
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karacas, A.,  
Klein, J., Landers, T., Largocque, K., Lehocsky, J., Levine, R.,  
Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N., McCarthy, M.,  
McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrum, J.,  
Meneas, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,  
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M.,  
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,  
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,  
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A.,  
Travers, M., Triggillo, J., Vasilev, H., Viel, R., Vo, A., Wilson, B.,  
Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, D., Zimmer, A. and  
Zody, M.

Direct Submission  
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 30, 2000 this sequence version replaced gi:6978288.  
All repeats were identified using RepeatMasker:  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIRB  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center Project Name: L6803  
Center clone name: 574\_J\_7

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

\* NOTE: This record contains 166 individual.  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1	714: contig of 714 bp in length	24771	25448: contig of 678 bp in length
715	814: gap of 100 bp	25449	25548: gap of 100 bp
815	1518: contig of 704 bp in length	25549	26230: contig of 682 bp in length
1519	1618: gap of 100 bp	26231	26330: gap of 100 bp
1619	2321: contig of 703 bp in length	26331	27021: contig of 691 bp in length
2322	2421: gap of 100 bp	27022	27121: gap of 100 bp
2422	3108: contig of 687 bp in length	27122	27833: contig of 712 bp in length
3109	3208: gap of 100 bp	27834	27933: gap of 100 bp
3209	3915: contig of 708 bp in length	27934	28620: contig of 687 bp in length
3917	4016: gap of 100 bp	28621	28720: gap of 100 bp
4017	4721: contig of 705 bp in length	28721	29420: contig of 700 bp in length
4722	4821: gap of 100 bp	29421	29520: gap of 100 bp
4822	5530: contig of 709 bp in length	29521	30235: contig of 715 bp in length
5531	5630: gap of 100 bp	30236	30335: gap of 100 bp
5631	6340: contig of 710 bp in length	30336	31031: contig of 696 bp in length
6341	6440: gap of 100 bp	31032	31131: gap of 100 bp
6441	7124: contig of 684 bp in length	31132	31848: contig of 717 bp in length
7125	7224: gap of 100 bp	31849	31948: gap of 100 bp
7224	7922: contig of 698 bp in length	31949	32667: contig of 719 bp in length
7923	8022: gap of 100 bp	32668	32767: gap of 100 bp
8023	8737: contig of 715 bp in length	32768	33483: contig of 716 bp in length
8738	8837: gap of 100 bp	33484	33583: gap of 100 bp
8838	9520: contig of 683 bp in length	33584	34244: contig of 661 bp in length
9521	9620: gap of 100 bp	34245	34344: gap of 100 bp
9621	10304: contig of 684 bp in length	34345	35031: contig of 687 bp in length
10305	10404: gap of 100 bp	35032	35131: gap of 100 bp
10405	11118: contig of 714 bp in length	35132	35783: contig of 652 bp in length
11119	11218: gap of 100 bp	35784	35883: gap of 100 bp
11219	11926: contig of 708 bp in length	35884	36597: contig of 714 bp in length
11927	12026: gap of 100 bp	36598	36697: gap of 100 bp
12027	12719: contig of 693 bp in length	36698	37417: contig of 720 bp in length
12720	12819: gap of 100 bp	37418	37517: gap of 100 bp
12820	13544: contig of 725 bp in length	37518	38228: contig of 711 bp in length
13545	13644: gap of 100 bp	38229	38328: gap of 100 bp
13645	14339: contig of 695 bp in length	38329	39042: contig of 714 bp in length
14340	14439: gap of 100 bp	39043	39142: gap of 100 bp
14440	15153: contig of 714 bp in length	39143	39827: contig of 685 bp in length
15154	15253: gap of 100 bp	39828	39927: gap of 100 bp
15254	15959: contig of 706 bp in length	39928	40615: contig of 688 bp in length
15960	16059: gap of 100 bp	40616	40715: gap of 100 bp
16060	16734: contig of 675 bp in length	40716	41396: contig of 681 bp in length
16735	16834: gap of 100 bp	41397	41496: gap of 100 bp
16835	17501: contig of 667 bp in length	41497	42199: contig of 703 bp in length
17502	17601: gap of 100 bp	42200	42299: gap of 100 bp
17603	18238: contig of 637 bp in length	42300	43002: contig of 703 bp in length
18239	18338: gap of 100 bp	43003	43102: gap of 100 bp
18339	19048: contig of 710 bp in length	43103	43806: contig of 704 bp in length
19049	19148: gap of 100 bp	43807	43906: gap of 100 bp
19149	19804: contig of 656 bp in length	43907	44612: contig of 706 bp in length
19805	19904: gap of 100 bp	44613	44712: gap of 100 bp
19905	20630: contig of 726 bp in length	44713	45428: contig of 716 bp in length
20631	20730: gap of 100 bp	45429	45528: gap of 100 bp
20731	21437: contig of 707 bp in length	45529	46243: contig of 715 bp in length
21438	21537: gap of 100 bp	46244	47017: contig of 674 bp in length
21538	22248: contig of 711 bp in length	47018	47117: gap of 100 bp
22249	22348: gap of 100 bp	47118	47824: contig of 707 bp in length
22349	23072: contig of 724 bp in length	47825	47924: gap of 100 bp
23073	23172: gap of 100 bp	47925	48610: contig of 686 bp in length
23173	23878: contig of 706 bp in length	48611	48710: gap of 100 bp
23879	24670: contig of 692 bp in length	48711	49421: contig of 711 bp in length
24671	24770: gap of 100 bp	49422	49521: gap of 100 bp
		49522	50341: contig of 720 bp in length
		50342	51017: contig of 676 bp in length
		51018	51117: gap of 100 bp
		51118	51827: contig of 710 bp in length
		51828	51927: gap of 100 bp
		51928	52556: contig of 729 bp in length
		52557	52756: gap of 100 bp
		52757	53471: contig of 715 bp in length
		53472	53571: gap of 100 bp
		53572	54254: contig of 683 bp in length



```

* 19887 19886: gap of unknown length
* 19987 21267: contig of 1281 bp in length
* 21268 21367: gap of unknown length
* 21368 21384: contig of 2017 bp in length
* 23385 23484: gap of unknown length
* 23485 24781: contig of 1297 bp in length
* 24782 24881: gap of unknown length
* 26326 26325: contig of 1444 bp in length
* 26426 26425: gap of unknown length
* 27891 27891: contig of 1466 bp in length
* 27892 29249: contig of 1258 bp in length
* 29250 29349: gap of unknown length
* 29350 30511: contig of 1162 bp in length
* 30512 30612: gap of unknown length
* 30612 31639: contig of 1028 bp in length
* 31640 31739: gap of unknown length
* 31740 33262: contig of 1523 bp in length
* 33263 33362: gap of unknown length
* 33363 34819: contig of 1457 bp in length
* 34820 34919: gap of unknown length
* 34920 36444: contig of 1525 bp in length
* 36445 36544: gap of unknown length
* 36545 38154: contig of 1610 bp in length
* 38155 38254: gap of unknown length
* 38255 40652: contig of 2398 bp in length
* 40653 40752: gap of unknown length
* 40753 42596: contig of 1846 bp in length
* 42599 42698: gap of unknown length
* 45341 45341: contig of 2643 bp in length
* 45342 45441: gap of unknown length
* 45442 47416: contig of 1975 bp in length
* 47417 47516: gap of unknown length
* 47517 50148: contig of 2632 bp in length
* 50149 50248: gap of unknown length
* 50249 53066: contig of 2818 bp in length
* 53067 53166: gap of unknown length
* 53167 55931: contig of 2764 bp in length
* 55931 56030: gap of unknown length
* 56031 58774: contig of 2743 bp in length
* 58774 58873: gap of unknown length
* 58874 62176: contig of 3303 bp in length
* 62177 62276: gap of unknown length
* 62277 65607: contig of 3331 bp in length
* 65608 65707: gap of unknown length
* 65708 69755: contig of 4048 bp in length
* 69756 69855: gap of unknown length
* 69856 72866: contig of 3011 bp in length
* 72867 72966: gap of unknown length
* 72967 76494: contig of 3528 bp in length
* 76495 76594: gap of unknown length
* 76595 79874: contig of 3280 bp in length
* 79875 79974: gap of unknown length
* 82983 82982: contig of 3008 bp in length
* 82983 83083: gap of unknown length
* 83083 88834: contig of 5752 bp in length
* 88835 88934: gap of unknown length
* 88935 92177: contig of 3243 bp in length
* 92178 92277: gap of unknown length
* 92278 97659: contig of 5382 bp in length
* 97660 97759: gap of unknown length
* 102399 102398: contig of 4639 bp in length
* 102499 108654: gap of unknown length
* 108655 108754: gap of unknown length
* 108755 116575: contig of 7821 bp in length
* 116576 116675: gap of unknown length
* 116676 124086: contig of 7411 bp in length

```

```

Query Match 77.8%; Score 14; DB 2; Length 151097;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 5 UCCUGAGANNNNN 18
Db 144288 TCCTGGAGNNNNN 144275

RESULT 67
AC074261
LOCUS 151448 bp DNA linear HTG 24-AUG-2000
DEFINITION Homo sapiens chromosome 12 clone RP11-55F19, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
ACCESSION AC074261
VERSION AC074261.3 GI:9887786
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 151448)
AUTHORS Waterston,R.H.
TITLES The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 151448)
AUTHORS Waterston,R.H.
TITLES Direct Submission
JOURNAL Submitted (24-Jul-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 24, 2000 this sequence version replaced gi:9845165.

COMMENT ----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H.NH0055F19
----- Summary Statistics -----
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 145424 bases at least Q40
Consensus quality: 147251 bases at least Q30
Consensus quality: 147980 bases at least Q20
Insert size: 14600; agarose-fp
Insert size: 149444; sum-of-contigs
Quality coverage: 5.22 in Q20 bases;
Quality coverage: 5.13 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1452: contig of 1452 bp in length
1453 1552: gap of unknown length
1553 3954: contig of 2402 bp in length
3955 4054: gap of unknown length
4055 5943: contig of 1889 bp in length
5944 6043: gap of unknown length
6044 10527: contig of 4484 bp in length
10528 10627: gap of unknown length
10628 15918: contig of 5291 bp in length
15919 16019: gap of unknown length
16019 20749: contig of 4731 bp in length
20750 20849: gap of unknown length
20850 27240: contig of 6391 bp in length
27241 27340: gap of unknown length
27341 36787: contig of 9447 bp in length
36788 36887: gap of unknown length

```

\* 3688 47572: contig of 10685 bp in length  
\* 47573 47672: contig of unknown length  
\* 47673 66286: contig of 18614 bp in length  
\* 47674 66287 66386: gap of unknown length  
\* 66387 84036: contig of 17650 bp in length  
\* 84037 84137: gap of unknown length  
\* 84137 106069: contig of 21933 bp in length  
\* 106070 106169: gap of unknown length  
\* 106170 126375: contig of 20206 bp in length  
\* 126376 126475: gap of unknown length  
\* 126476 150744: contig of 24269 bp in length  
\* 150745 150844: gap of unknown length  
\* 150845 151448: contig of 604 bp in length.

## FEATURES

source

location/Qualifiers  
1. 151448  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="12"  
/clone="RP11-55F19"

misc\_feature  
1. 1452  
/note="assembly\_name:Contig11"  
1553. 3954  
/note="assembly\_name:Contig12"  
4055. 5943  
/note="assembly\_name:Contig13"  
6044. 10527  
/note="assembly\_name:Contig14"  
10628. 15918  
/note="assembly\_name:Contig15"  
16019. 20749  
/note="assembly\_name:Contig16"  
20850. 27240  
/note="assembly\_name:Contig17"  
27341. 36787  
/note="assembly\_name:Contig18"  
36888. 47572  
/note="assembly\_name:Contig19"  
47673. 66286  
/note="assembly\_name:Contig20  
clone\_end:T7  
vector\_side:right"  
66387. 84036  
/note="assembly\_name:Contig21"  
84137. 106069  
/note="assembly\_name:Contig22"  
106170. 126375  
/note="assembly\_name:Contig23"  
126476. 150744  
/note="assembly\_name:Contig24"  
150845. 151448  
/note="assembly\_name:Contig7"

## ORIGIN

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 68

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

77.8%; Score 14; DB 2; Length 151448;

Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;

3947 TCCTGAGANNNNN 3960

5 UCCUGAGANNNNNN 18

:|||||

BX927200

BX927200

BX927200

BX927200

BX927200

BX927200

152420 bp DNA linear HTG 24-JAN-2004

WORKING DRAFT SEQUENCE, 8 unordered

pieces.

HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_FULLTOP.

Danio rerio (zebrafish)

Danio rerio

## REFERENCE

AUTHORS

TITLE

JOURNAL

## COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostrariophysi; Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 152420)  
Burton, J.  
Direct Submission  
Submitted (23-JUN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk On Jan 25, 2004 this sequence version replaced gi:41223462.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: ZC116A20  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 10% of reads  
Consensus quality: 150420 bases at least Q40  
Consensus quality: 151102 bases at least Q30  
Consensus quality: 151513 bases at least Q20  
Insert size: 151720; sum-of-contigs  
Insert size: 167766; 4.0% error; agarose-fp  
Quality coverage: 9.55x in Q20 bases; sum-of-contigs Quality coverage: 8.84x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 33759: contig of 33759 bp in length  
\* 33760 33859: gap of 100 bp  
\* 33860 43530: contig of 9671 bp in length  
\* 43531 43630: gap of 100 bp  
\* 43631 48335: contig of 4705 bp in length  
\* 48336 48435: gap of 100 bp  
\* 48436 65568: contig of 17133 bp in length  
\* 65569 65668: gap of 100 bp  
\* 65669 69685: contig of 4017 bp in length  
\* 69686 69785: gap of 100 bp  
\* 69786 76321: contig of 6536 bp in length  
\* 76322 76421: gap of 100 bp  
\* 76422 120851: contig of 44430 bp in length  
\* 120852 120951: gap of 100 bp  
\* 120952 152420: contig of 31469 bp in length.  
Location/Qualifiers

## FEATURES

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misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

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/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="CH211-116A20"  
/clone\_lib="CHORI-211"  
1. 33759  
/note="assembly\_fragment:01133  
fragment\_chain:1  
clone\_end:T7  
vector\_side:left"  
33860. 43530  
/note="assembly\_fragment:00194  
fragment\_chain:1"  
43631. 48335  
/note="assembly\_fragment:00100  
fragment\_chain:1"  
48436. 65568  
/note="assembly\_fragment:00346  
fragment\_chain:1"  
65669. 69685

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/nc="assembly_fragment:00012
fragment_chain:1"
misc_feature
69786..76321
/nc="assembly_fragment:00044
fragment_chain:1"
misc_feature
76422..120851
/nc="assembly_fragment:01745
fragment_chain:1"
misc_feature
120952..152420
/nc="assembly_fragment:00585
fragment_chain:1
clone_end:SP6
vector_side:right"

ORIGIN

Query Match      77.8%; Score 14; DB 2; Length 152420;
Best Local Similarity 85.7%; Pred. NO. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGAGNNNNN 18
Db      43523 TCCTGAGNNNNN 43536

RESULT 69
AC117546/c 154474 bp DNA linear HTG 24-FEB-2003
LOCUS      Mus musculus clone RP23-220E20, WORKING DRAFT SEQUENCE, 23
DEFINITION unorderd pieces.
AC117546
AC117546 GI:28475947
VERSION HTG; HTGS PHASE1; HTGS DRAFT.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 154474)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-220E20
Unpublished
2 (bases 1 to 154474)
Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhalter,B., Brown,A., Camarata,J., Campolano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Deakellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagge,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Labrecque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Margulis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Menesh,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,W., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 154474)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., Deakellano,K.,
Diaz,J.S., Dodge,S., Doolley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,

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TITLE
JOURNAL
COMMENT
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Menesh,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 24, 2003 this sequence version replaced gi:21306852.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RV/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L17227
Center clone name: 220_E_20
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 148512 bases at least Q40
Consensus quality: 150760 bases at least Q30
Consensus quality: 151523 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 152274; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; agarose-fp
Quality coverage: 6.1 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 11: contig of 11 bp in length
12 111: gap of 100 bp
112 945: contig of 834 bp in length
946 1045: gap of 100 bp
1046 1775: contig of 730 bp in length
1776 1875: gap of 100 bp
1876 3355: contig of 1380 bp in length
3356 3355: gap of 100 bp
3356 4362: contig of 1007 bp in length
4363 4462: gap of 100 bp
4463 5745: contig of 1283 bp in length
5746 5845: gap of 100 bp
5846 7326: contig of 1481 bp in length
7327 7426: gap of 100 bp
7427 8111: contig of 685 bp in length
8112 8211: gap of 100 bp
8212 10181: contig of 1970 bp in length
10182 10281: gap of 100 bp
10282 12496: contig of 2215 bp in length
12497 12596: gap of 100 bp
12597 14720: contig of 2124 bp in length
14721 14820: gap of 100 bp
14821 17328: contig of 2508 bp in length
17329 17428: gap of 100 bp

```



```

misc_feature
/notes="assembly_fragment"
141829..154474
/notes="assembly_fragment
clone end:T7
vector_side:right"

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 154474;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGGAGNNNNN 18
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Db 1053 TCCTGAGANNNNN 1040

RESULT 70
AC025626/c 154696 bp DNA linear HTG 28-MAY-2000
LOCUS Homo sapiens clone RP11-216B13, WORKING DRAFT SEQUENCE, 35
DEFINITION Unordered pieces.
AC025626
AC025626 3 GI:8093800
AC025626 3 GI:8093800
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 154696)
Birren,B., Lincon,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-216B13
Unpublished
2 (bases 1 to 154696)
Birren,B., Lincon,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barra,N., Baetien,V., Beda,F.,
Boguslavsky,L., Bouknighter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galgas,J., Gardyna,S., Glnde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Illev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N.,
McCarthy,M., McEwan,P., McGuck,L., McKernan,K., McPheters,R.,
Meldrum,J., Menues,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olyvar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tsefaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,
Vassaliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 330 Charles Street, Cambridge, MA 02141, USA
On May 28, 2000 this sequence version replaced gi:7657088.
All repeats were identified using RepeatMasker:
Smt,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: LS807
Center clone name: 216.B.13
Summary Statistics
Sequencing vector: M13; M77815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

```

Consensus quality: 135951 bases at least Q40  
Consensus quality: 145629 bases at least Q30  
Consensus quality: 148984 bases at least Q20  
Insert size: 149000; agarose-fp  
Insert size: 151296; sum-of-contigs  
Quality coverage: 3.7 in Q20 bases; agarose-fp  
Quality coverage: 3.7 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence, as soon as it is available and the accession number will be preserved.

1 1088: contig of 1088 bp in length  
1089 1188: gap of 100 bp  
1189 2246: contig of 1058 bp in length  
2247 2346: gap of 100 bp  
2347 3505: contig of 1159 bp in length  
3506 3605: gap of 100 bp  
3606 4777: contig of 1172 bp in length  
4778 4878: gap of 100 bp  
4878 6634: contig of 1757 bp in length  
6635 6735: gap of 100 bp  
6735 8097: contig of 1363 bp in length  
8098 8197: gap of 100 bp  
8198 10306: contig of 2109 bp in length  
10307 10406: gap of 100 bp  
10407 12406: contig of 2000 bp in length  
12407 12506: gap of 100 bp  
12507 14219: contig of 1713 bp in length  
14220 14319: gap of 100 bp  
14320 16072: contig of 1753 bp in length  
16073 16173: gap of 100 bp  
16173 17723: contig of 1551 bp in length  
17724 17823: gap of 100 bp  
17824 19608: contig of 1785 bp in length  
19609 19708: gap of 100 bp  
19709 22007: contig of 2299 bp in length  
22008 22107: gap of 100 bp  
22108 23950: contig of 1843 bp in length  
23951 24050: gap of 100 bp  
24051 26881: contig of 2831 bp in length  
26882 26981: gap of 100 bp  
26982 29772: contig of 2791 bp in length  
29773 29872: gap of 100 bp  
29873 32507: contig of 2635 bp in length  
32508 32607: gap of 100 bp  
32608 36314: contig of 3707 bp in length  
36315 36414: gap of 100 bp  
36415 38938: contig of 2424 bp in length  
38939 42279: contig of 3341 bp in length  
42280 42379: gap of 100 bp  
42380 44940: contig of 2561 bp in length  
44941 45041: gap of 100 bp  
45041 48483: contig of 3443 bp in length  
48484 48584: gap of 100 bp  
48584 52752: contig of 4169 bp in length  
52753 52852: gap of 100 bp  
52853 57771: contig of 4919 bp in length  
57772 57871: gap of 100 bp  
57872 61962: contig of 4091 bp in length  
61963 62062: gap of 100 bp  
62063 65728: contig of 3666 bp in length  
65729 65828: gap of 100 bp  
65829 69752: contig of 3924 bp in length  
69753 69853: gap of 100 bp  
69853 76487: contig of 6635 bp in length  
76488 76587: gap of 100 bp  
76588 84995: contig of 8408 bp in length

84996 85095: gap of 100 bp  
85096 91863: contig of 6768 bp in length  
91864 91963: gap of 100 bp  
91964 104501: contig of 12538 bp in length  
104502 104601: gap of 100 bp  
104602 116857: contig of 12256 bp in length  
116858 116957: gap of 100 bp  
116958 127000: contig of 10043 bp in length  
127001 127100: gap of 100 bp  
127101 140329: contig of 13229 bp in length  
140330 140429: gap of 100 bp  
140430 154696: contig of 14267 bp in length.

FEATURES  
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1. 154696  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone\_lib="RP11-216B13"  
/clone\_1ib="RP11-11 Human Male BAC"  
1. 1088  
/note="assembly\_fragment"  
1189. 2246  
/note="assembly\_fragment"  
2347. 3505  
/note="assembly\_fragment"  
3606. 4777  
/note="assembly\_fragment"  
4878. 6634  
/note="assembly\_fragment"  
6735. 8097  
/note="assembly\_fragment"  
8198. 10306  
/note="assembly\_fragment"  
10407. 12406  
/note="assembly\_fragment"  
12507. 14219  
/note="assembly\_fragment"  
14320. 16072  
/note="assembly\_fragment"  
16173. 17723  
/note="assembly\_fragment"  
17824. 19608  
/note="assembly\_fragment"  
19709. 22007  
/note="assembly\_fragment"  
22108. 23950  
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24051. 26881  
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26982. 29772  
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29873. 32507  
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32608. 36314  
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36415. 38938  
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38939. 42279  
/note="assembly\_fragment"  
42380. 44940  
/note="assembly\_fragment"  
45041. 48483  
/note="assembly\_fragment"  
48584. 52752  
/note="assembly\_fragment"  
52853. 57771  
/note="assembly\_fragment"  
57872. 61962

Query Match 77.8%; Score 14; DB 2; Length 154696;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNN 18  
 :||:|||||  
 Db 76595 TCCGAGAGNNNNN 76582

RESULT 71  
 AC144021 158981 bp DNA linear HTG 09-APR-2003  
 DEFINITION Macaca mulatta clone CH250-272M19, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 AC144021  
 AC144021.1 GI:29649612  
 HTG; HTGS\_PHASE2; HTGS\_PGI  
 Macaca mulatta (rhesus monkey)  
 Macaca mulatta  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.  
 1 (bases 1 to 158981)  
 Cauros, M. and Mlosovajevic, A.  
 Pooled genomic indexing (PGI): mathematical analysis and experiment design

REFERENCE  
 AUTHORS (in) Guiso R. and Gusfield, D. (Eds.);  
 TITLE ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI  
 2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;  
 Springer (2002)  
 2 (bases 1 to 158981)  
 Mlosovajevic, A., Sodergren, E., Cauros, M., Li, B., Jackson, A.R.,  
 Adams, C., Adio-oduola, B., Ali-osman, F.R., Allen, C., Alshrocks, S.L.,  
 Amaratunga, H.C., Are, J.R., Ayale, M., Banks, T., Barbata, J.,  
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 Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulhay, C.,  
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 Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D.,  
 Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,  
 Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,  
 Denu, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,  
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 Zorrilla, S., Zuchterlapp, R., Weinstein, G. and Gibbs, R.  
 Direct Submission

JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 158981)  
 AUTHORS Worley, K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-APR-2003) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 COMMENT  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: LCV0  
 Center clone name: CH250-272M19  
 ----- Summary Statistics  
 Chemistry: Dye-terminator Big Dye; Intf of reads  
 Chemistry: Dye-terminator Big Dye; Intf of reads  
 Consensus quality: 8998 bases at least Q40  
 Consensus quality: 10656 bases at least Q30  
 Consensus quality: 12610 bases at least Q20  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html)  
 \* NOTE: The config are based on the application  
 \* of the PGI method using the human genome (NCBI build 31)  
 \* as the comparative genome.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 1 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 1 158981: config of 158981 bp in length.  
 Location/Qualifiers  
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 CONFIDENCE: 0.83"

ORIGIN  
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 Query Match 77.8%; Score 14; DB 2; Length 158981;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNN 18  
 :||:|||||  
 Db 125578 TCCGAGAGNNNNN 125591

RESULT 72  
 AC144013 159732 bp DNA linear HTG 13-JUN-2002  
 DEFINITION Rattus norvegicus clone RPCI-31-40B13 strain Brown Norway, WORKING  
 DRAFT SEQUENCE, 208 unordered pieces.  
 AL627241  
 AL627241.2 GI:17154521  
 HTG; HTGS\_PHASE1; HTGS\_DRAFT  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1  
 Subtrak, R., Borzym, K., Mueller, I., Klages, S., Kojima, A.,  
 Walter, L., Guenther, E., Hurt, P., Lehrach, H., Himmelbauer, H. and

Reinhardt, R.  
Unpublished  
2 (bases 1 to 159732)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Direct Submission  
Submitted (22-OCT-2001) MPIMG, Abt. Lehrach, Max Planck Institut  
Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany  
On Nov 29, 2001 this sequence version replaced gi:16416083.  
COMMENT  
contig 01 1..485  
contig 02 586..2139  
contig 03 2240..2622  
contig 04 2723..3242  
contig 05 3343..3741  
contig 06 3842..4514  
contig 07 4615..5100  
contig 08 5201..6281  
contig 09 6382..6795  
contig 10 6896..7823  
contig 11 7924..8859  
contig 12 8960..9970  
contig 13 10071..10603  
contig 14 10704..11117  
contig 15 11218..11541  
contig 16 11642..11836  
contig 17 11937..12664  
contig 18 12765..13209  
contig 19 13310..13840  
contig 20 13941..14593  
contig 21 14694..15088  
contig 22 15189..15436  
contig 23 15537..15720  
contig 24 15821..16949  
contig 25 17050..17480  
contig 26 17581..18457  
contig 27 18558..19109  
contig 28 19210..20433  
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contig 31 21210..21547  
contig 32 21648..21971  
contig 33 22072..22343  
contig 34 22444..22643  
contig 35 22744..22962  
contig 36 23063..23416  
contig 37 23517..23979  
contig 38 24080..24360  
contig 39 24461..24929  
contig 40 25030..25430  
contig 41 25531..25701  
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contig 43 26038..26430  
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contig 108 77555..77994  
contig 109 78095..78534  
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contig 111 79230..80615  
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Query Match 77.8%; Score 14; DB 2; Length 159732;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18  
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 Db 2132 TCCTGAGAGNNNNN 2145

RESULT 73  
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 LOCUS Homo sapiens chromosome 3 clone RP11-80B17 map 3, WORKING DRAFT  
 DEFINITION SEQUENCE, 20 unordered pieces.  
 AC027535  
 VERSION AC027535.2 GI:8705144  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
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 Anderson,S., Baldwin,J., Barna,N., Baetsen,V., Bedalov,F.,  
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# TITLE JOURNAL

## COMMENT

Galagan J., Gardyna S., Ginde S., Goyette M., Graham L.,  
 Grand-Pierre N., Grant G., Hagoe B., Heaford A., Horton L.,  
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 Vassiliev H., Viel R., Vo A., Wilson B., Wu X., Wyman D., Ye W.J.,  
 Young G., Zainoun J., Zimmer A. and Zody M.  
 Direct Submission  
 Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jun 25, 2000 this sequence version replaced gi:7342280.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WtBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L8663  
 Center clone name: 80 B.17  
 ----- Summary Statistics  
 Sequencing vector: M13, M7815, 100% of reads  
 Chemistry: Dye-terminator Big Dye, 100% of reads  
 Assembly program: Phrap, version 0.960731  
 Consensus quality: 150530 bases at least Q40  
 Consensus quality: 15616 bases at least Q30  
 Consensus quality: 158784 bases at least Q20  
 Insert size: 157000; agarose-fp  
 Insert size: 159929; sum-of-contigs  
 Quality coverage: 4.1 in Q20 bases; sum-of-contigs  
 Quality coverage: 4.1 in Q20 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 20 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 1 1220: contig of 1220 bp in length  
 \* 1221 1320: gap of 100 bp  
 \* 1321 2400: contig of 1080 bp in length  
 \* 2401 2500: gap of 100 bp  
 \* 2501 4030: contig of 1530 bp in length  
 \* 4031 4130: gap of 100 bp  
 \* 4131 6165: contig of 2035 bp in length  
 \* 6166 6265: gap of 100 bp  
 \* 6266 8351: contig of 2086 bp in length  
 \* 8352 8451: gap of 100 bp  
 \* 8452 11132: contig of 2681 bp in length  
 \* 11133 11232: gap of 100 bp  
 \* 11233 14754: contig of 3522 bp in length  
 \* 14755 14854: gap of 100 bp  
 \* 14855 18511: contig of 3657 bp in length  
 \* 18512 18611: gap of 100 bp  
 \* 18612 21628: contig of 3017 bp in length  
 \* 21629 21728: gap of 100 bp  
 \* 21729 26262: contig of 4534 bp in length  
 \* 26263 31430: contig of 5066 bp in length  
 \* 31431 31530: gap of 100 bp  
 \* 31531 37366: contig of 5836 bp in length

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* 37367 37466: gap of 100 bp
* 37467 44372: contig of 6906 bp in length
* 44373 44472: gap of 100 bp
* 44473 54509: contig of 10037 bp in length
* 54510 54609: gap of 100 bp
* 54610 64622: contig of 9913 bp in length
* 64623 64623: gap of 100 bp
* 64623 74692: contig of 10070 bp in length
* 74693 74792: gap of 100 bp
* 74793 85848: contig of 11056 bp in length
* 85849 108162: contig of 22214 bp in length
* 108163 108262: gap of 100 bp
* 108263 129110: contig of 20848 bp in length
* 129111 129210: gap of 100 bp
* 129211 161829: contig of 32619 bp in length.
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ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 161829;

Best Local Similarity 85.7%; Pred. No. 1e+02;

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Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 UCCUGAGANNNNNN 18
Db 108270 TCCTGAGANNNNNN 108257

RESULT 74
BX908804/c
LOCUS
DEFINITION
ACCESSION
BX908804.5 GI:42592630
VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
SOURCE
Dario rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 163732)
Sims,S.
Direct Submission
Submitted (13-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
fish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 17, 2004 this sequence version replaced gi:42538895.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: fish-help@sanger.ac.uk
----- Project Information
Center project name: zc163M16
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 160023 bases at least Q40
Consensus quality: 160800 bases at least Q30
Consensus quality: 160800 bases at least Q20
Insert size: 162732; sum-of-contigs
Insert size: 173608; 1.2% error; agarose-fp
Quality coverage: 11.84x in Q20 bases; sum-of-contigs Quality
coverage: 11.22x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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    * 6996 7095: gap of 100 bp
    * 16711 16711: contig of 9616 bp in length
    * 16712 16811: gap of 100 bp
    * 16812 35552: contig of 18741 bp in length
    * 35553 35652: gap of 100 bp
    * 35653 38371: contig of 2719 bp in length
    * 38372 38471: gap of 100 bp
    * 38472 64553: contig of 2682 bp in length
    * 64554 64553: gap of 100 bp
    * 64554 109139: contig of 44486 bp in length
    * 109140 109239: gap of 100 bp
    * 109240 113076: contig of 3837 bp in length
    * 113077 113176: gap of 100 bp
    * 113177 137707: contig of 2431 bp in length
    * 137708 137807: gap of 100 bp
    * 137808 152500: contig of 14693 bp in length
    * 152501 152600: gap of 100 bp
    * 152601 160231: contig of 7631 bp in length
    * 160232 160331: gap of 100 bp
```

```

FEATURES          *      160332      163732: contig of 3401 bp in length.
SOURCE
1..163732
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-163M16"
/clone_1ib="CHORI-211"
1..6995
/note="assembly_fragment:00139
fragment_chain:1
clone_end:SP6
vector_side:left"
misc_feature
7096..16711
/note="assembly_fragment:00375
fragment_chain:1"
16812..35552
/note="assembly_fragment:00531
fragment_chain:1"
35653..38371
/note="assembly_fragment:00082
fragment_chain:1"
38472..64553
/note="assembly_fragment:01682
fragment_chain:1"
64654..109139
/note="assembly_fragment:02187.
fragment_chain:1"
109240..113076
/note="assembly_fragment:00033
fragment_chain:1"
113177..137707
/note="assembly_fragment:01180
fragment_chain:1"
137808..152500
/note="assembly_fragment:00845
fragment_chain:1"
152601..160231
/note="assembly_fragment:00222
fragment_chain:1"
160332..163732
/note="assembly_fragment:00057"

ORIGIN
Query Match      77.8%; Score 14; DB 2; Length 163732;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGGAGNNNNNN 18
      :||:|||||||
Db      35660 TCCTGAGNNNNNN 35647

RESULT 75
AC026082      173423 bp      DNA      linear      HTG 01-SEP-2000
LOCUS        Homo sapiens chromosome 12 clone RP11-424B7, WORKING DRAFT
DEFINITION   AC026082
SEQUENCE     AC026082, 8 unordered pieces.
ACCESSION    AC026082.4 GI:9958252
VERSION      HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 173423)
AUTHORS      Waterston, R.H.
TITLE        The sequence of Homo sapiens clone
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 173423)
AUTHORS      Waterston, R.H.
TITLE        Direct Submission
JOURNAL      Submitted (19-MAR-2000) Genome Sequencing Center, Washington

```

```

COMMENT
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:7523968.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0424B07
----- Summary Statistics -----
Sequencing vector: M13, 100%
Sequencing vector: plasmid, 0%
Chemistry: Dye-Primer ET; 100% of reads
Chemistry: Dye-Terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 169510 bases at least Q40
Consensus quality: 170826 bases at least Q30
Consensus quality: 171573 bases at least Q20
Insert size: 155000; agarose-fp
Insert size: 172723; sum-of-contigs
Quality coverage: 5.33 in Q20 bases; agarose-fp
Quality coverage: 4.79 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 14541: contig of 14541 bp in length
* 14542 14641: gap of unknown length
* 14642 24352: contig of 9711 bp in length
* 24353 24453: gap of unknown length
* 24453 55873: contig of 31421 bp in length
* 55874 55974: gap of unknown length
* 55974 96384: gap of unknown length
* 96384 96484: gap of 40410 bp in length
* 96484 141828: contig of 45345 bp in length
* 141828 141928: gap of unknown length
* 141928 150796: contig of 8766 bp in length
* 150796 150797: gap of unknown length
* 150797 162246: contig of 11450 bp in length
* 162246 162347: gap of unknown length
* 162347 173423: contig of 11077 bp in length.

FEATURES
SOURCE
1..173423
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-424B7"
1..14541
/note="assembly_name:Contig10
clone_end:SP6
vector_side:left"
14642..24352
/note="assembly_name:Contig8
clone_end:T7
vector_side:right"
24453..55873
/note="assembly_name:Contig11"
55974..96383
/note="assembly_name:Contig12"
96484..141828
/note="assembly_name:Contig13"
141929..150696
/note="assembly_name:Contig16"
150797..162246
/note="assembly_name:Contig7"
162347..173423

```

```

ORIGIN /note="assembly_name:Contig9"

Query Match 77.8%; Score 14; DB 2; Length 173423;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGGNNNNN 18
Db 162239 TCCTGAGGNNNNN 162252

RESULT 76
CR339046 173705 bp DNA linear HTG 11-MAR-2004
LOCUS Danio rerio clone CH211-112C15, *** SEQUENCING IN PROGRESS ***, 9
DEFINITION unordered pieces.
ACCESSION CR339046
VERSION CR339046.4 GI:45381861
KEYWORDS HTG: HTGS PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 173705)
McLay, K.
Direct Submission
Submitted (08-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf1sh-help@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
On Mar 11, 2004 this sequence version replaced gi:45238479.

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf1sh-help@sanger.ac.uk
----- Project Information
Center project name: ZC112C15
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 171047 bases at least Q40
Consensus quality: 171468 bases at least Q30
Consensus quality: 171906 bases at least Q20
Insert size: 172905; sum-of-contigs
Insert size: 176004; 4.4% error; agarose-fp
Quality coverage: 10.13x in Q20 bases; sum-of-contigs Quality
Coverage: 9.95x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 17494: contig of 17494 bp in length
* 17495 17594: gap of 100 bp
* 17595 30952: contig of 13358 bp in length
* 30953 31052: gap of 100 bp
* 31053 56754: contig of 25702 bp in length
* 56755 56854: gap of 100 bp
* 56855 61530: contig of 4676 bp in length
* 61531 61630: gap of 100 bp
* 61631 83635: contig of 22005 bp in length
* 83636 83735: gap of 100 bp
* 83736 87791: contig of 4056 bp in length
* 87792 87891: gap of 100 bp
* 87892 91726: contig of 3835 bp in length
* 91727 91826: gap of 100 bp
* 91827 139371: contig of 47545 bp in length

```

```

FEATURES
* 139372 139471: gap of 100 bp
* 139472 173705: contig of 34234 bp in length.
source
1. 173705
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-112C15"
/clone_1b="CHORI-211"
1. 17494
/note="assembly fragment:00399
fragment chain:1
clone_end:17
vector_side:left"
17595. 30952
/note="assembly fragment:00171
fragment chain:1"
31053. 56754
/note="assembly fragment:00394
fragment chain:1"
56855. 61530
/note="assembly fragment:00107
fragment chain:1"
61631. 83635
/note="assembly fragment:00638
fragment chain:1"
83736. 87791
/note="assembly fragment:00001
fragment chain:1"
87892. 91726
/note="assembly fragment:00050
fragment chain:1"
91827. 139371
/note="assembly fragment:01987
fragment chain:1"
139472. 173705
/note="assembly fragment:01449
fragment chain:1
clone_end:886
vector_side:right"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 173705;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGGNNNNN 18
Db 61523 TCCTGAGGNNNNN 61536

RESULT 77
AP002368 175056 bp DNA linear HTG 31-MAY-2000
LOCUS Homo sapiens chromosome 11 clone RP11-152017 map 11q, WORKING DRAFT
DEFINITION SEQUENCE, 38 unordered pieces.
ACCESSION AP002368
VERSION AP002368.1 GI:8131632
KEYWORDS HTG: HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 175056)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Home sapiens 175,056 genomic DNA of 11q
Published Only in Database (2000)
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical

```



## COMMENT

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
Japan (E-mail: hactori@gsc.riken.go.jp,  
URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923,  
Fax: 81-42-778-9924)

## ----- Genome Center

Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hactori@gsc.riken.go.jp

## ----- Project Information

Center project name: HumDrafc11

Center Clone name: RP11-152017

## ----- Summary Statistics

Sequencing vector: PCR products; 100% of reads  
Chemistry: Dye-terminator ET-amersham; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 15284 bases at least Q40  
Consensus quality: 163107 bases at least Q30  
Consensus quality: 168285 bases at least Q20  
Insert size: 171356; sum-of-contigs  
Quality coverage: 4.55x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of  
38 contigs. The true order of the pieces is not known and their  
order in this sequence record is arbitrary. Gaps between the  
contigs are represented as runs 'N', but the exact sizes of the gaps  
are unknown. This record will be updated with the finished sequence  
as soon as it is available and the accession number will be  
preserved

```
1 27556 contig of 27556 bp in length
27657 47715 contig of 20059 bp in length
47816 58290 contig of 10475 bp in length
58391 65882 contig of 7492 bp in length
65983 75140 contig of 9158 bp in length
75241 83735 contig of 8495 bp in length
83836 91075 contig of 7240 bp in length
91176 97301 contig of 6126 bp in length
97402 102966 contig of 5565 bp in length
103067 108296 contig of 5230 bp in length
108397 114679 contig of 6283 bp in length
114780 116966 contig of 2187 bp in length
117067 121663 contig of 4597 bp in length
121764 125369 contig of 3606 bp in length
125470 129037 contig of 3568 bp in length
129138 133165 contig of 4027 bp in length
133265 136081 contig of 2817 bp in length
136182 138969 contig of 2788 bp in length
139070 140960 contig of 1891 bp in length
141061 143612 contig of 2552 bp in length
143713 144408 contig of 666 bp in length
144509 147057 contig of 2549 bp in length
147158 149315 contig of 2158 bp in length
149416 151589 contig of 2184 bp in length
151680 153973 contig of 1952 bp in length
153974 155925 contig of 1952 bp in length
155926 156025 contig of 1648 bp in length
156026 157673 contig of 1745 bp in length
157674 159518 contig of 2055 bp in length
159519 161673 contig of 1451 bp in length
161674 163325 contig of 1223 bp in length
163325 165447 contig of 1927 bp in length
165448 166675 contig of 1342 bp in length
166675 168016 contig of 1702 bp in length
168017 169818 contig of 1416 bp in length
169819 171334 contig of 1150 bp in length
171335 173766 contig of 1082 bp in length
173767 175056 contig of 1180 bp in length
```

\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

```
1 27556: contig of 27556 bp in length
27657 47715: gap of 100 bp
47816 58290: contig of 20059 bp in length
58391 65882: gap of 100 bp
65983 75140: gap of 10475 bp in length
75241 83735: gap of 100 bp
83836 91075: gap of 7492 bp in length
91176 97301: gap of 8495 bp in length
97402 102966: gap of 9158 bp in length
103067 108296: gap of 100 bp
108397 114679: gap of 100 bp
114780 116966: gap of 6283 bp in length
117067 121663: gap of 100 bp
121764 125369: gap of 2187 bp in length
125470 129037: gap of 4597 bp in length
129138 133165: gap of 3606 bp in length
133265 136081: gap of 100 bp
136182 138969: gap of 2788 bp in length
139070 140960: gap of 1891 bp in length
141061 143612: gap of 2552 bp in length
143713 144408: gap of 666 bp in length
144509 147057: gap of 2549 bp in length
147158 149315: gap of 2158 bp in length
149416 151589: gap of 2184 bp in length
151680 153973: gap of 1952 bp in length
153974 155925: gap of 1952 bp in length
155926 156025: gap of 1648 bp in length
156026 157673: gap of 1745 bp in length
157674 159518: gap of 2055 bp in length
159519 161673: gap of 1451 bp in length
161674 163325: gap of 1223 bp in length
163325 165447: gap of 1927 bp in length
165448 166675: gap of 1342 bp in length
166675 168016: gap of 1702 bp in length
168017 169818: gap of 1416 bp in length
169819 171334: gap of 1150 bp in length
171335 173766: gap of 1082 bp in length
173767 175056: gap of 1180 bp in length
```

FEATURES

171435 172584: contig of 1150 bp in length

172885 172684: gap of 100 bp

173766 173766: contig of 1082 bp in length

173767 173866: gap of 100 bp

173867 175056: contig of 1190 bp in length.

Location/Qualifiers

1. 175056

organism="Homo sapiens"

mol\_type="genomic DNA"

db\_xref="taxon:9606"

chromosome="11"

map="11g"

clone="RP11-152017"

misc\_feature 1. 27556

misc\_feature 27657. 47715

misc\_feature 47816. 58290

misc\_feature 58391. 65882

misc\_feature 65983. 75140

misc\_feature 75241. 83735

misc\_feature 83836. 91075

misc\_feature 91176. 97301

misc\_feature 97402. 102966

misc\_feature 103067. 108296

misc\_feature 108397. 114679

Query Match 77.8%; Score 14; DB 2; Length 175056;

Best Local Similarity 85.7%; Pred. No. 1e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGNNNNNN 18

DB 58283 TCCTGAGNNNNNN 58296

RESULT 78

AC144311 176565 bp DNA linear HTG 09-APR-2003

DEFINITION Macaca mulatta clone CH250-271024, \*\*\* SEQUENCING IN PROGRESS \*\*\*.

AC144311

AC144311.1 GI:29650159

KEYWORDS HTG; HTGS PHASE2; HTGS\_PGI.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae; Macaca.

1 (bases 1 to 176565)

REFERENCE

AUTHORS Csuros,M. and Milosavljevic,A.

TITLE Pooled genomic indexing (PGI): mathematical analysis and experiment design

JOURNAL (in) Guigo,R. and Gusfield,D. (Eds.);

REFERENCE

AUTHORS

ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI

2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;

Springer (2002)

2 (bases 1 to 176565)

Milosavljevic,A., Sodergren,E., Csuros,M., Li,B., Jackson,A.R., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Albrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbara,J., Benton,J., Binsag,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D.,

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Duan,A.L., Ding,Y., Dinl,H.H., Douthwaite,K.J., Dirper,H., Dugan-Rocha,S., Durbin,K.J., Egan,A., Earnhart,C., Edwards,C.C., Elhaj,C., Emeling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,A.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hune,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Kovach,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louised,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meader,M., Mei,G., Merscher,S., Metzger,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokemwo,S., Ogih,M., Okunou,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L., Quiles,M., Ren,Y., Rivers,M., Rojase,A., Rojoudkan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shum,C., Shooshtrai,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,O., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williams,A., Wleczek,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kuchelapatti,R., Weinstein,G. and Gibbs,R.

Direct Submission

Unpublished

3 (bases 1 to 176565)

Worley,K.C.

Direct Submission

Submitted (09-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

----- Genome Center -----

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information -----

Center project name: LCIP

Center clone name: CH250-271024

----- Summary Statistics -----

Chemistry: Dye-primer Bodyby: inf% of reads

Chemistry: Dye-terminator Big Dye: inf% of reads

Consensus quality: 7017 bases at least Q40

Consensus quality: 8529 bases at least Q30

Consensus quality: 10199 bases at least Q20

----- NOTE: -----

NOTE: Estimated insert size may differ from sequence length

NOTE: (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))

NOTE: The contigs are based on the application

NOTE: of the PGI method using the Human genome (NCBI build 31)

NOTE: as the comparative genome.

NOTE: This is a 'working draft' sequence. It currently

NOTE: consists of 1 contigs. Gaps between the contigs

NOTE: are represented as runs of N. The order of the pieces

NOTE: is believed to be correct as given, however the sizes

NOTE: of the gaps between them are based on estimates that have

NOTE: provided by the submitter.

NOTE: This sequence will be replaced

NOTE: by the finished sequence as soon as it is available and

NOTE: the accession number will be preserved.

1 176565: contig of 176565 bp in length.

Location/Qualifiers

```

source
1. 176565
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"
/clone="CH250-271024"
1. 176565
/notes="assembly name:CH250-271024.1B
CONFIDENCE:_0.83"

mloc_feature

Query Match 77.8%; Score 14; DB 2; Length 176565;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0

ORIGIN

Oy 5 UCCUGAGAGNNNNN 18
:::|||||
Db 29695 TCCTGAGAGNNNNN 29708

RESULT 79
AC151062 177380 bp DNA linear HTG 04-SEP-2004
LOCUS AC151062
DEFINITION Bos taurus clone CH240-503M8, WORKING DRAFT SEQUENCE, 23 unordered
AC151062
VERSION AC151062.1 GI:51468321
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Bos taurus (cow)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 177380)
Muzny,D., Metzker,M., Adams,C., Agbai II,O., Allen,C.,
Alpbrooks,S., Archer,P., Arredondo,H., Bandaranaike,D., Bangura,L.,
Beltran,B., Beltran,R., Beraducci,A., Biswal,K., Blyth,P.,
Bonham,H., Bunay,C., Burch,C., Cadore,I., Canada,A., Cardenas,V.,
Carter,K., Cavazos,I., Chacko,J., Chahrouh,M., Chavez,D., Chen,A.,
Chen,G., Chen,R., Cheng,M.-T., Chu,J., Cleric,K., Cockrell,R.,
Coyle,M., Cree,A., Curry,S., Dai,M., Davila,M.L., Davis,C.,
Davy-Carroll,L., De Anda,C., Delgado,O., Denson,S., Derramo,C.,
Ding,Y., Dinh,H., Donlin,J., McCalley,S., Dugan-Rocha,S., Dunn,A.,
Durdin,K., Dzude,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C.,
Fa,M., Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T.,
Gaekin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D.,
Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeblerlen,K.,
Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Haylak,P.,
Haves,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J.,
Hines,S., Hitchens,M., Hodgeson,A., Hogues,M., Hollins,B.,
Howell,L.T., Hulky,S., Hume,J., Imo,K., Jackson,A., Jackson,L.,
Jacob,L., Jiang,H., Johnson,B., Johnson,R., Kalatus,K., Kelly,S.,
Key,T., Khan,Z., King,L., Kovar,C., Kovis,A., Kovis,C., Lara,F.,
Lee,S., Lee,K., Lee,S., Legall,F.I., Lemon,S., Lewis,L., Li,B.,
Li,Y., Li,Z., Linnell,M., Liu,W., Liu,Y.-S., Liu,Y., Llyanage,D.,
London,P., Lopez,J., Lorenzshwa,L., Lozado,R., Luk,T., Madu,R.,
Maleshvari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E.,
McClennan,H., McPherson,J., Mercedao,C., Milosavljevic,A.,
Miyaj,E., Morgan,M., Morris,S., Muniasa,M., Murray,D.,
Nasarith,L., Ngo,D., Nguyen,N., Norwig-Bastugun,E., Nott,A.,
Nwokoleh.O., Obregon,M., Ochi-Okoie,C., Odoh,E., Okwunou,G.,
Okwunou,K., Parker,D., Pasternak,S., Patel,B., Patel,V., Paul,H.,
Petrez,A., Perez,L., Petrosino,J., Pham,T., Prius,E., Pu,L.-L.,
Puzo,M., Qin,X., Quinn,A., Quiroz,J., Rabata,D., Rachlin,E.,
Reisig,R., Ren,Y., Reuter,M., Richards,S., Rives,C., Rodriguez,F.,
Rojas,A., Ruiz,S.-J., Sana,M., Sanders,W., Santibanez,J., Santos,R.,
Savery,G., Scherer,S., Shen,H., Shen,Y., Sisson,I., Sneed,A.,
Sodergren,E., Song,X.-Z., Sorelle,R., Svatok,A., Taylor,E.,
Taylor,T., Thomas,N., Thorn,R., Thornton,R., Trejos,Z., Usmani,K.,
Vargio,C., Verdusco,D., Villaseana,D., Vitk,D., Volkov,A.,
Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,J., Wei,X.,
Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R., Wu,J.,
Yakub,S., Yan,K., Yaun,Y., Yu,F., Zhang,J., Zhang,L., Zhang,Z.,

```

TITLE	Zhou, J., Weinstock, G. and Gibbs, R.
JOURNAL	Direct Submission
REFERENCE	2 (bases 1 to 177380)
AUTHORS	Worley, K. C.
TITLE	Direct Submission
JOURNAL	Submitted (20-AUG-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 177380)
AUTHORS	Worley, K. C.
TITLE	Direct Submission
JOURNAL	Submitted (04-SEP-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	----- Center: Baylor College of Medicine Genome Center ----- Center code: BCM Web site: <a href="http://www.hgsc.bcm.tmc.edu/">http://www.hgsc.bcm.tmc.edu/</a> Contact: hgsc-help.tmc.edu ----- Project Information ----- Center project name: FBTU Center clone name: CH240-503N8 ----- Summary Statistics ----- Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 182338 bases at least Q40 Consensus quality: 185027 bases at least Q30 Consensus quality: 188535 bases at least Q20 Estimated insert size: 150732; sum-of-contigs estimation Estimated insert size: 189442; agarose-fp estimation Quality coverage: 3x in Q20 bases; agarose-fp estimation Quality coverage: 3x in Q20 bases; sum-of-contigs estimation ----- * NOTE: Estimated insert size may differ from sequence length * (see <a href="http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html">http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html</a> ) * NOTE: This is a "working draft" sequence. It currently * consists of 23 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. ----- * 1 2833: contig of 2833 bp in length * 2834 2933: gap of unknown length * 2934 6260: contig of 3327 bp in length * 6261 6360: gap of unknown length * 6361 12441: contig of 6081 bp in length * 12442 12541: gap of unknown length * 12542 15522: contig of 2981 bp in length * 15523 15622: gap of unknown length * 15623 22934: contig of 7312 bp in length * 22935 23034: gap of unknown length * 23035 37402: contig of 14368 bp in length * 37403 37502: gap of unknown length * 37503 41711: contig of 4209 bp in length * 41712 41811: gap of unknown length * 41812 49591: contig of 7780 bp in length * 49592 49691: gap of unknown length * 49692 70289: contig of 20598 bp in length * 70290 70389: gap of unknown length * 70390 77856: contig of 7467 bp in length * 77857 77956: gap of unknown length * 77957 80000: contig of 2044 bp in length * 80001 80100: gap of unknown length * 80101 83813: contig of 3713 bp in length * 83814 83913: gap of unknown length * 83914 89178: contig of 5265 bp in length * 89179 89278: gap of unknown length * 89279 98605: contig of 9327 bp in length * 98606 98705: gap of unknown length

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* 98706 101016: contig of 2311 bp in length
* 101017 101116: gap of unknown length
* 101117 106474: contig of 5358 bp in length
* 106475 106574: gap of unknown length
* 106575 116243: contig of 9669 bp in length
* 116244 116343: gap of unknown length
* 116344 122675: contig of 6332 bp in length
* 122676 122775: gap of unknown length
* 122776 137611: contig of 14836 bp in length
* 137612 143280: contig of 5569 bp in length
* 143281 143381: gap of unknown length
* 143382 155847: contig of 12467 bp in length
* 155848 155947: gap of unknown length
* 155948 164900: contig of 8953 bp in length
* 164901 165001: gap of unknown length
* 165001 177380: contig of 12380 bp in length.

FEATURES
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      /organism="Bos taurus"
      /mol_type="genomic DNA"
      /db_xref="taxon:9913"
      /clone="CH240-503N8"

ORIGIN
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  Best Local Similarity 85.7%; Pred. No. 1e+02;
  Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGAGNNNNNN 18
   |||:|||||
Db 15515 TCCTGAGAGNNNNN 15528

RESULT 80
LOCUS AC125597/c
DEFINITION Rattus norvegicus clone CH230-341P19, *** SEQUENCING IN PROGRESS
ACCESSION AC125597
VERSION AC125597.3 GI:25074793
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
  1 (bases 1 to 178472)
  Muzny,D,Marie, Metzker,M,Lee, Abramzon,S, Adams,C, Alder,J,
  Allen,C, Allen,H, Alsbrooks,S, Amin,A, Anguiano,D,
  Anyalebechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
  Baldwin,D, Bandatanaike,D, Barber,M, Barnstead,M, Benahmed,F,
  Bissalo,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M,
  Bryant,N, Buhay,C, Burch,P, Butrell,K, Calderon,E,
  Cardenas,V, Carter,K, Cavazos,I, Caesar,H, Center,A,
  Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
  Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
  Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
  Delgado,O, Denson,S, Detamo,C, Ding,Y, Dinh,H, Divya,K,
  Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Evans,K,
  Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
  Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
  Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
  Gebregregis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,W,
  Gunaratne,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,J,
  Hernandez,R, Hines,S, Hui,Y,S, Hume,J, Idelbird,D, Jackson,A,
  Hollins,B, Howells,S, Hu,Y,S, Hudson,S,L, Hodgson,A, Hogue,M,
  Hernandez,R, Hines,S, Hui,Y,S, Hume,J, Idelbird,D, Jackson,A,
  Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A,
  Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Koyar,C,
  Kowals,C, Kratz,C,L, Ledow,H, Levan,J, Lewis,L, Li,Z, Liu,J,
  Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
  Lorenshewa,L, Louisedge,H, Lozano,R,J, Lu,X, Ma,J,

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TITLE JOURNAL
AUTHORS Mageshwar,M, Mahindartne,M, Mahmoud,M, Malloy,K, Mangum,A,
Mangum,B, Mapua,P, Martin,K, Martin,R, Martinez,E,
Mawhinney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S,
Morgan,M, Morris,K, Morris,S, Mundasa,M, Murphy,M, Nair,L,
Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S,
Nwaokweme,O, Okunolu,G, Olarnunsegun,A, Pal,S, Parks,K,
Pasternak,S, Paul,H, Perez,A, Perez,L, Pfankuch,C,
Plopper,F, Polndexter,A, Popovic,D, Prims,E, Pu,L,
Puzo,M, Quiroz,J, Rachlin,E, Reeves,K, Regier,M,A, Reigh,R,
Reilly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F,
Rives,C, Rodery,T, Rojas,A, Rose,M, Rose,R, Ruiz,S,U,
Sanders,M, Savery,G, Scherer,S, Scott,G, Shatman,S, Shen,H,
Shetty,J, Shvartbeyn,A, Sisson,I, Sitter,C,D, Smaj,D,
Sneed,A, Sodergren,E, Song,X,-Z, Sorelle,R, Soosa,J,
Steinle,M, Strong,R, Sutton,A, Svatek,A, Taber,P, Taylor,C,
Taylor,T, Thomas,N, Thomas,S, Tingey,A, Trejos,Z, Usmani,K,
Valas,R, Vera,V, Villaseana,D, Waldron,L, Walker,B, Wang,J,
Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,F,
Williams,G, Willson,R, Wlezyk,R, Wooden,H, Worley,K,
Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V,
Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von
Niederhausern,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O,
Weinstock,G, and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 178472)
Worley,K.C.
Direct Submission
Submitted (29-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 178472)
Rat Genome Sequencing Consortium.
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23196214.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: KADM
Center clone name: CH230-341P19
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 172947 bases at least Q40
Consensus quality: 174279 bases at least Q30
Consensus quality: 175219 bases at least Q20
Estimated insert size: 177582; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

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* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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  * 91458: contig of 91458 bp in length
  * 91459 91558: gap of unknown length
  * 91559 176692: contig of 85134 bp in length
  * 176693 176792: gap of unknown length
  * 176793 178472: contig of 1680 bp in length.
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      /db_xref="taxon:10116"
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              clone_end:T7"
              3845..4697
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                  clone_end:T7
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                    end_sequence:BZ205473"
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    Query Match 77.8%; Score 14; DB 2; Length 178472;
    Best Local Similarity 85.7%; Pred. No. 1e+02;
    Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGGNNNNN 18
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   DB 91566 TCCTGAGGNNNNN 91553

RESULT 81
BX927248/c 180506 bp DNA linear HTG 01-MAR-2004
DEFINITION
  BX927248
  Danio rerio clone CH211-140C22, WORKING DRAFT SEQUENCE, 9 unordered
  pieces.
ACCESSION
  BX927248.2 GI:41392805
KEYWORDS
  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
  Danio rerio (zebrafish)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Danio.
  1 (bases 1 to 180506)
REFERENCE
  Sime, S.
  Direct Submission
  Submitted (26-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries@sanger.ac.uk
  zfish-help@sanger.ac.uk
  On Jan 29, 2004 this sequence version replaced gi:4139613.
  ----- Genome Center
  Center: Wellcome Trust Sanger Institute
  Center code: SC
  Web site: http://www.sanger.ac.uk
  Contact: zfish-help@sanger.ac.uk
  ----- Project Information
  Center project name: zc140C22
  ----- Summary Statistics
  Assembly program: XGAP4; version 4.5
  Chemistry: Dye-terminator; 10% of reads
  Consensus quality: 178181 bases at least Q40
  Consensus quality: 178549 bases at least Q30
  Consensus quality: 178864 bases at least Q20
  Insert size: 179706; sum-of-contigs
  Insert size: 181854; 4.4% error; agarose-fp
  Quality coverage: 7.68x in Q20 bases; sum-of-contigs Quality
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coverage: 8.04x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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  * 21382: contig of 21382 bp in length
  * 21383 21482: gap of 100 bp
  * 21483 39908: contig of 18426 bp in length
  * 39909 40008: gap of 100 bp
  * 40009 71058: contig of 31050 bp in length
  * 71059 71159: gap of 100 bp
  * 71159 81805: contig of 10647 bp in length
  * 81806 81905: gap of 100 bp
  * 81906 89850: contig of 7945 bp in length
  * 89851 89951: gap of 100 bp
  * 89951 95146: contig of 5196 bp in length
  * 95147 95247: gap of 100 bp
  * 95247 167183: contig of 71937 bp in length
  * 167184 167283: gap of 100 bp
  * 167284 170213: contig of 2930 bp in length
  * 170214 170314: gap of 100 bp
  * 170314 180506: contig of 10193 bp in length.
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      /clone_1b="CHOR-211"
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          fragment_chain:1
          clone_end:SP6
          vector_side:left"
          21483..39908
            /note="assembly_fragment:00790
            fragment_chain:1"
            40009..71058
              misc_feature
                /note="assembly_fragment:01068
                fragment_chain:1"
                71159..81805
                  misc_feature
                    /note="assembly_fragment:00401
                    fragment_chain:1"
                    81906..89850
                      misc_feature
                        /note="assembly_fragment:00278
                        fragment_chain:1"
                        89951..95146
                          misc_feature
                            /note="assembly_fragment:00106
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                            95247..167183
                              misc_feature
                                /note="assembly_fragment:01493
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                                167284..170213
                                  misc_feature
                                    /note="assembly_fragment:00077
                                    fragment_chain:1"
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                                        /note="assembly_fragment:00160
                                        fragment_chain:1"
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    Query Match 77.8%; Score 14; DB 2; Length 180506;
    Best Local Similarity 85.7%; Pred. No. 1e+02;
    Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGGNNNNN 18
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   DB 170321 TCCTGAGGNNNNN 170308
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RESULT 82  
AC015622  
LOCUS  
DEFINITION  
Homo sapiens clone RP11-45J14, WORKING DRAFT SEQUENCE, 33 unordered  
pieces.  
AC015622  
AC015622.4 GI:8096821  
HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 184869) Nusbaum, C. and Lander, E.  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens, clone RP11-45J14  
Unpublished  
2 (bases 1 to 184869)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
Baldwin, J., Barna, N., Beckert, R., Boguslavsky, L., Boukhalter, B.,  
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
Cooke, P., Deatellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
Ferrera, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,  
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Headford, A., Horton, L.,  
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karst, A., Klein, J.,  
Lehoczky, J., Lien, C., Locke, K., MacDonald, P., Marquis, N.,  
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Teste, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 26, 2000 this sequence version replaced gi:5604528.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L1170  
Center clone name: 45-J\_14  
Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 147749 bases at least Q40  
Consensus quality: 168400 bases at least Q30  
Consensus quality: 176223 bases at least Q20  
Insert size: 152000; agarose-fp  
Insert size: 181669; sum-of-contigs  
Quality coverage: 4.6 in Q20 bases; agarose-fp  
Quality coverage: 3.8 in Q20 bases; sum-of-contigs  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 33 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1226: contig of 1226 bp in length  
\* 1227 1326: gap of 100 bp  
\* 1327 1360: contig of 1034 bp in length  
\* 2361 2460: gap of 100 bp  
\* 2461 3510: contig of 1050 bp in length  
\* 3511 3610: gap of 100 bp

3611 4882: contig of 1272 bp in length  
\* 4883 4982: gap of 100 bp  
\* 4983 6425: contig of 1443 bp in length  
\* 6426 6525: gap of 100 bp  
\* 6526 7693: contig of 1168 bp in length  
\* 7694 7793: gap of 100 bp  
\* 7794 8950: contig of 1157 bp in length  
\* 8951 9050: gap of 100 bp  
\* 9051 10082: contig of 1032 bp in length  
\* 10083 10182: gap of 100 bp  
\* 10183 11513: contig of 1331 bp in length  
\* 11514 11614: gap of 100 bp  
\* 11614 12762: contig of 1149 bp in length  
\* 12763 12862: gap of 100 bp  
\* 12863 14245: contig of 1383 bp in length  
\* 14246 14345: gap of 100 bp  
\* 14346 15528: contig of 1183 bp in length  
\* 15529 15628: gap of 100 bp  
\* 15629 16803: contig of 1175 bp in length  
\* 16804 16903: gap of 100 bp  
\* 16904 18547: contig of 1644 bp in length  
\* 18548 18647: gap of 100 bp  
\* 18648 19920: contig of 1273 bp in length  
\* 19921 20020: gap of 100 bp  
\* 20021 22262: contig of 2242 bp in length  
\* 22263 22362: gap of 100 bp  
\* 22363 24001: contig of 1639 bp in length  
\* 24002 24101: gap of 100 bp  
\* 24102 26655: contig of 2554 bp in length  
\* 26656 26755: gap of 100 bp  
\* 26756 28646: contig of 1891 bp in length  
\* 28647 28746: gap of 100 bp  
\* 28747 31056: contig of 2310 bp in length  
\* 31057 31156: gap of 100 bp  
\* 31157 33922: contig of 2766 bp in length  
\* 33923 34022: gap of 100 bp  
\* 34023 36450: contig of 2428 bp in length  
\* 36451 36550: gap of 100 bp  
\* 36551 40183: contig of 3633 bp in length  
\* 40184 40283: gap of 100 bp  
\* 40283 45282: contig of 4999 bp in length  
\* 45283 45382: gap of 100 bp  
\* 45383 50884: contig of 5502 bp in length  
\* 50885 50984: gap of 100 bp  
\* 50985 61265: contig of 10281 bp in length  
\* 61266 61365: gap of 100 bp  
\* 61366 71108: contig of 9743 bp in length  
\* 71109 71208: gap of 100 bp  
\* 71209 85877: contig of 14669 bp in length  
\* 85878 85977: gap of 100 bp  
\* 85978 97906: contig of 11929 bp in length  
\* 97907 98006: gap of 100 bp  
\* 98007 112916: contig of 14910 bp in length  
\* 112917 113016: gap of 100 bp  
\* 113017 129210: contig of 16194 bp in length  
\* 129211 129310: gap of 100 bp  
\* 129311 152603: contig of 23293 bp in length  
\* 152604 152703: gap of 100 bp  
\* 152704 184869: contig of 32166 bp in length.  
Location/Qualifiers  
1..184869  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="RP11-45J14"  
/clone\_lib="RP11-45J14 Human Male BAC"  
1..1226  
/note="assembly\_fragment"  
1327..2360  
/note="assembly\_fragment"  
2461..3510  
/note="assembly\_fragment"  
3611..4882

```

misc_feature      /note="assembly_fragment"
4983. .6425
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
6526. .7693
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
7794. .8950
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
9051. .10082
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
10183. .11513
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
11614. .12762
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
12863. .14245
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
14346. .15528
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
15629. .16803
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
16904. .18547
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
18648. .19920
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
20021. .22262
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
22363. .24001
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
24102. .26655
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
26756. .28646
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
28747. .31056
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
31157. .33922
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
34023. .36450
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
36551. .40183
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
40284. .45282
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
45383. .50884
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
50985. .61265
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
61366. .71108
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
71209. .85877
/note="assembly_fragment"
misc_feature      /note="assembly_fragment"
clone_end:T7
vector_side:left"
misc_feature      85978. .97906
/note="assembly_fragment"
misc_feature      98007. .112916
/note="assembly_fragment"
misc_feature      113017. .129210
/note="assembly_fragment"

Query Match      77.8%; Score 14; DB 2; Length 184869;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGAGNNNNNN 18
       :|||:|||||
Db      22255 TCCTGAGNNNNNN 22268

RESULT 83
BX927379      187478 bp      DNA      linear      HTG 05-FEB-2004
LOCUS      Danio rerio clone DKEX-111H12, *** SEQUENCING IN PROGRESS ***, 5
DEFINITION      unordered pieces.
ACCESSION      BX927379

```

```

VERSION      BX927379.3      GI:42414941
KEYWORDS      HTG; HTGS PHASE1.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE      1 (bases 1 to 187478)
AUTHORS      McIay,K.
TITLE      Direct Submission
JOURNAL      Submitted (04-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
fish-help@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk
On Feb 5, 2004 this sequence version replaced gi.42406562.
COMMENT      ----- Genome Center
Center: Wellcome Trust Sanger Institute
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----
Center project name: ZK111H12
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 186191 bases at least Q40
Consensus quality: 186506 bases at least Q30
Consensus quality: 186799 bases at least Q20
Insert size: 187078; sum-of-coverage
Insert size: 179723; 3.4% error; agarose-fp
Quality coverage: 8.73x in Q20 bases; sum-of-coverage
Quality coverage: 9.09x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 75787: contig of 75787 bp in length
* 75788 75887: gap of 100 bp
* 75888 82568: contig of 6681 bp in length
* 82568 82669: gap of 100 bp
* 82669 87993: contig of 5325 bp in length
* 87993 88094: gap of 100 bp
* 88094 130375: contig of 42282 bp in length
* 130375 130476: gap of 100 bp
* 130476 187478: contig of 57003 bp in length.
*
FEATURES
Location/Qualifiers
Source
1. 187478
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-111H12"
/clone_1lb="DanioKey"
1. 75787
/note="assembly_fragment:01538
fragment chain:1"
75888. 82568
/note="assembly_fragment:00004
fragment chain:1"
82669. 87993
/note="assembly_fragment:00091.0"
88094. 130375
/note="assembly_fragment:00180"
130476. 187478
/note="assembly_fragment:00791"

ORIGIN
Query Match      77.8%; Score 14; DB 2; Length 187478;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```





```

ORIGIN
Query Match      77.8%  Score 14;  DB 2;  Length 188931;
Best Local Similarity 85.7%:  Pred. No. 1e+02;
Matches 12;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      5  UCCUGAGAGNNNNNN 18
      :||:|||||
Db      66759  TCCTGAGAGNNNNN 66746

RESULT 85
CR356244      189756 bp  DNA      linear  HTG 29-MAR-2004
LOCUS
DEFINITION  Dario rerio clone DKEX-149J12, *** SEQUENCING IN PROGRESS ***, 8
unordered pieces.
ACCESSION  CR356244
VERSION    CR356244.4  GI:45824946
KEYWORDS   HTG; HTGS PHASE1.
SOURCE     Dario rerio (zebrafish)
ORGANISM   Dario rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
            1 (bases 1 to 189756)
REFERENCE  1  (bases 1 to 189756)
AUTHORS    McIay, K.
JOURNAL    Direct Submission
            Submitted (28-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
            On Mar 29, 2004 this sequence version replaced gi:45772257.
            ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: zfish-help@sanger.ac.uk
            ----- Project Information
            Center project name: zK149J12
            ----- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: Dye-terminator; 100% of reads
            Consensus quality: 186149 bases at least Q40
            Consensus quality: 186609 bases at least Q30
            Consensus quality: 187115 bases at least Q20
            Insert size: 189056; sum-of-contigs
            Insert size: 166597; 3.0% error; agarose-gel
            Quality coverage: 8.42x in Q20 bases; sum-of-contigs Quality
            coverage: 9.70x in Q20 bases; agarose-gel
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            *
            1
            3426: contig of 3426 bp in length
            3427      3526: gap of 100 bp
            3527      14421: contig of 10895 bp in length
            14422      14521: gap of 100 bp
            14522      36714: contig of 22193 bp in length
            36715      36814: gap of 100 bp
            36815      41106: contig of 4292 bp in length
            41107      41207: gap of 100 bp
            41207      50698: contig of 9492 bp in length
            50699      50798: gap of 100 bp
            50799      113926: contig of 63128 bp in length
            113927      114026: gap of 100 bp
            114027      121029: contig of 7003 bp in length
            121030      121130: gap of 100 bp
            121130      189756: contig of 68627 bp in length.
            Location/Qualifiers
FEATURES

```

```

source
1. .189756
/organism="Dario rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-149J12"
/clone_1fb="DanioKey"
1. .3426
/note="assembly fragment:00068
fragment_chain:1"
3527. .14421
/note="assembly fragment:00313
fragment_chain:1"
14522. .36714
/note="assembly fragment:00434
fragment_chain:1"
36815. .41106
/note="assembly fragment:00033
fragment_chain:1"
41207. .50698
/note="assembly fragment:00212
fragment_chain:1"
50799. .113926
/note="assembly fragment:00697
fragment_chain:1"
114027. .121029
/note="assembly fragment:00118"
121130. .189756
/note="assembly fragment:01588.0"

ORIGIN
Query Match      77.8%  Score 14;  DB 2;  Length 189756;
Best Local Similarity 85.7%:  Pred. No. 1e+02;
Matches 12;  Conservative 2;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      5  UCCUGAGAGNNNNNN 18
      :||:|||||
Db      113919  TCCTGAGAGNNNNN 113932

RESULT 86
CR293534      189787 bp  DNA      linear  HTG 01-MAR-2004
LOCUS
DEFINITION  Dario rerio clone CH211-13J1, *** SEQUENCING IN PROGRESS ***, 10
unordered pieces.
ACCESSION  CR293534
VERSION    CR293534.2  GI:44850216
KEYWORDS   HTG; HTGS PHASE1.
SOURCE     Dario rerio (zebrafish)
ORGANISM   Dario rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
            1 (bases 1 to 189787)
REFERENCE  1  (bases 1 to 189787)
AUTHORS    Sims, S.
JOURNAL    Direct Submission
            Submitted (26-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
            On Mar 1, 2004 this sequence version replaced gi:42821021.
            ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: zfish-help@sanger.ac.uk
            ----- Project Information
            Center project name: zC13J1
            ----- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: Dye-terminator; 100% of reads
            Consensus quality: 187978 bases at least Q40
            Consensus quality: 188341 bases at least Q30
            Consensus quality: 188615 bases at least Q20
            Insert size: 188887; sum-of-contigs

```

Query Match	77.8%;	Score 14;	DB 2;	Length 189787;
Best Local Similarity	85.7%;	Pred. No. 1e+02;		

```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
-----
Center project name: H_NH0520F07
-----
Project Information -----
-----
Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: PHRAP; version 0.990319
Consensus quality: 178105 bases at least Q40
Consensus quality: 182135 bases at least Q30
Consensus quality: 184620 bases at least Q20
Insert size: 182000; agarose-fp
Quality coverage: 189102; sum-of-coverage
Quality coverage: 4.18 in Q20 bases; agarose-fp
Quality coverage: 3.94 in Q20 bases; sum-of-coverage
-----
** NOTE: This is a 'working draft' sequence. It currently
** consists of 26 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
1
1798 1797: contig of 1797 bp in length
1897 1897: gap of unknown length
1898 3447: contig of 1550 bp in length
3448 3547: gap of unknown length
3548 5261: contig of 1714 bp in length
5262 5361: gap of unknown length
5362 7030: contig of 1669 bp in length
7031 7130: gap of unknown length
7131 9374: contig of 2244 bp in length
9375 9474: gap of unknown length
9475 11907: contig of 2433 bp in length
11908 12007: gap of unknown length
12008 14972: contig of 2965 bp in length
14973 15072: gap of unknown length

```

```
* 15073 17812: contig of 2740 bp in length
* 17813 17912: gap of unknown length
* 17913 20959: contig of 3047 bp in length
* 20960 21059: gap of unknown length
* 21060 26055: contig of 4996 bp in length
* 26056 26155: gap of unknown length
* 26156 30231: contig of 4076 bp in length
* 30232 30331: gap of unknown length
* 30332 34743: contig of 4412 bp in length
* 34744 34843: gap of unknown length
* 34844 39428: contig of 4585 bp in length
* 39429 39528: gap of unknown length
* 39529 45798: contig of 6269 bp in length
* 45799 45898: gap of unknown length
* 45899 51353: contig of 5456 bp in length
* 51354 51453: gap of unknown length
* 51454 57595: contig of 6142 bp in length
* 57596 57695: gap of unknown length
* 57696 64225: contig of 6530 bp in length
* 64226 64325: gap of unknown length
* 64326 71971: contig of 7646 bp in length
* 71972 72071: gap of unknown length
* 72072 80420: contig of 8349 bp in length
* 80421 80520: gap of unknown length
* 80521 88981: contig of 8461 bp in length
* 88982 89081: gap of unknown length
* 89082 96199: contig of 7118 bp in length
* 96200 96299: gap of unknown length
* 96300 108298: contig of 11999 bp in length
* 108299 108398: gap of unknown length
* 108399 121805: contig of 13407 bp in length
* 121806 121905: gap of unknown length
* 121906 138416: contig of 16511 bp in length
* 138417 138516: gap of unknown length
* 138517 163956: contig of 25440 bp in length
* 163957 164057: gap of unknown length
* 164057 191602: contig of 27546 bp in length.
```

## FEATURES

## SOURCE

```
1. .191602
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/clone="RP11-52087"
1. .11797
/note="assembly_name:Contig10"
1898. .3447
/note="assembly_name:Contig11"
3548. .5261
/note="assembly_name:Contig12"
5362. .7030
/note="assembly_name:Contig13"
7131. .9374
/note="assembly_name:Contig14"
9475. .11907
/note="assembly_name:Contig15"
12008. .14972
/note="assembly_name:Contig16"
15073. .17812
/note="assembly_name:Contig17"
17913. .20959
/note="assembly_name:Contig18"
21060. .26055
/note="assembly_name:Contig19"
26156. .30231
/note="assembly_name:Contig20"
30332. .34743
/note="assembly_name:Contig21"
34844. .39428
/note="assembly_name:Contig22
clone end:T7
vector_side:right"
39529. .45797
misc_feature
```

## ORIGIN

Query Match

Best Local Similarity 85.7%; Pred. No. 1e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGAGNNNNNN 18

Db 5254 TCCGCGAGNNNNN 5267

## RESULT 88

CR524482

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```
/note="assembly_name:Contig23"
45898. .51353
/note="assembly_name:Contig24"
51454. .57595
/note="assembly_name:Contig25"
57696. .64225
/note="assembly_name:Contig26
clone_end:SP6
vector_side:left"
64326. .71971
/note="assembly_name:Contig27"
72072. .80420
/note="assembly_name:Contig28"
80521. .88981
/note="assembly_name:Contig29"
89082. .96199
/note="assembly_name:Contig30"
96300. .108298
/note="assembly_name:Contig31"
108399. .121805
/note="assembly_name:Contig32"
121906. .138416
/note="assembly_name:Contig33"
138517. .163956
/note="assembly_name:Contig34"
164057. .191602
/note="assembly_name:Contig35"
```

CR524482 194513 bp DNA linear HTG 19-AUG-2004

Danio rerio clone DKEX-109F24, WORKING DRAFT SEQUENCE, 15 unordered pieces.

CR524482 GI:51470689

HTG; HTGS PHASIS; HTGS DRAFT; HTGS\_FULFILLTOP.

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 194513)

Burton,J.

Direct Submission

Submitted (16-AUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 20, 2004 this sequence version replaced gi:51242031.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: zfish-help@sanger.ac.uk

----- Project Information

Center project name: ZK109F24

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 188805 bases at least Q40

Consensus quality: 189699 bases at least Q30

Consensus quality: 190483 bases at least Q20

Insert size: 19313; sum-of-contigs

Insert size: 203739; 6.5% error; agarose-gel

Quality coverage: 6.93x in Q20 bases; sum-of-contigs Quality coverage: 6.71x in Q20 bases; agarose-tp

\*\*\*\*\*  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 15 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

```
1 38721: contig of 38721 bp in length
* 38722 38821: gap of 100 bp
* 38822 59895: contig of 21074 bp in length
* 59895 59995: gap of 100 bp
* 59995 65918: contig of 5923 bp in length
* 65918 66019: gap of 100 bp
* 66019 74644: contig of 8626 bp in length
* 74644 74744: gap of 100 bp
* 74744 89717: contig of 14973 bp in length
* 89717 89817: gap of 100 bp
* 89817 98513: contig of 8696 bp in length
* 98513 98614: gap of 100 bp
* 98614 100848: contig of 2235 bp in length
* 100848 100949: gap of 100 bp
* 100949 108230: contig of 7282 bp in length
* 108230 108330: gap of 100 bp
* 108330 120926: contig of 12596 bp in length
* 120926 121027: gap of 100 bp
* 121027 129164: contig of 8138 bp in length
* 129164 129264: gap of 100 bp
* 129264 162823: contig of 33558 bp in length
* 162823 162922: gap of 100 bp
* 162922 170559: contig of 7636 bp in length
* 170559 188732: contig of 18074 bp in length
* 188732 188832: gap of 100 bp
* 188832 191673: contig of 2841 bp in length
* 191673 191774: gap of 100 bp
* 191774 194513: contig of 2740 bp in length.
```

## FEATURES

## source

```
1. 194513
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKF1-109F24"
/clone_lib="DantolKey"
1. 38721
/note="assembly fragment:01832
fragment chain:1"
38822. 59895
/note="assembly fragment:01070
fragment chain:1"
59996. 65918
/note="assembly fragment:00149
fragment chain:1"
66019. 74644
/note="assembly fragment:00417
fragment chain:1"
74745. 89717
/note="assembly fragment:00739
fragment chain:1"
89818. 98513
/note="assembly fragment:00331
fragment chain:1"
98614. 100848
/note="assembly fragment:00067
fragment chain:2"
100949. 108230
/note="assembly fragment:00185
fragment chain:2"
108331. 120926
/note="assembly fragment:00618
```

```
misc_feature      fragment chain:2"
121027. 129164
/note="assembly fragment:00504
fragment chain:2"
129265. 162822
/note="assembly fragment:01355
fragment chain:2"
162923. 170558
/note="assembly fragment:00253
fragment chain:3"
170659. 188732
/note="assembly fragment:00889
fragment chain:3"
188833. 191673
/note="assembly fragment:00089"
191774. 194513
/note="assembly fragment:00116.0"
```

## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 194513;  
Best Local Similarity 85.7%; Pred. No. 16+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy 5 UCCUGAGNNNNNN 18
Db 191666 TCCTGGAGNNNNNN 191679
```

## RESULT 89

AC150020/c  
LOCUS  
DEFINITION Papio anubis clone RP41-380L14, WORKING DRAFT SEQUENCE, 11 ordered  
pieces.

AC150020.2 GI:51241824  
VERSION HTG; HTGS PHASE2; HTGS DRAFT.  
KEYWORDS Papio anubis (olive baboon)  
SOURCE Papio anubis  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopitheciinae; Papio.

## REFERENCE

AUTHORS Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,  
Boutfard, G.G., Brinkley, C., Brooks, S., Chu, S., Coleman, B.,  
Coleman, H., Dakl, N., Engle, J., Guan, X., Gupta, J., Haghighi, P.,  
Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Jones, C.,  
Karlsen, E., Kim, H., Kwong, P., Latic, P., Larson, S., Lee-Lin, S.-O.,  
Legaspi, R., Madden, M., Maduro, Q.L., Maduro, Y.B., Margulies, E.H.,  
Maselli, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C.,  
Park, M., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Dugue, N.,  
Schandler, K., Schneider, M.G., Shah, K., Sison, C., Stancitop, S.,  
Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D.,  
Young, A. and Green, E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2. (bases 1 to 202456)  
Green, E.D.  
Direct Submission  
Submitted (30-JUN-2004) NIH Intramural Sequencing Center, 8717  
Grovermont Circle, Gaithersburg, MD 20877, USA  
3 (bases 1 to 202456)  
Green, E.D.  
Direct Submission  
Submitted (14-AUG-2004) NIH Intramural Sequencing Center, 8717  
Grovermont Circle, Gaithersburg, MD 20877, USA  
On Aug 14, 2004 this sequence version replaced gi:49457902.  
Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc.zoo@hgrl.nih.gov  
Project Information  
Center project name: hot

```
/note="assembly_fragment"
```

```

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----
Project Information
Center project name: zkp85E10
-----
Summary Statistics
Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 208982 bases at least Q40
Consensus quality: 209266 bases at least Q30
Consensus quality: 209525 bases at least Q20
Insert size: 209810; sum-of-contigs
Insert size: 208739; 3.5% error; agarose-fp
Quality coverage: 8.69% in Q20 bases; sum-of-contigs
Quality coverage: 8.73% in Q20 bases; agarose-fp

```

```

* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 37505: contig of 37505 bp in length
* 37506: gap of 100 bp
* 37606: contig of 18649 bp in length
* 56354: gap of 100 bp
* 56355: contig of 35547 bp in length
* 91901: gap of 100 bp
* 92001: contig of 26216 bp in length
* 118217: gap of 100 bp
* 118218: contig of 42865 bp in length
* 16182: gap of 100 bp
* 16183: contig of 49028 bp in length.
* 161283
*
* Location/Qualifiers
* 1..210310
*   /organism="Danio rerio"
*   /mol_type="genomic DNA"
*   /db_xref="taxon:7955"
*   /clone_lib="DKEXP-85B10"
*   /clone_id="DanioKeyPilot"
*
* misc_feature
* 1..37505
*   /note="assembly_fragment:01090"
*   fragment_chain:1
* 37606..56254
*   /note="assembly_fragment:00006"
*   fragment_chain:1
* 56355..91901
*   /note="assembly_fragment:00639"
*   fragment_chain:1
* 92002..118217
*   /note="assembly_fragment:00271"
*   118318..161182
*   /note="assembly_fragment:01599"
*   161283..210310
*   /note="assembly_fragment:02149.0"
*
* ORIGIN
* Query Match 77.8%; Score 14; DB 2; Length 210310;
* Best Local Similarity 85.7%; Pred. No. 99;
* Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
*
* QY 5 UCCUGAGNNNNNN 18
* :||:|||||||
* Db 37498 TCCTGAGNNNNNN 37511
*
* RESULT 91
* CR376743/c 210481 bp DNA linear HTG 21-MAR-2004
* LOCUS
* DEFINITION
*   Danio rerio clone CH211-215N20, *** SEQUENCING IN PROGRESS ***, 14
*   unordered pieces.
* ACCESSION
*   CR376743
* CR376743.2 GI:45598670
* VERSION
*   HTG; HTGS PHASE1.
* KEYWORDS
*   Danio rerio (zebrafish)
* SOURCE
*   Danio rerio
* ORGANISM
*   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
*   Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
*   Cypriniformes; Cyprinidae; Danio.
*   1 (bases 1 to 210481)
*   Sims, S.
*   Direct Submission
*   Submitted (20-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
*   Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
*   zfish-help@sanger.ac.uk Clone requests: clonesrequest@sanger.ac.uk
*   On Mar 21, 2004 this sequence version replaced gi:45598211.
*   ----- Genome Center
*   Center: Wellcome Trust Sanger Institute

```

```

Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: ZC215N20
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 204148 bases at least Q40
Consensus quality: 205280 bases at least Q30
Consensus quality: 206024 bases at least Q20
Insert size: 209181; sum-of-contigs
Insert size: 187345; 2.5% error; agarose-fp
Quality coverage: 5.75x in Q20 bases; sum-of-contigs Quality
coverage: 6.45x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 5312: contig of 5312 bp in length
* 5313: gap of 100 bp
* 5412: gap of 100 bp
* 5413: contig of 4983 bp in length
* 10396: gap of 100 bp
* 10495: gap of 100 bp
* 16368: contig of 5873 bp in length
* 16369: gap of 100 bp
* 16468: gap of 100 bp
* 58037: contig of 4169 bp in length
* 58038: gap of 100 bp
* 58138: contig of 14663 bp in length
* 73001: gap of 100 bp
* 73100: gap of 100 bp
* 92512: contig of 19412 bp in length
* 92612: gap of 100 bp
* 92613: contig of 2381 bp in length
* 116193: contig of 100 bp
* 116293: gap of 100 bp
* 116294: contig of 14669 bp in length
* 130963: gap of 100 bp
* 131063: contig of 40897 bp in length
* 171960: gap of 100 bp
* 172059: gap of 100 bp
* 172060: contig of 9000 bp in length
* 181060: gap of 100 bp
* 181159: gap of 100 bp
* 181160: contig of 3058 bp in length
* 184218: gap of 100 bp
* 184317: gap of 100 bp
* 184318: contig of 4758 bp in length
* 189076: gap of 100 bp
* 189175: gap of 100 bp
* 189176: contig of 7734 bp in length
* 196909: gap of 100 bp
* 196910: gap of 100 bp
* 197010: contig of 13472 bp in length.
*
* Location/Qualifiers
* 1..210481
*   /organism="Danio rerio"
*   /mol_type="genomic DNA"
*   /db_xref="taxon:7955"
*   /clone="CH211-215N20"
*   /clone_lib="CHORI-211"
*   1..5312
*   /note="assembly_fragment:00187"
*   clone_end:SP6
*   vector_side:left"
* 5413..10395
*   /note="assembly_fragment:00136"
*   fragment_chain:1
* 10496..16368
*   /note="assembly_fragment:00092"
*   fragment_chain:1
* 16469..58037
*   /note="assembly_fragment:01222"
*   fragment_chain:1
* 58138..73000
*   /note="assembly_fragment:00496"

```

```

misc_feature      fragment chain:1"
73101..52512
/note="assembly_fragment:00766
fragment chain:1"
misc_feature      92613..116193
/note="assembly_fragment:00962
fragment chain:1"
misc_feature      116294..1130962
/note="assembly_fragment:00628
fragment chain:1"
misc_feature      131063..171959
/note="assembly_fragment:01601
fragment chain:1"
misc_feature      172060..181059
/note="assembly_fragment:00245
fragment chain:1"
misc_feature      181160..184217
/note="assembly_fragment:00029
fragment chain:1"
misc_feature      184318..189075
/note="assembly_fragment:00052
fragment chain:1"
misc_feature      189176..196909
/note="assembly_fragment:00309
fragment chain:1"
misc_feature      197010..210481
/note="assembly_fragment:00376
fragment chain:1"

ORIGIN

Query Match      77.8% Score 14; DB 2; Length 210481;
Best Local Similarity 85.7% Pred. NO. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      5 UCCUGAGAGNNNNNN 18
Db      58145 TCCGCGAGNNNNNN 58132

RESULT 92
AC122949
LOCUS      AC122949
DEFINITION Rattus norvegicus clone CH230-290B6, *** SEQUENCING IN PROGRESS
ACCESSION AC122949
VERSION    AC122949.5 GI:25089514
KEYWORDS   HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 213181)
AUTHORS    Muzny D, Marie E, Metzker M, Lee S, Abramzon S, Adams C, Alder J,
            Allen C, Allen H, Albrooke S, Amin A, Angiano D,
            Anyalbech V, Aoyagi A, Ayodeji M, Baca E, Baden H,
            Baldwin D, Bandaranaike D, Barber M, Barnstead M, Benahmed F,
            Biewald K, Blair J, Blankenburg K, Blyth P, Brown M,
            Bryant N, Buhay C, Burch P, Burrell K, Calderon E,
            Cardenas V, Carter K, Cavazos I, Ceasar H, Center A,
            Chacko J, Chavez D, Chen G, Chen R, Chen Y, Chen Z, Chu J,
            Cleveland C, Cockrell R, Cox C, Coyle M, Cree A, D'Souza J,
            Devilla M, Davis C, Davy-Carroll L, De Anda C, Dederich D,
            Delgado O, Denison S, Deramo C, Ding Y, Dinh H, Divya K,
            Draper H, Dugan-Rocha S, Dunn A, Durbin K, Duval B, Eaves K,
            Egan A, Escotto M, Eugene C, Evans C, A, Falls T, Fan G,
            Fernandez S, Finley M, Flagg N, Forbes L, Foster M, Foster P,
            Fraser C, Gabisi A, Ganta R, Garcia A, Garner J, Garza M,
            Gebegeorgis E, Geer K, Gill R, Grady M, Guerra W, Guevara W,
            Gunaratne P, Haaland W, Hamli C, Hamilton C, Hamilton K,
            Harvey Y, Havlak P, Hawes A, Henderson N, Hernandez J,
            Hernandez R, Hines S, Hladun S, L, Hodgson A, Hogues M,
            Hollins B, Howells S, Hulik S, Hume J, Idlebird D, Jackson A,

```

```

TITLE      JOURNAL
AUTHORS    Karpachy S, Kelly S, Kelly S, Khan Z, King L, Kovar C,
            Kowitz C, Kraft C, L, Lebow H, Levan J, Lewis L, Li Z, Liu J,
            Liu J, Liu W, Liu Y, London P, Longacre S, Lopez J,
            Lorenshuwa L, Louissege H, Lozano R, J, Lu X, Ma J,
            Maheshwari M, Mahindratne M, Mahmood M, Malloy K, Mangum A,
            Mangum B, Mapa P, Martin K, Martin K, Martinez E,
            Mawhney S, McLeod M, P, McNeill T, Z, Meenen E,
            Milosavljevic A, Miner G, Ming E, Montemayor J, Moore S,
            Morgan M, Morris K, Morris S, Munidasa M, Murphy M, Naik L,
            Nankervis C, Neal D, Newton N, Nguyen N, Norris S,
            Paackelemech O, Okunou G, Olarnpooagoon A, Pal S, Parks K,
            Paaternak S, Paul H, Perez A, Perez L, Pfannkuch C,
            Plopper F, Poindecker A, Popovic D, Primm E, Pu L, L,
            Piazzi M, Quiroz J, Rachlin E, Reeves K, Regier M, A, Reigh R,
            Reilly B, Reilly M, Ren Y, Reuter M, Richard S, Riggs F,
            Rives C, Rodkey T, Rojas A, Rose M, Rose R, Ruiz S, J,
            Sanders M, Savery G, Scherer S, Scott G, Shatsman S, Shen H,
            Shetty J, Shvartsbeyn A, Sison I, Sitter C, D, Smajic D,
            Sneed A, Sodergren E, Song X, Z, Sorelle R, Sosa J,
            Steimle M, Strong R, Sutton A, Svaltek A, Tabor P, Taylor C,
            Taylor T, Thomas N, Thomas S, Tingey A, Trejos Z, Usmani K,
            Valas R, Vera V, Villaseana D, Waldron L, Walker B, Wang J,
            Wang O, Wang S, Warren J, Warren R, Wei X, White F,
            Williams G, Willson R, Wleczek R, Wooden H, Worley K,
            Wright D, Wright R, Wu J, Yakub S, Yen J, Yoon L, Yoon V,
            Yu F, Zhang J, Zhou J, Zhou X, Zhao S, Dunn D, von
            Niederhausern A, Weis R, Smith D, R, Holt R, A, Smith H, O,
            Weinstock G, and Gibbs R, A.

REFERENCE   2 (bases 1 to 213181)
AUTHORS    Worley K, C.
TITLE      Direct Submission
JOURNAL    Submitted (26-MAY-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 213181)
            Rat Genome Sequencing Consortium.
            Direct Submission
            Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On Nov 19, 2002 this sequence version replaced gi:22907669.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/atlantis/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.

REFERENCE   3 (bases 1 to 213181)
AUTHORS    Center: Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            Project Information
            Center project name: GW2W
            Center clone name: CH230-290B6
            Summary Statistics
            Assembly program: Phrap; version 0.990329
            Consensus quality: 187583 bases at least Q40
            Consensus quality: 189673 bases at least Q30
            Consensus quality: 191228 bases at least Q20
            Estimated insert size: 184726; sum-of-contigs estimation
            Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

```





TITLE Direct Submission  
JOURNAL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## COMMENT

On May 10, 2003 this sequence version replaced gi:23269275. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

## ----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GFTL

Center clone name: CH230-137022

## ----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 204318 bases at least Q40

Consensus quality: 205639 bases at least Q30

Consensus quality: 206762 bases at least Q20

Estimated insert size: 213544; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 89642: contig of 89642 bp in length  
\* 89643 89742: gap of unknown length  
\* 89743 107775: contig of 18033 bp in length  
\* 107776 107875: gap of unknown length  
\* 107876 120148: contig of 12273 bp in length  
\* 120149 120248: gap of unknown length  
\* 120249 214156: contig of 93908 bp in length  
\* 214157 214256: gap of unknown length  
\* 214257 215479: contig of 1223 bp in length.

## Location/Qualifiers

1. 215479  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-137022"  
1. 1132  
/note="wge\_contig"

## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 215479;

Best Local Similarity 85.7%; Pred. No. 99;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGANNNNN 18

Db 126882 TCCTGAGANNNNN 126866

RESULT 94  
CR376804/c

## LOCUS

CR376804 215604 bp DNA linear HTG 27-MAR-2004

DEFINITION Danio rerio clone DKEX-42P14, \*\*\* SEQUENCING IN PROGRESS \*\*\*; 18.

UNORDERED PIECES.

Accession CR376804

VERSION CR376804.2 GI:45772275

KEYWORDS HTG; HTGS PHASE1.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 215604)

McLay, K.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission  
Submitted (26-MAR-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: [zfish-help@sanger.ac.uk](mailto:zfish-help@sanger.ac.uk) Clone requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk) On Mar 27, 2004 this sequence version replaced gi:45598604.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: [zfish-help@sanger.ac.uk](mailto:zfish-help@sanger.ac.uk)

Project Information

Center project name: ZK42P14

## ----- Summary Statistics

Assembly program: XGAP; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 210686 bases at least Q40

Consensus quality: 211687 bases at least Q30

Consensus quality: 212503 bases at least Q20

Insert size: 213904; sum-of-contigs

Insert size: 207062; 4.5% error; agarose-fp

Quality coverage: 6.90x in Q20 bases; sum-of-contigs Quality

coverage: 7.33x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 2616: contig of 2616 bp in length  
\* 2617 2716: gap of 100 bp  
\* 2717 17492: contig of 14776 bp in length  
\* 17493 17592: gap of 100 bp  
\* 17593 47621: contig of 30029 bp in length  
\* 47622 47721: gap of 100 bp  
\* 47722 54207: contig of 6486 bp in length  
\* 54208 54307: gap of 100 bp  
\* 54308 60090: contig of 5783 bp in length  
\* 60091 60190: gap of 100 bp  
\* 60191 64267: contig of 4077 bp in length  
\* 64268 64367: gap of 100 bp  
\* 64368 80144: contig of 15777 bp in length  
\* 80145 80244: gap of 100 bp  
\* 80245 93958: contig of 13714 bp in length  
\* 93959 94058: gap of 100 bp  
\* 94059 121790: contig of 27732 bp in length  
\* 121791 121890: gap of 100 bp  
\* 121891 144599: contig of 22709 bp in length  
\* 144600 144699: gap of 100 bp  
\* 144700 151660: contig of 6961 bp in length  
\* 151661 151760: gap of 100 bp  
\* 151761 163632: contig of 11872 bp in length  
\* 163633 163732: gap of 100 bp  
\* 163733 177690: contig of 13958 bp in length  
\* 177691 177791: gap of 100 bp  
\* 177792 183034: contig of 5244 bp in length  
\* 183035 183134: gap of 100 bp  
\* 183135 187729: contig of 4595 bp in length



```
misc_feature 1..40662
/note="assembly_fragment:01484
fragment_chain:1"
misc_feature 40763..70874
/note="assembly_fragment:01075
fragment_chain:1"
misc_feature 70975..75647
/note="assembly_fragment:00094
fragment_chain:1"
misc_feature 75748..80091
/note="assembly_fragment:00038
fragment_chain:1"
misc_feature 80192..94544
/note="assembly_fragment:00458
fragment_chain:1"
misc_feature 94645..163121
/note="assembly_fragment:01993
fragment_chain:1"
misc_feature 163322..174523
/note="assembly_fragment:00157
fragment_chain:1"
misc_feature 174624..204483
/note="assembly_fragment:00687
fragment_chain:1"
misc_feature 204584..216013
/note="assembly_fragment:00285.0"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 216013;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNNN 18
Db 94537 TCCTGAGANNNNN 94550

RESULT 96
BX901905/c 217309 bp DNA linear HTG 04-JAN-2004
LOCUS Danio rerio clone CH211-208N20, ** SEQUENCING IN PROGRESS ***, 14
DEFINITION unorderd piecec.
ACCESSION BX901905
VERSION BX901905.1 GI:40556537
KEYWORDS HTG; HTGS PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 217309)
Sim8.S.
Direct Submission
Submitted (03-JAN-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zc208N20
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 213096 bases at least Q40
Consensus quality: 213787 bases at least Q40
Consensus quality: 214425 bases at least Q20
Insert size: 216009; sum-of-contigs
Insert size: 210494; 5.9% error; agarose-fp
Quality coverage: 8.71x in Q20 bases; sum-of-contigs Quality
coverage: 9.06x in Q20 bases; agarose-fp
```

```
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
* 9698: contig of 9698 bp in length
* 9699: gap of 100 bp
* 9799: contig of 6750 bp in length
* 16548: gap of 100 bp
* 16649: contig of 5309 bp in length
* 21958: gap of 100 bp
* 22058: contig of 22103 bp in length
* 44160: gap of 100 bp
* 44261: contig of 7879 bp in length
* 52140: gap of 100 bp
* 52240: contig of 4918 bp in length
* 57158: gap of 100 bp
* 57258: contig of 19348 bp in length
* 57258: gap of 100 bp
* 76605: contig of 8958 bp in length
* 76706: gap of 100 bp
* 85663: contig of 58923 bp in length
* 85764: gap of 100 bp
* 144687: contig of 5468 bp in length
* 144787: gap of 100 bp
* 150254: contig of 21537 bp in length
* 150355: gap of 100 bp
* 171892: contig of 7461 bp in length
* 171992: gap of 100 bp
* 179453: gap of 100 bp
* 179552: contig of 27543 bp in length
* 207096: gap of 100 bp
* 207196: contig of 10114 bp in length.
* Location/Qualifiers
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/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-208N20"
/clone_1bp="CHOR1-211"
1..9638
/note="assembly_fragment:00393
fragment_chain:1
clone_end:T7
vector_side:left"
9799..16548
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fragment_chain:1"
16649..21957
/note="assembly_fragment:00110
fragment_chain:1"
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44261..52139
/note="assembly_fragment:00249
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52240..57157
/note="assembly_fragment:00072.0"
57258..76605
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76706..85663
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144787..150254
/note="assembly_fragment:00194
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misc_feature      150355..171891      /note="assembly_fragment:01196
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misc_feature      171992..179452      /note="assembly_fragment:00318
                                fragment_chain:2"
misc_feature      179553..207095      /note="assembly_fragment:01531
                                fragment_chain:2"
misc_feature      207196..217309      /note="assembly_fragment:00504
                                fragment_chain:2
                                clone_end:SP6
                                vector_side:right"

ORIGIN
Query Match      77.8%; Score 14; DB 2; Length 217309;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGGAGNNNNNN 18
        :||:|||||||
Db      171999 TCCTGGAGNNNNNN 171986

RESULT 97
AC106115/c      222632 bp      DNA      linear      HTG 10-MAY-2003
LOCUS      Rattus norvegicus clone CH230-137L21, *** SEQUENCING IN PROGRESS
DEFINITION      *** 3 unordered pieces.
ACCESSION      AC106115
VERSION      AC106115.6 GI:30521579
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus
ORGANISM      Rattus norvegicus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
        Rattus.
REFERENCE      1 (bases 1 to 222632)
AUTHORS      Muzny,D,Marie, Metzker,M, Lee, Abramson,S, Adams,C, Alder,J,
        Allen,C, Allen,H, Alsbrooks,S, Amin,A, Anguiano,D,
        Anyalobechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
        Baldwin,D, Bandaruaike,D, Barber,M, Barnstead,M, Benahmed,F,
        Biswal,K, Blair,J, Blankenburg,K, Blych,P, Brown,M,
        Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
        Cardenas,V, Carter,K, Cavazos,I, Ceasar,H, Center,A,
        Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
        Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
        Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
        Delgado,O, Denson,S, Deramo,C, Ding,Y, Dinh,H, Diya,K,
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        Egan,A, Escoto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
        Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
        Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
        Gebregeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W,
        Gunaratne,P, Haaland,W, Hamil,C, Hamilton,C, Hamilton,K,
        Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J,
        Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogue,M,
        Hollins,B, Howells,S, Huily,S, Hume,J, Idlebird,D, Jackson,A,
        Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A,
        Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C,
        Kowitz,C, Kraft,C,L, Lebow,H, Levran,J, Lewis,L, Li,Z, Liu,J,
        Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
        Lorensuwa,L, Loulsegad,H, Lozano,R,J, Lu,X, Ma,J,
        Maheshwari,M, Mahndarine,M, Mahmoud,M, Malloy,K, Mangum,A,
        Mangum,B, Mapua,P, Martin,K, Martin,R, Martinez,E,
        Mawhney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
        Migaavijevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S,
        Morgan,M, Morris,K, Morris,S, Munidasa,M, Murphy,M, Nair,L,
        Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S, Nair,L,
        Nwackelmen,O, Okwuonu,G, Olarnpunsagoon,A, Pal,S, Parks,K,
        Pasternak,S, Paul,H, Perez,A, Perez,L, Pfankoch,C,

```

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TITLE      JOURNAL
REFERENCE      Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
AUTHORS      of Molecular and Human Genetics, Baylor College of Medicine, One
        Baylor Plaza, Houston, TX 77030, USA
        3 (bases 1 to 222632)
REFERENCE      Rat Genome Sequencing Consortium.
AUTHORS      Direct Submission
        Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
        of Molecular and Human Genetics, Baylor College of Medicine, One
        Baylor Plaza, Houston, TX 77030, USA
        On May 10, 2003 this sequence version replaced gi:24953991.
        The sequence in this assembly is a combination of BAC based reads
        and whole genome shotgun sequencing reads assembled using Atlas
        (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
        in the feature table below represents a scaffold in the Atlas
        assembly (a 'contig-scaffold'). Within each contig-scaffold,
        individual sequence contigs are ordered and oriented, and separated
        by sized gaps filled with Ns to the estimated size. The sequence
        may extend beyond the ends of the clone and there may be sequence
        contigs within a contig-scaffold that consist entirely of whole
        genome shotgun sequence reads. Both end sequences and whole genome
        shotgun sequence only contigs will be indicated in the feature
        table.
COMMENT

```

```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHKJ
Center clone name: CH230-137L21
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 182183 bases at least Q40
Consensus quality: 186060 bases at least Q30
Consensus quality: 189005 bases at least Q20
Estimated insert size: 191530; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_diff_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 202667: contig of 202667 bp in length
* 202668 202767: gap of unknown length
* 202768 221218: contig of 18451 bp in length
* 221219 221318: gap of unknown length

```

```
FEATURES      * 221319 222632: contig of 1314 bp in length.
SOURCE
  .222632
  /organism="Rattus norvegicus"
  /mol_type="genomic DNA"
  /db_xref="taxon:10116"
  /clone="CH230-137L21"
  misc_feature 4877..7300
    /note="wgs_contig"
  misc_feature 48572..50625
    /note="wgs_contig"
  misc_feature 152768..154725
    /note="wgs_contig"
  misc_feature 155213..156643
    /note="wgs_contig"
ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 222632;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 5 UCCUGAGAGNNNNN 18
Db 72066 TCCTGAGAGNNNNN 72053

RESULT 98
CR382363/c 222961 bp DNA linear HTG 03-APR-2004
DEFINITION Danio rerio clone DKEX-23p11, *** SEQUENCING IN PROGRESS ***, 22
unordered pieces.
ACCESSION CR382363.2 GI:46194580
VERSION HTG; HTGS_PHASE1.
KEYWORDS Danio rerio (zebrafish)
SOURCE Danio rerio
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 222961)
REFERENCE 1
AUTHORS McIlroy, K.
JOURNAL Direct Submission
Submitted (01-APR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Apr 3, 2004 this sequence version replaced gi:46019166.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zK23p11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 21673 bases at least Q40
Consensus quality: 217636 bases at least Q30
Consensus quality: 218438 bases at least Q20
Insert size: 220861; sum-of-contigs
Insert size: 207717; 1.0% error; agarose-fp
Quality coverage: 6.70x in Q20 bases; sum-of-contigs Quality
coverage: 7.25x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 5743: contig of 5743 bp in length
```

```
FEATURES
SOURCE
  .222961
  /organism="Danio rerio"
  /mol_type="genomic DNA"
  /db_xref="taxon:7955"
  /clone="DKEX-23p11"
  /clone_1fb="DantioKey"
  1..5743
  /note="assembly_fragment:00234
  fragment_chain:1"
  misc_feature 5844..8760
    /note="assembly_fragment:00065
    fragment_chain:1"
  misc_feature 8861..38667
    /note="assembly_fragment:01842
    fragment_chain:1"
  misc_feature 38768..46216
    /note="assembly_fragment:00330
    fragment_chain:1"
  misc_feature 46317..49904
    /note="assembly_fragment:00196
    fragment_chain:1"
  misc_feature 50005..80575
    /note="assembly_fragment:02173
    fragment_chain:1"
  misc_feature 80676..83226
    /note="assembly_fragment:00047
    fragment_chain:1"
  misc_feature 83327..101361
    /note="assembly_fragment:01036
    fragment_chain:1"
  5744 5843: gap of 100 bp
  * 5844 8760: contig of 2917 bp in length
  * 8761 8860: gap of 100 bp
  * 8861 38667: contig of 29807 bp in length
  * 38668 38767: gap of 100 bp
  * 38768 46216: contig of 7449 bp in length
  * 46217 46316: gap of 100 bp
  * 46317 49904: contig of 3588 bp in length
  * 49905 50004: gap of 100 bp
  * 50005 80575: contig of 30571 bp in length
  * 80576 80675: gap of 100 bp
  * 80676 83226: contig of 2551 bp in length
  * 83227 83325: gap of 100 bp
  * 83327 101361: contig of 18035 bp in length
  * 101362 101461: gap of 100 bp
  * 101462 108527: contig of 7066 bp in length
  * 108528 108627: gap of 100 bp
  * 108628 110978: contig of 2351 bp in length
  * 110979 111078: gap of 100 bp
  * 111079 113982: contig of 2904 bp in length
  * 113983 114082: gap of 100 bp
  * 114083 116877: contig of 2795 bp in length
  * 116878 116977: gap of 100 bp
  * 116978 121962: contig of 4985 bp in length
  * 121963 122062: gap of 100 bp
  * 122063 128775: contig of 7713 bp in length
  * 128776 129875: gap of 100 bp
  * 129876 133929: contig of 4054 bp in length
  * 133930 134029: gap of 100 bp
  * 134030 138068: contig of 4039 bp in length
  * 138069 138168: gap of 100 bp
  * 138169 143235: contig of 5067 bp in length
  * 143236 143335: gap of 100 bp
  * 143336 151982: contig of 8647 bp in length
  * 151983 152082: gap of 100 bp
  * 152083 161834: contig of 9752 bp in length
  * 161835 161934: gap of 100 bp
  * 161935 174485: contig of 12351 bp in length
  * 174486 174585: gap of 100 bp
  * 174586 200738: contig of 26153 bp in length
  * 200739 200838: gap of 100 bp
  * 200839 222961: contig of 22123 bp in length.
Location/Qualifiers
  1..222961
  /organism="Danio rerio"
  /mol_type="genomic DNA"
  /db_xref="taxon:7955"
  /clone="DKEX-23p11"
  /clone_1fb="DantioKey"
  1..5743
  /note="assembly_fragment:00234
  fragment_chain:1"
  misc_feature 5844..8760
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  misc_feature 8861..38667
    /note="assembly_fragment:01842
    fragment_chain:1"
  misc_feature 38768..46216
    /note="assembly_fragment:00330
    fragment_chain:1"
  misc_feature 46317..49904
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    fragment_chain:1"
  misc_feature 50005..80575
    /note="assembly_fragment:02173
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misc_feature      101462..108527
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misc_feature      108628..110978
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misc_feature      200839..222961
                    /note="assembly_fragment:01522.0"
ORIGIN
Query Match      77.8% Score 14; DB 2; Length 222961;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 UCCUGAGAGNNNNN 18
DB      174593 TCCTGGAGNNNNN 174580

RESULT 99
AC097049
LOCUS      AC097049
DEFINITION AC097049 224370 bp DNA linear HTG 10-MAY-2003
            Rattus norvegicus clone CH230-204H23, *** SEQUENCING IN PROGRESS
            *** 9 unordered pieces.
ACCESSION  AC097049
VERSION     AC097049.7 GI:30521039
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 224370)
REFERENCE   1 (bases 1 to 224370)
AUTHORS    Muzny,D.,Mettzer,M.,Lee,J.,Abramson,S.,Adams,C.,Alder,J.,
            Allen,C.,Allen,H.,Alsbrooks,S.,Amin,A.,Anguiano,D.,
            Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,
            Baldwin,D.,Bandaranaike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,
            Biswal,K.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M.,
            Bryant,N.,Buhay,C.,Burch,P.,Burrell,K.,Calderson,E.,
            Cardenas,V.,Carter,K.,Cavazos,I.,Ceasar,H.,Center,A.,

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            Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,
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            Davila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Deckerich,D.,
            Delgado,O.,Denson,S.,Denson,S.,Ding,Y.,Dinh,H.,Diyra,K.,
            Draper,H.,Dugan-Rocha,S.,Dum,A.,Durbin,K.,Duvall,B.,Eaves,K.,
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            Fraser,C.M.,Gabriel,A.,Ganta,R.,Garcia,A.,Gartner,T.,Garza,M.,
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            Gunaratne,P.,Haaland,M.,Hamil,C.,Hamilton,C.,Hamilton,K.,
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            Jackson,L.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolivet,A.,
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            Kowis,C.,Kraft,C.L.,Lebow,H.,Levan,J.,Lewis,L.,Li,Z.,Liu,J.,
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            Mangum,B.,Mapua,P.,Martin,K.,Martin,R.,Martinez,E.,
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            Nwackelamen,O.,Okunomu,G.,Olafunso,A.,Pal,S.,Parks,K.,
            Pasternak,S.,Paul,H.,Perez,A.,Perez,L.,Plankkoch,C.,
            Plopper,F.,Polindexter,A.,Popovic,D.,Primus,E.,Pu,D.-L.,
            Puazo,M.,Quiroz,J.,Rachlin,E.,Reeves,K.,Regier,M.A.,Reigh,R.,
            Reilly,B.,Reilly,M.,Ren,Y.,Reuter,M.,Richards,S.,Riggs,F.,
            Rives,C.,Rodkey,T.,Rojas,R.,Rose,M.,Rose,R.,Rutz,S.J.,
            Sanders,W.,Savery,G.,Scherer,S.,Scott,G.,Shatsman,S.,Shen,H.,
            Shetty,J.,Shvartsbeyn,A.,Slison,I.,Sitter,C.D.,Smajls,D.,
            Sheed,A.,Sodergren,E.,Song,X.-Z.,Sorelle,R.,Sosa,D.,
            Steimle,M.,Strong,R.,Sutton,A.,Svatek,A.,Taber,P.,Taylor,C.,
            Taylor,T.,Thomas,N.,Thomas,S.,Tingey,A.,Tretos,Z.,Umanan,K.,
            Vals,R.,Vera,V.,Villasana,D.,Waldron,L.,Walker,B.,Wang,J.,
            Wang,Q.,Wang,S.,Warren,J.,Warren,R.,Wei,X.,White,F.,
            Williams,G.,Willson,R.,Wleczkyk,R.,Wooden,H.,Worley,K.,
            Wright,D.,Wright,R.,Wu,J.,Yakub,S.,Yen,J.,Yoon,L.,Yoon,V.,
            Yu,F.,Zhang,J.,Zhou,J.,Zhou,X.,Zhao,S.,Zhu,D.,von
            Niederhausern,A.,Weiss,R.,Smith,D.R.,Holt,R.A.,Smith,H.O.,
            Weinstock,G.,and Gibbs,R.A.
            Direct Submission
            Unpublished
            2 (bases 1 to 224370)
            Worley,K.C.
            Direct Submission
            Submitted (06-OCT-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 224370)
            Rat Genome Sequencing Consortium.
            Direct Submission
            Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On May 10, 2003 this sequence version replaced gi:25186677.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            ----- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/

```

Contact: hgsc-help@bcm.tmc.edu

----- Project Information -----

Center project name: GIDP

Center clone name: CH230-204H23

----- Summary Statistics -----

Assembly program: Atlas 3.0;

Consensus quality: 189343 bases at least Q40

Consensus quality: 194891 bases at least Q30

Consensus quality: 198424 bases at least Q20

Estimated insert size: 218744; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently  
 consists of 9 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 206236: contig of 206236 bp in length

\* 206237 206336: gap of unknown length

\* 206337 207904: contig of 1568 bp in length

\* 207905 208004: gap of unknown length

\* 208005 209107: contig of 1103 bp in length

\* 209108 209207: gap of unknown length

\* 209208 210423: contig of 1216 bp in length

\* 210424 210523: gap of unknown length

\* 210524 212598: contig of 2075 bp in length

\* 212599 212698: gap of unknown length

\* 212699 214271: contig of 1573 bp in length

\* 214272 214371: gap of unknown length

\* 214372 217564: contig of 3193 bp in length

\* 217565 222371: gap of unknown length

\* 222372 222371: contig of 4607 bp in length

\* 222372 224370: contig of 1999 bp in length.

Location/Qualifiers

1..224370

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-204H23"

3387..3510

misc\_feature

/note="clone boundary"

clone end: T7

site: EcoRI

end sequence: BZ106407"

133012..133520

misc\_feature

/note="wgs contig"

139324..151199

misc\_feature

/note="clone boundary"

clone end: Sp6

site: EcoRI

end sequence: BZ106411"

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 224370;

Best Local Similarity 85.7%; Pred. No. 99;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18

143235 TCCTGAGAGNNNNN 143248

RESULT 100

BX927188/c 228022 bp DNA linear HTG 10-OCT-2004

LOCUS BX927188

DEFINITION Danio rerio clone DKEX-264N13, WORKING DRAFT SEQUENCE, 9 unordered

pieces.

ACCESSION BX927188

VERSION GI:41630180

KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.

SOURCE Danio rerio (zebrafish)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 228022)

AUTHORS McLaren, S.

TITLE Submitted (08-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk

COMMENT On Feb 2, 2004 this sequence version replaced gi:41322817.

----- Genome Center -----

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: zfish-help@sanger.ac.uk

----- Project Information -----

Center project name: ZK264N13

----- Summary Statistics -----

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 225138 bases at least Q40

Consensus quality: 225502 bases at least Q30

Consensus quality: 225841 bases at least Q20

Insert size: 227222; sum-of-contigs

Insert size: 221727; 4.7% error; agarose-fp

Quality coverage: 8.04x in Q20 bases; sum-of-contigs Quality coverage: 8.28x in Q20 bases; agarose-fp

-----

\* NOTE: This is a 'working draft' sequence. It currently  
 consists of 9 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 16758: contig of 16758 bp in length

\* 16759 16858: gap of 100 bp

\* 16859 20882: contig of 4024 bp in length

\* 20883 20982: gap of 100 bp

\* 20983 75976: contig of 54994 bp in length

\* 75977 76076: gap of 100 bp

\* 76077 82135: contig of 6059 bp in length

\* 82136 82235: gap of 100 bp

\* 82236 89535: contig of 7301 bp in length

\* 89537 89636: gap of 100 bp

\* 89637 101310: contig of 11674 bp in length

\* 101311 101410: gap of 100 bp

\* 101411 120443: contig of 19033 bp in length

\* 120444 120543: gap of 100 bp

\* 120544 168466: contig of 47923 bp in length

\* 168467 168566: gap of 100 bp

\* 168567 228022: contig of 59456 bp in length.

Location/Qualifiers

1..228022

/organism="Danio rerio"

/mol\_type="genomic DNA"

/db\_xref="taxon:7955"

/clone="DKEX-264N13"

/clone\_1lb="DanioKey"

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/note="assembly fragment:00363

fragment chain: I"

16859..20882

/note="assembly fragment:00009

fragment chain: I"

20983..75976

/note="assembly fragment:02092

misc\_feature

misc\_feature

misc\_feature

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misc_feature      fragment chain:1"
                    76077..82135
                    /note="assembly: fragment:00052
                    fragment chain:1"
misc_feature      82236..89536
                    /note="assembly: fragment:00113
                    fragment chain:2"
misc_feature      89637..101310
                    /note="assembly: fragment:00225
                    fragment chain:2"
misc_feature      101411..120443
                    /note="assembly: fragment:00552
                    fragment chain:2"
misc_feature      120544..168466
                    /note="assembly: fragment:00801.0"
                    168567..228022
                    /note="assembly: fragment:01385"

ORIGIN
Query Match      77.8%; Score 14; DB 2; Length 228022;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy      5 UCCUGAGAGNNNNNN 18
        |||:|||||
Db      82243 TCCCTGAGNNNNNN 82230

RESULT 101
AC107590/c      232490 bp DNA linear HTG 13-NOV-2002
LOCUS           Rattus norvegicus clone CH230-99F11, *** SEQUENCING IN PROGRESS
DEFINITION      *** 8 unordered pieces.
ACCESSION      AC107590
VERSION        AC107590.4 GI:24941933
KEYWORDS       HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE         Rattus norvegicus (Norway rat)
ORGANISM       Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
                1 (bases 1 to 232490)
REFERENCE
AUTHORS        Muzny,D.,Marie,,Metzker,M.,Lee,,Abramzon,S.,Adams,C.,Alder,J.,
                Allen,C.,Allen,H.,Aisbrooks,S.,Amin,A.,Anguiano,D.,
                Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,
                Baldwin,D.,Bandaranaike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,
                Biswalio,K.,Blair,J.,Blankenburg,K.,Blych,P.,Brown,M.,
                Bryant,N.,Buhay,C.,Burch,P.,Burrell,K.,Calderon,E.,
                Cardenas,V.,Carter,K.,Cavazos,I.,Cassar,H.,Center,A.,
                Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,
                Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,
                Davila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,
                Delgado,O.,Denson,S.,Derramo,C.,Ding,Y.,Dinh,H.,Diyak,K.,
                Draper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Dval,B.,Eaves,K.,
                Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G.,
                Fernandez,S.,Finley,M.,Flagg,N.,Forbes,L.,Foster,M.,Foster,P.,
                Fraser,C.M.,Gabisi,A.,Ganta,R.,Garcia,A.,Garner,T.,Garza,M.,
                Gebregergis,E.,Geer,K.,Gill,R.,Grady,M.,Guerra,M.,Guevara,W.,
                Gunaratne,P.,Haaland,W.,Hamill,C.,Hamilton,C.,Hamilton,K.,
                Harvery,Y.,Havlak,P.,Hawes,A.,Henderson,N.,Hernandez,J.,
                Hernandez,R.,Hines,S.,Hladun,S.L.,Hodgson,A.,Hogues,M.,
                Hollins,B.,Howells,S.,Hulky,S.,Hume,J.,Idlebird,D.,Jackson,A.,
                Jackson,B.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolyvet,A.,
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                Kows,C.,Krat,C.L.,Ledow,H.,Levan,J.,Lewis,L.,Li,Z.,Liu,J.,
                Liu,J.,Liu,W.,Liu,Y.,London,P.,Longacre,S.,Lopez,J.,
                Loshenshew,L.,Loulesged,H.,Lozado,R.J.,Lu,X.,Ma,J.,
                Maheshwari,M.,Mahindaratne,M.,Mahmoud,M.,Malloy,K.,Mangum,A.,
                Mawhney,S.,McLeod,M.P.,McNeill,T.Z.,Meenen,E.,
                Milosavljevic,A.,Miner,G.,Ming,E.,Montemayor,J.,Moore,S.,
                Morgan,M.,Morris,K.,Morris,S.,Munidas,M.,Murphy,M.,Nair,L.,
                Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,

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TITLE           Nwaokemelele, O., Okunnu, G., Olarunpasegun, A., Pal, S., Parks, K.,
                Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
                Plopper, F., Poindexter, A., Popovic, D., Prims, E., Pu, L.-L.,
                Prazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reich, R.,
                Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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                Sanders, M., Savary, G., Scherer, S., Scott, G., Shateman, S., Shen, H.,
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                Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
                Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
                Neiderhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
                Direct Submission
                Unpublished
                2 (bases 1 to 232490)
                Worley, K.C.
                Direct Submission
                Submitted (23-JAN-2002) Human Genome Sequencing Center, Department
                of Molecular and Human Genetics, Baylor College of Medicine, One
                Baylor Plaza, Houston, TX 77030, USA
                3 (bases 1 to 232490)
                Rat Genome Sequencing Consortium.
                Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
                of Molecular and Human Genetics, Baylor College of Medicine, One
                Baylor Plaza, Houston, TX 77030, USA
                On Nov 13, 2002 this sequence version replaced gi:23267838.
                The sequence in this assembly is a combination of BAC based reads
                and whole genome shotgun sequencing reads assembled using Atlas
                (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                in the feature table below represents a scaffold in the Atlas
                assembly (a 'contig-scaffold'). Within each contig-scaffold,
                individual sequence contigs are ordered and oriented, and separated
                by sized gaps filled with Ns to the estimated size. The sequence
                may extend beyond the ends of the clone and there may be sequence
                contigs within a contig-scaffold that consist entirely of whole
                genome shotgun sequence reads. Both end sequences and whole genome
                shotgun sequence only contigs will be indicated in the feature
                table.
                ----- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
                ----- Project Information
                Center project name: GOPW
                Center clone name: CH230-99F11
                ----- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 199275 bases at least Q40
                Consensus quality: 205373 bases at least Q20
                Consensus quality: 206713 bases at least Q20
                Estimated insert size: 201384; sum-of-contigs estimation
                Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                -----
                * NOTE: Estimated insert size may differ from sequence length
                * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
                * NOTE: This is a 'working draft' sequence. It currently
                * consists of 8 contigs. The true order of the pieces
                * is not known and their order in this sequence record is
                * arbitrary. Gaps between the contigs are represented as
                * runs of N, but the exact sizes of the gaps are unknown.
                * This record will be updated with the finished sequence
                * as soon as it is available and the accession number will
                * be preserved.
                *
                1 6116: contig of 6116 bp in length
                *
                6117 6216: gap of unknown length

```



\* 6217 62242: contig of 56026 bp in length  
\* 62342 62342: gap of unknown length  
\* 62343 135755: contig of 73413 bp in length  
\* 135756 135855: gap of unknown length  
\* 135856 227081: contig of 91226 bp in length  
\* 227082 227181: gap of unknown length  
\* 227182 226618: contig of 1437 bp in length  
\* 226619 228719: gap of unknown length  
\* 228719 230002: contig of 1284 bp in length  
\* 230003 230102: gap of unknown length  
\* 231206 231206: contig of 1104 bp in length  
\* 231207 231306: gap of unknown length  
\* 231307 232490: contig of 1184 bp in length.  
Location/Qualifiers  
1. 232490  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-99F11"  
674. 1283  
/note="clone\_boundary  
clone\_end:5p6  
site:  
end\_sequence:BH334967"  
6217. 7733  
/note="wgs\_contig"  
189472. 151092  
/note="wgs\_contig"  
200912. 202317  
/note="wgs\_contig"

Query Match 77.8% Score 14; DB 2; Length 232490;  
Best Local Similarity 85.7%; Pred. No. 99;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNNNN 18  
Db 228726 TCCTGAGANNNNNN 228713

RESULT 102  
BX950179  
LOCUS BX950179 239166 bp DNA linear HTG 18-FEB-2004  
DEFINITION Danio rerio clone DKY-27P23, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 14  
unordered pieces.  
ACCESSION BX950179  
VERSION BX950179.3 GI:42627395  
KEYWORDS HTG: HTGS PHASE1.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 239166)  
Sims.S.  
REFERENCE  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (17-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zf1sh-help@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk  
On Feb 18 2004 this sequence version replaced gi:42600214.  
COMMENT  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zf1sh-help@sanger.ac.uk  
----- Project Information  
Center project name: ZK27P23  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 234745 bases at least Q40  
Consensus quality: 235466 bases at least Q30

Consensus quality: 236100 bases at least Q20  
Insert size: 237866; sum-of-contigs  
Insert size: 235442; 3.9% error; agarose-fp  
Quality coverage: 9.54x in Q20 bases; sum-of-contigs Quality  
coverage: 9.64x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 14 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 11014: contig of 11014 bp in length  
\* 11015 11114: gap of 100 bp  
\* 11115 15181: contig of 4067 bp in length  
\* 15182 15281: gap of 100 bp  
\* 15282 84366: contig of 69085 bp in length  
\* 84367 84466: gap of 100 bp  
\* 84467 97522: contig of 13056 bp in length  
\* 97523 97622: gap of 100 bp  
\* 97623 109674: contig of 12052 bp in length  
\* 109675 109774: gap of 100 bp  
\* 109775 139344: contig of 29570 bp in length  
\* 139345 139444: gap of 100 bp  
\* 139445 145157: contig of 5713 bp in length  
\* 145158 145257: gap of 100 bp  
\* 145258 163330: contig of 18073 bp in length  
\* 163331 163430: gap of 100 bp  
\* 163431 175658: contig of 12228 bp in length  
\* 175659 175759: gap of 100 bp  
\* 175759 192348: contig of 16590 bp in length  
\* 192349 192448: gap of 100 bp  
\* 192449 198785: contig of 6337 bp in length  
\* 198786 198885: gap of 100 bp  
\* 198886 216179: contig of 17294 bp in length  
\* 216180 216279: gap of 100 bp  
\* 216280 219430: contig of 3151 bp in length  
\* 219431 219530: gap of 100 bp  
\* 219531 239166: contig of 19636 bp in length.  
Location/Qualifiers  
1. 239166  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKY-27P23"  
/clone\_1ib="DanioKey"  
1. 11014  
/note="assembly\_fragment:00357  
fragment\_chain:1"  
11115. 15181  
/note="assembly\_fragment:00012  
fragment\_chain:1"  
15282. 84366  
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84467. 97522  
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97623. 109674  
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109775. 139344  
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139445. 145157  
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145258. 163330  
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163431. 175658

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/note="assembly_fragment:00233
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misc_feature
175759..192348
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198886..216179
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216280..219430
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219531..239166
/note="assembly_fragment:01645.0"

ORIGIN

Query Match 77.8% Score 14; DB 2; Length 239166;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGANNNNNN 18
Db 139337 TCCTGAGAGNNNNN 139350.

RESULT 103
AC110826
LOCUS
DEFINITION
Rattus norvegicus clone CH230-19912, *** SEQUENCING IN PROGRESS
***, 7 unordered pieces.
AC110826
AC110826.5 GI:24818668
HTG: HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 241934)
Muzny,D,Marle, Metzker,M, Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyte, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregregis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
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Hollins, B., Howells, S., Hu, Y. S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, B., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowls, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensueta, L., Louie, H., Lozano, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Mallory, K., Mangum, A.,
Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Muniasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwachukwu, O., Okwuonu, G., Olarinmusa, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
3 (bases 1 to 241934)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (16-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:2321713.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.bsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.bsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCGI
Center clone name: CH230-19912
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 217093 bases at least Q40
Consensus quality: 221891 bases at least Q30
Consensus quality: 225435 bases at least Q20
Estimated insert size: 227785; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbankdraft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 10980: contig of 10980 bp in length
* 10981 11080: gap of unknown length
* 11081 20228: contig of 9148 bp in length
* 20229 20328: gap of unknown length

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*      20329      98047: contig of 77719 bp in length
*      98048      98147: gap of unknown length
*      98148      179247: contig of 81100 bp in length
*      179248      179347: gap of unknown length
*      179348      239002: contig of 59655 bp in length
*      239003      239102: gap of unknown length
*      239103      240128: contig of 1026 bp in length
*      240129      240228: gap of unknown length
*      240229      241934: contig of 1706 bp in length.
*      240230      Location/Qualifiers
*      241934
*      Location="Rattus norvegicus"
*      mol_type="genomic DNA"
*      db_xref="taxon:10116"
*      clone="CH230-19912"
*      1..1019
*      misc_feature
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*      /note="wgs_contig"
*      32300..33356
*      /note="wgs_contig"
*      102325..103591
*      /note="wgs_contig"
*      179348..181311
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*      181504..183523
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*      /note="wgs_contig"

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Query Match      77.8% Score 14; DB 2; Length 241934;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy      5 UCCUGAGNNNNNN 18
Db      103584 TCCTGAGNNNNNN 103597

RESULT 104
AC131536      243490 bp DNA linear HTG 10-MAY-2003
LOCUS      AC131536
DEFINITION      Rattus norvegicus clone CH230-4992, *** SEQUENCING IN PROGRESS ***
ACCESSION      AC131536
VERSION      AC131536.4 GI:30520641
KEYWORDS      HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 243490)
Munry,D,Marle,M,Mezker,M, Lee, A, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alebrooke, S., Amin, A., Anguiano, D.,
Ayala-Beche, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryan, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Devila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Drepper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Gant, R., Garcia, A., Garner, F., Garza, M.,
Georgiev, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Guarinate, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolliver, A.,
Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Koval, C.,
Kovis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshew, L., Louisedge, H., Lozano, R., Lu, X., Ma, J.,
Maheshwari, M., Mahlstedt, M., Mahmud, M., Malloy, K., Mangum, A.,
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Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
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Pasternak, S., Paul, H., Perez, A., Perez, L., Pfennoch, C.,
Plopper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L.,
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reig, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.,
Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smaj, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission

TITLE
Unpublished
2 (bases 1 to 243490)
REFERENCE
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 243490)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24819714.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

REFERENCE
AUTHORS
JOURNAL
COMMENT
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GPCR
Center clone name: CH230-4992
----- Summary Statistics
Assembly program: Atlas 3.0:
Consensus quality: 214615 bases at least Q40
Consensus quality: 219225 bases at least Q30
Consensus quality: 222545 bases at least Q20
Estimated insert size: 228801; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
* NOTE: Estimated insert size may differ from sequence length

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```

      (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
      * NOTE: This is a working draft sequence. It currently
      * consists of 1 contigs. Gaps between the contigs
      * are represented as runs of N. The order of the pieces
      * is believed to be correct as far as possible, however the sizes
      * of the gaps between them are based on estimates that have
      * provided by the submitter.
      * This sequence will be replaced
      * by the finished sequence as soon as it is available and
      * the accession number will be preserved.
      *
      1 243490: contig of 243490 bp in length.
      Location/Qualifiers
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           /mol_type="genomic DNA"
           /db_xref="taxon:10116"
           /clone="CH230-49B2"
           1. 1169
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              clone_end:Sp6
              complement(6360..6720)
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              end_sequence:BH280612"
              131675..134466
              /note="wgs contig"
              172018..173754
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ORIGIN

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Query Match      77.8%; Score 14; DB 2; Length 243490;
Best Local Similarity 85.7%; Pred.No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
    
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Qy 5 UCCUGGAGNNNNNN 18  
 13326 TCCTGAGANNNNNN 13339

RESULT 105  
 AC112470/c  
 LOCUS  
 DEFINITION  
 AC112470 244594 bp DNA linear HTG 19-NOV-2002  
 Rattus norvegicus clone CH230-120K2, WORKING DRAFT SEQUENCE, 3  
 unrounded pieces.  
 AC112470  
 VERSION  
 HTG: HTGS PHASE1; HTGS DRAFT; HTGS\_FULLTOP.  
 KEYWORDS  
 Rattus norvegicus (Norway rat)  
 SOURCE  
 Rattus norvegicus  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 244594)  
 Muzny,D,Marle,,Metzker,M,Lea,,Abramson,S,,Adams,C,,Alder,J,,  
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 Anyalebechi,V,,Aoyagi,A,,Ayodeji,M,,Baca,B,,Baden,H,,  
 Baldwin,D,,Bandaranaike,D,,Barber,M,,Barnstead,M,,Behamed,F,,  
 Biswalio,K,,Blair,J,,Blankenburg,K,,Blyth,P,,Brown,M,,  
 Bryant,N,,Buhay,C,,Burck,P,,Burrell,K,,Calderson,E,,  
 Cardenas,V,,Carter,K,,Cavazos,I,,Caesar,H,,Center,A,,  
 Chacko,J,,Chavez,D,,Chen,G,,Chen,R,,Chen,Y,,Chen,Z,,Chu,J,,  
 Cleveland,C,,Cockrell,R,,Cox,C,,Coyle,M,,Cree,A,,D'Souza,L,,  
 Davila,M,L,,Davis,C,,Davy-Carroll,L,,De Anda,C,,Dederich,D,,  
 Delgado,O,,Denson,S,,Deramo,C,,Ding,Y,,Dinh,H,,Divya,K,,

Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,  
 Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,  
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,  
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,  
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 Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,  
 Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,  
 Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,  
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 Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,  
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 Milosavljevic,A., Miner,G., Mirza,E., Montemayor,J., Moore,S.,  
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 Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,  
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 Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,  
 Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.,  
 Puazo,M., Quiroz,J., Rachlin,B., Reeves,K., Reister,M.A., Reigh,R.,  
 Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,  
 Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,  
 Sanders,M., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,  
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 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Soza,J.,  
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 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Tjorja,Z., Umami,K.,  
 Vals,O., Vera,V., Villanueva,D., Waldron,L., Walker,B., Wang,J.,  
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,  
 Williams,G., Willson,R., Wleczky,R., Woodman,H., Wolley,K.,  
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,  
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von  
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
 Weinstock,G. and Gibbs,R.A.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 244594)  
 Worley,K.C.  
 Direct Submission  
 Submitted (21-FEB-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 244594)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Nov 19, 2002 this sequence version replaced gi:23195038.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GSRF  
 Center clone name: CH230-120K2

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----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 22983 bases at least Q40
Consensus quality: 23259 bases at least Q30
Consensus quality: 23496 bases at least Q20
Estimated insert size: 236805; sum-of-coverage estimation
Quality coverage: 7x in Q20 bases; sum-of-coverage estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 116449: contig of 116449 bp in length
* 116450 116549: gap of unknown length
* 116550 128724: contig of 12175 bp in length
* 128725 128825: gap of unknown length
* 128825 244594: contig of 115770 bp in length.
Location/Qualifiers
1. 244594
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/db_xref="taxon:10116"
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1. 1266
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ORIGIN
Query Match 77.8% Score 14; DB 2; Length 244594;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18
Db 148237 TCCTGAGAGNNNNN 148224

RESULT 106
AC117977 245318 bp DNA linear HTG 26-SEP-2002
LOCUS Rattus norvegicus clone CH230-13311, *** SEQUENCING IN PROGRESS
DEFINITION *** 12 unordered pieces.
AC117977
VERSION AC117977.5 GI:33322207
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 245318)
Muzny,D,Marle, Metzker,M, Lee, Abramson,S, Adams,C, Alder,J,
Allen,C, Allen,H, Alsbrooks,S, Amin,A, Angiano,D,
Anyalebechi,V, Aoyagi,A, Ayodeji,M, Bacc,E, Baden,H,
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Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
Cardenas,V, Carter,K, Cavazos,I, Caesar,H, Center,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,D,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
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Georgievski,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W,
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Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
Hollins,B, Howells,S, Huliyk,S, Hume,J, Idlebird,D, Jackson,A,
Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A,
Karpachy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C,
Kovis,C, Kraft,C,L, Lebow,H, Levay,J, Lewis,L, Li,Z, Liu,J,
Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
Lorenshuber,L, Louisedge,H, Lozada,R,J, Lu,X, Ma,J,
Maheshwari,M, Mahindartine,M, Mahmud,M, Malloy,K, Mangum,A,
Mangum,B, Mapa,P, Martin,K, Martin,R, Martinez,E,
Mawhinney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S,
Morgan,M, Morris,K, Morris,S, Mundasa,M, Murphy,M, Nair,L,
Nankervill,C, Neal,D, Newton,N, Nguyen,N, Norris,S,
Nwokeneme,O, Okwunnu,G, Olarinpoogoon,A, Pal,S, Parks,K,
Pasternak,S, Paul,H, Perez,A, Perez,L, Pfamknoch,C,
Plopper,F, Poinexter,A, Popovic,D, Primus,E, Pu,L,L,
Piazo,M, Quiroz,J, Rachin,E, Reeves,K, Regier,M,A, Reigh,R,
Reilly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F,
Rivers,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ruiz,S,
Sanders,W, Savary,G, Scherer,S, Scott,G, Shatsman,S, Shen,H,
Shetty,J, Shvartsbeyn,A, Sisson,I, Sitter,C,D, Smaiz,D,
Sneed,A, Sodergren,E, Song,X-Z, Sorelle,R, Sosa,J,
Steinle,M, Strong,R, Sutton,A, Swatek,A, Taber,P, Taylor,C,
Taylor,T, Thomas,N, Thomas,S, Tinney,A, Trejos,Z, Uemami,K,
Valas,R, Vera,V, Villaseana,D, Waldron,L, Walker,B, Wang,J,
Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,F,
Williams,G, Willson,R, Wleczkyk,R, Wooden,H, Worley,K,
Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V,
Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von
Niederhausern,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O,
Weinstock,G, and Gibbs,R,A.
Direct Submission
Unpublished
2 (bases 1 to 245318)
REFERENCE
AUTHORS
Worley,K,C.
TITLE
Direct Submission
JOURNAL
Submitted (12-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 245318)
REFERENCE
AUTHORS
Rat Genome Sequencing Consortium.
TITLE
Direct Submission
JOURNAL
Submitted (26-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT
On Sep 26, 2002 this sequence version replaced gi:21903166.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only

```

contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GWIE

Center clone name: CH230-13311

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 207818 bases at least Q40

Consensus quality: 212673 bases at least Q30

Consensus quality: 215838 bases at least Q20

Estimated insert size: 248658; sum-of-contigs estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length

(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 12 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

```

* 1 6825: contig of 6825 bp in length
* 6826 6925: gap of unknown length
* 6926 112025: contig of 105100 bp in length
* 112026 112125: gap of unknown length
* 112126 200613: contig of 88487 bp in length
* 200613 200713: gap of unknown length
* 200713 213425: contig of 12713 bp in length
* 213426 213525: gap of unknown length
* 213526 216973: contig of 3448 bp in length
* 216974 217073: gap of unknown length
* 217074 221686: contig of 4613 bp in length
* 221687 223129: contig of 1343 bp in length
* 223130 224222: gap of unknown length
* 224223 224522: contig of 1193 bp in length
* 224523 225689: contig of 1167 bp in length
* 225690 225789: gap of unknown length
* 225790 226872: contig of 1083 bp in length
* 226873 226972: gap of unknown length
* 226973 229239: contig of 2267 bp in length
* 229240 229339: gap of unknown length
* 229340 245318: contig of 15979 bp in length.
Location/Qualifiers
1. .245318
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-13311"
112126..113262
/notes="wgs contig"
203834..205488
/notes="wgs contig"
217074..218922
/notes="wgs contig"

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FEATURES

source

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1. .245318
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-13311"
112126..113262
/notes="wgs contig"
203834..205488
/notes="wgs contig"
217074..218922
/notes="wgs contig"

```

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 245318;  
Best Local Similarity 85.7%; Pred. No. 99;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18

Db 163709 TCCTGAGAGNNNNNN 163722

RESULT 107

CR812481/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CR812481 247436 bp DNA linear HTG 03-OCT-2004  
Dario rerio clone DKEX-225D17, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
unnumbered pieces.  
CR812481.3 GI:53755942  
HTG; HTGS PHASE1.  
Dario rerio (zebrafish)  
Dario rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 247436)  
McLay, K.  
Direct Submission  
Submitted (02-OCT-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
fish-help@sanger.ac.uk Clone request: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
On Oct 3, 2004 this sequence version replaced gi:52851212.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [fish-help@sanger.ac.uk](mailto:fish-help@sanger.ac.uk)  
----- Project Information  
Center project name: ZK225D17

----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 245295 bases at least Q40  
Consensus quality: 245732 bases at least Q30  
Consensus quality: 246014 bases at least Q20  
Insert size: 246836; sum-of-contigs  
Insert size: 225419; 4.4% error; agarose-fp  
Quality coverage: 6.92x in Q20 bases; sum-of-contigs Quality  
coverage: 7.58x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

```

* 1 55502: contig of 55502 bp in length
* 55503 55602: gap of 100 bp
* 55603 72285: contig of 16683 bp in length
* 72286 72385: gap of 100 bp
* 72386 80502: contig of 8117 bp in length
* 80503 80602: gap of 100 bp
* 80603 129020: contig of 48418 bp in length
* 129021 129120: gap of 100 bp
* 129121 195746: contig of 66626 bp in length
* 195747 195846: gap of 100 bp
* 195847 205719: contig of 9873 bp in length
* 205720 205819: gap of 100 bp
* 205820 247436: contig of 41617 bp in length.
Location/Qualifiers
1. .247436
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7953"
/clone="DKEX-225D17"
/clone_lib="DanioKey"
1..55502
/notes="assembly fragment: 01325
fragment chain:1"
55603..72285
/notes="assembly fragment: 00168
fragment chain:1"
72386..80502

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FEATURES

source

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1. .247436
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7953"
/clone="DKEX-225D17"
/clone_lib="DanioKey"
1..55502
/notes="assembly fragment: 01325
fragment chain:1"
55603..72285
/notes="assembly fragment: 00168
fragment chain:1"
72386..80502

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misc\_feature

misc\_feature

misc\_feature

[illegible]

REILLY, B., REILLY, M., REN, Y., REUTER, M., RICHARDS, S., RIGGS, F.,  
RAVES, S., RODKEY, T., ROJAS, A., ROSE, M., ROSE, R., RUIZ, S. J.,  
SANDERS, W., SAREVY, G., SCHERER, S., SCOTT, G., SHATEMAN, S., SHEN, H.,  
SHELLEY, J., SHVARTSBEYN, A., SJOBORN, I., SILLER, C. D., SNAPE, D.,  
SNEED, A., SODERGREN, E., SONG, X. -2., SORRELL, R., SOSA, J.,  
STEINLE, M., STRONG, R., SUTTON, A., STAVEK, A., TABOR, P., TAYLOR, C.,  
TAYLOR, T., THOMAS, N., THOMAS, S., TINGEE, A., TRJOS, Z., UEMATI, K.,  
VALAS, R., VERA, V., VILLASANA, D., WALDRON, L., WALKER, B., WANG, J.,  
WANG, Q., WANG, S., WARREN, J., WARREN, R., WEI, X., WHITE, F.,  
WILLIAMS, G., WILSON, R., WLECZYK, R., WOODEN, H., WORLEY, K.,  
WU, F. D., WRIGHT, R., WU, J., YAKUB, S., YEN, J., YOON, L., YOON, V.,  
YU, F., ZHANG, J., ZHOU, J., ZHOU, X., ZHAO, S., ZHUN, D., VON  
NIEDERHAUSEN, A., WEISS, R., SMITH, D. R., HOLT, R. A., SMITH, H. O.,  
WEINSTECK, G. and GIBBS, R. A.

Direct Submission  
Unpublished  
2 (bases 1 to 248358)  
Worley, K. C.

Direct Submission  
Submitted (26-MAY-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 248358)  
Rat Genome Sequencing Consortium.

Direct Submission  
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:23265699.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information -----  
Center project name: GAPX  
Center clone name: CH230-4P17

----- Summary Statistics -----  
Assembly program: Atlas;  
Consensus quality: 225281 bases at least Q40  
Consensus quality: 228208 bases at least Q30  
Consensus quality: 231758 bases at least Q20  
Estimated insert size: 236600; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 246878: contig of 246878 bp in length  
\* 246879 246978: gap of unknown length  
\* 246979 248358: contig of 1380 bp in length.  
Location/Qualifiers  
1. 248358  
/organism="Rattus norvegicus"

FEATURES  
Source

```

/misc_feature
      /mol_type="genomic DNA"
      /db_xref="taxon:10116"
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      /note="clone_boundary
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      site:ECORI
      end_sequence:BH305410"
      complement(243979..244808)
      /note="clone_boundary
      clone_end:Sp6
      site:ECORI
      end_sequence:BH305412"

ORIGIN

Query Match      77.8%; Score 14; DB 2; Length 248358;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGAGAGNNNNNN 18
      :||:|||||
Db      246871 TCCTGGAGNNNNNN 246884

RESULT 109
AC127927      250161 bp      DNA      linear      HTG 21-SEP-2002
LOCUS      AC127927
DEFINITION      Rattus norvegicus clone CH230-129119, *** SEQUENCING IN PROGRESS
ACCESSION      AC127927
VERSION      AC127927.2 GI:23265377
KEYWORDS      HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus
ORGANISM      Rattus norvegicus
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
      Rattus.
      1 (bases 1 to 250161)
REFERENCE      1 (bases 1 to 250161)
AUTHORS      Muzny,D,Marle,M,et al., Lee,S., Abramson,S., Adams,C., Alder,J.,
      Allen,C., Allen,H., Alsbrooke,S., Amin,A., Angulano,D.,
      Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
      Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
      Biswal,K., Blair,J., Blankenburg,K., Blythe,P., Brown,M.,
      Bryant,N., Burch,C., Burch,P., Burrell,K., Calderon,E.,
      Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
      Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
      Cleveland,C., Cockrell,R., Cox,C., Coyte,M., Cree,A., D'Souza,L.,
      Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
      Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
      Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
      Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
      Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
      Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
      Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
      Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hernandez,J.,
      Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,K.,
      Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M.,
      Hollins,B., Howells,S., Huylk,S., Hume,J., Idlebird,D., Jackson,A.,
      Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
      Karpach,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
      Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
      Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
      Lorensueta,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
      Maheshwari,M., Mahindartine,M., Mahmoud,M., Mallory,K., Mangum,A.,
      Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
      Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenan,E.,
      Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
      Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
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      Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,

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Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primm,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Raculin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rivers,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ritz,S.J.,
Sanders,M., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajd,D.,
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Steinle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umanan,K.,
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Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willeon,R., Wleczek,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,U., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 250161)
REFERENCE      2 (bases 1 to 250161)
AUTHORS      Worley,K.C.
TITLE      Direct Submission
JOURNAL      Submitted (19-JUN-2002) Human Genome Sequencing Center, Department
      of Molecular and Human Genetics, Baylor College of Medicine, One
      Baylor Plaza, Houston, TX 77030, USA
      3 (bases 1 to 250161)
REFERENCE      3 (bases 1 to 250161)
AUTHORS      Rat Genome Sequencing Consortium.
TITLE      Direct Submission
JOURNAL      Submitted (21-SEP-2002) Human Genome Sequencing Center, Department
      of Molecular and Human Genetics, Baylor College of Medicine, One
      Baylor Plaza, Houston, TX 77030, USA
      On Sep 21, 2002 this sequence version replaced gi:21908454.
      The sequence in this assembly is a combination of BAC based reads
      and whole genome shotgun sequencing reads assembled using Actis
      (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
      sequence may extend beyond the ends of the clone and there may be
      contigs that consist entirely of whole genome shotgun sequence
      reads. Both end sequences and whole genome shotgun sequence only
      contigs will be indicated in the feature table.

-----Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----Project Information
Center project name: GXRV
Center clone name: CH230-129119
-----Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 22156 bases at least Q40
Consensus quality: 223903 bases at least Q30
Consensus quality: 225468 bases at least Q20
Estimated insert size: 240281; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 250161: contig of 250161 bp in length.
Location/Qualifiers
1.250161
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-129119"
FEATURES
source

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                  site:ECORI
                  end_sequence:BH307614"
misc_feature      /note="complement(246893..247494)
                  /note="clone_boundary
                  clone_end:T7
                  site:ECORI
                  end_sequence:BH307613"

ORIGIN
Query Match      77.8% Score 14; DB 2; Length 250161;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      5 UCCUGAGAGNNNNNN 18
       :||:|||||||
Db      138792 TCCTGAGAGNNNNNN 138805

RESULT 110
AC11204/C
LOCUS
DEFINITION
AC11204      256409 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-31G2, *** SEQUENCING IN PROGRESS ***,
3 unordered pieces.
AC11204
VERSION
AC11204.5 GI:30522768
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 256409)
Muzny,D,Marie., Metzker,M,lee., Abramson,S., Adams,C., Alder,J.,
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Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Caesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
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Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rivers,C., Rodkey,T., Rojao,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,

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AUTHORS
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REFERENCE
AUTHORS
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JOURNAL
COMMENT
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GENC
Center clone name: CH230-31G2
----- Summary Statistics
Assembly program: Atlas 3.0:
Consensus quality: 224869 bases at least Q40
Consensus quality: 230824 bases at least Q20
Estimated insert size: 239124; sum-of-coverage estimation
Quality coverage: 6x in Q20 bases; sum-of-coverage estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
253304: contig of 253304 bp in length
253305 253404: gap of unknown length
253405 254643: contig of 1239 bp in length
254644 254743: gap of unknown length
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Location/Qualifiers
1. 256409
/organism="Rattus norvegicus"
/mol_type="genomic DNA"

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/db xref="taxon:10116"
/c1one="CH230-3162"
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Query Match 77.8% Score 14; DB 2; Length 256409;
Best Local Similarity 85.7% Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Cy 5 UCCUGAGANNNNNN 18
Db 254751 TCCTGAGANNNNNN 254738

RESULT 111
AC106994/c
LOCUS
DEFINITION
AC106994 259219 bp DNA linear HTG 08-OCT-2002
Rattus norvegicus clone CH230-121024, *** SEQUENCING IN PROGRESS
*** 8 unordered pieces.
AC106994
AC106994.4 GI:23270269
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 259219)
Muzny,D,Marie,, Metzker,M,Lee,, Abramson,S,, Adams,C,, Alder,J,,
Allen,C,, Allen,H,, Alsbrooke,S,, Amin,A,, Anguiano,D,,
Anyalebechi,V,, Aoyagi,A,, Ayodeji,M,, Baca,E,, Baden,H,,
Baldwin,D,, Bandaranaike,D,, Barber,M,, Barnstead,M,, Benahmed,F,,
Biswal,K,, Blair,J,, Blankenburg,K,, Blyth,P,, Brown,M,,
Bryant,N,, Buhay,C,, Burch,P,, Burrell,K,, Calderon,E,,
Cardenas,V,, Carter,K,, Cavazos,I,, Ceasar,H,, Center,A,,
Chacko,J,, Chavez,K,, Chen,G,, Chen,R,, Chen,Y,, Chen,Z,, Chu,J,,
Cleveland,C,, Cockrell,R,, Cox,C,, Coyle,M,, Cree,A,, D'Souza,L,,
Davila,M,L,, Davis,C,, Davy-Carroll,L,, De Anda,C,, Dederich,D,,
Delgado,O,, Denson,S,, Deramo,C,, Ding,Y,, Dinh,H,, Diya,K,,
Draper,H,, Dugan-Rocha,S,, Dunn,A,, Durbin,K,, Duval,B,, Eaves,K,,
Egan,A,, Escotto,M,, Eugene,C,, Evans,C,A,, Falls,T,, Fan,G,,
Fernandez,S,, Finley,M,, Flaggs,N,, Forbes,L,, Foster,M,, Foster,P,,
Gebrgeorgis,E,, Geer,K,, Galli,R,, Grady,A,, Gartner,T,, Garza,M,,
Gunnatarte,P,, Haaland,W,, Hamill,C,, Hamilton,C,, Hamilton,K,,
Harvey,Y,, Havlak,P,, Hawes,A,, Henderson,N,, Hernandez,J,,
Hernandez,R,, Hines,S,, Hladun,S,L,, Hodgson,A,, Hogue,M,,
Hollins,B,, Howells,S,, Hulik,S,, Hume,J,, Idlebird,D,, Jackson,A,,
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Karpeth,S,, Kelly,S,, Kelly,S,, Khan,Z,, King,L,, Kovar,C,,
Kows,C,, Kraft,C,L,, Ledow,H,, Levan,J,, Lewis,L,, Li,Z,, Liu,D,,
Liu,J,, Liu,W,, Liu,Y,, London,P,, Longacre,S,, Lopez,J,,
Lorenshuwa,L,, Louised,H,, Lozano,R,J,, Lu,X,, Ma,J,,
Maheshwari,M,, Mahindaratne,M,, Mahmoud,M,, Malloy,K,, Mangum,A,,
Mangum,B,, Mapua,P,, Martin,K,, Martin,R,, Martinez,E,,
Mawhinney,S,, McLeod,M,P,, McNeill,T,Z,, Meenen,E,,
Miloavjevic,A,, Miner,G,, Minja,E,, Montemayor,J,, Moore,S,,
Morgan,M,, Morris,K,, Morris,S,, Mundasa,M,, Murphy,M,, Nait,L,,
Nwaokemele,O,, Okunolu,G,, Olarnunsgoon,A,, Pal,S,, Parks,K,,
Pasternak,S,, Paul,H,, Perez,A,, Perez,L,, Pfankoch,C,,
Plopper,F,, Polindexter,A,, Popovic,D,, Primus,B,, Fu,L,,-L,,
Puzos,M,, Quiroz,J,, Rachlin,E,, Reeves,K,, Regier,M,A,, Reigh,R,,
Reilly,B,, Reilly,M,, Ren,Y,, Reuter,M,, Richards,S,, Riggs,F,,
Rivers,C,, Rodkey,T,, Rojas,A,, Rose,M,, Rose,R,, Ruiz,S,J,,
Sanders,M,, Savery,G,, Scherer,S,, Scott,G,, Shatman,S,, Shen,H,,
Shetty,J,, Shvartbeyn,A,, Sison,I,, Sitter,C,D,, Smajic,D,,
Sneed,A,, Sodergren,E,, Song,X,-Z,, Sorrelle,R,, Sosa,J,,
Steinle,M,, Strong,R,, Sutton,A,, Svatek,A,, Tabori,P,, Taylor,C,,
Taylor,T,, Thomas,N,, Thomas,S,, Tingey,A,, Trejos,Z,, Uemant,K,,

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TITLE
JOURNAL
AUTHORS
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JOURNAL
COMMENT
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 259219)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 23, 2002 this sequence version replaced gi:21737508.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GPGQ
Center clone name: CH230-121024
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 222280 bases at least Q40
Consensus quality: 226331 bases at least Q30
Consensus quality: 228820 bases at least Q20
Estimated insert size: 250992; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html) .
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 87120: contig of 87120 bp in length
87121 87220: gap of unknown length
87221 230567: contig of 143347 bp in length
230568 230667: gap of unknown length
230668 253361: contig of 22694 bp in length
253362 254461: gap of unknown length
254462 254494: contig of 1033 bp in length
254495 254594: gap of unknown length
254595 255966: contig of 1002 bp in length
255967 256734: gap of unknown length
256735 256834: gap of unknown length

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* 256835 258095: contig of 1261 bp in length
* 258096 258195: gap of unknown length
* 258196 259219: contig of 1024 bp in length.
FEATURES
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            /db_xref="taxon:10116"
            /clone="CH230-121024"
            1. 1440
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            7279. 8766
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            /note="wgs_contig"
ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 259219;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 5 UCCUGAGNNNNN 18
Db 30898 TCCTGAGNNNNN 30885
RESULT 112
AC128915 272053 bp DNA linear HTG 19-NOV-2002
LOCUS Rattus norvegicus clone CH230-332D13, *** SEQUENCING IN PROGRESS
ACCESSION AC128915
VERSION AC128915.3 GI:25073567
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
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TITLE
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COMMENT
Plapper,F., Polidexter,A., Popovic,D., Primus,E., Pu.L.-L.,
Puzo,M., Quiror,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
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Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 272053)
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 272053)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23196153.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KBD0
Center clone name: CH230-332D13
----- Summary Statistics8
Assembly program: Phrap; version 0.990329
Consensus quality: 245349 bases at least Q40
Consensus quality: 250712 bases at least Q30
Consensus quality: 254043 bases at least Q20
Estimated insert size: 256776; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a "working draft" sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 27109: contig of 27109 bp in length
* 27110 27209: gap of unknown length
* 27210 270524: contig of 243315 bp in length

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* 270525 270624: gap of unknown length
* 270625 272053: contig of 1429 bp in length.
FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:10116"
            /clone="CH230-332D13"
            complement(633..1531)
            /note="clone boundary"
            clone_end:17
            site:
                end_sequence: BZ232511"
            misc_feature
                68676..70602
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                258419..259483
                /note="wgs_contig"
            misc_feature
                263476..264931
                /note="wgs_contig"
            misc_feature
                268470..270524
                /note="wgs_contig"
ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 272053;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 UCCUGGAGNNNNNN 18
Db 237761 TCCTGGAGNNNNNN 237774

RESULT 113
AC097979/c
LOCUS AC097979 276376 bp DNA linear HTG 21-SEP-2002
DEFINITION Rattus norvegicus clone CH230-44022. *** SEQUENCING IN PROGRESS ***
ACCESSION AC097979
VERSION AC097979.6 GI:23264455
KEYWORDS HTG; HTG_PHASE1; HTG_DRAFT; HTG_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
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REFERENCE
    Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
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    Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
    Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,
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    Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
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    Maheshwari, M., Mahindaratne, M., Mahmoud, R., Mallory, K., Mangum, A.,
    Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,

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AUTHORS
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COMMENT
    The sequence in this assembly is a combination of BAC based reads
    and whole genome shotgun sequencing reads assembled using Atlas
    (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
    sequence may extend beyond the ends of the clone and there may be
    contigs that consist entirely of whole genome shotgun sequence
    reads. Both end sequences and whole genome shotgun sequence only
    contigs will be indicated in the feature table.
    ----- Genome Center
    Center: Baylor College of Medicine
    Center code: BCM
    Web site: http://www.hgsc.bcm.tmc.edu/
    Contact: hgsc-help@bcm.tmc.edu
    ----- Project Information
    Center project name: GRTH
    Center clone name: CH230-44022
    ----- Summary Statistics
    Assembly program: Phrap; version 0.9903229
    Consensus quality: 203480 bases at least Q40
    Consensus quality: 205742 bases at least Q30
    Consensus quality: 207204 bases at least Q20
    Estimated insert size: 231400; sum-of-contigs estimation
    Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
    * NOTE: Estimated insert size may differ from sequence length
    * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
    * NOTE: This is a "working draft" sequence. It currently
    * consists of 6 contigs. The true order of the pieces
    * is not known and their order in this sequence record is
    * arbitrary. Gaps between the contigs are represented as
    * runs of N, but the exact sizes of the gaps are unknown.
    * This record will be updated with the finished sequence
    * as soon as it is available and the accession number will
    * be preserved.
    * 1 231096: contig of 231096 bp in length
    * 231097 231196: gap of unknown length
    * 231197 233408: contig of 2212 bp in length

```

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* 233409 233508: contig of unknown length
* 233509 234638: contig of 1130 bp in length
* 234639 234738: gap of unknown length
* 234739 238474: contig of 3736 bp in length
* 238475 238574: gap of unknown length
* 238575 257956: contig of 19382 bp in length
* 257957 258056: gap of unknown length
* 258057 276376: contig of 18320 bp in length.

FEATURES
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        /mol_type="genomic DNA"
        /db_xref="taxon:10116"
        /clone="CH230-44022"
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        clone_end:5p6"
        2214..3072
        /note="clone boundary"
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        site:ECORI
        end_sequence:BH295921"
    misc_feature
        229632..230700
        /note="clone boundary"
        clone_end:T7
        site:ECORI
        end_sequence:BH295918"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 276376;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCGCGAGNNNNNN 18
    :||:|||||||
Db 171866 TCCTGAGNNNNNN 171853

RESULT 114
AC095110/c 278311 bp DNA linear HTG 09-MAY-2003
LOCUS Rattus norvegicus clone CH230-7M3, ** SEQUENCING IN PROGRESS **
DEFINITION 6 uncloned pieces.
AC095110
VERSION AC095110.6 GI:30467662
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
    Rattus.
    1 (bases 1 to 278311)
    Muzny,D,Marle,M,Mezker,M,lee,A, Abramson,S, Adams,C, Alder,J,
    Allen,C, Allen,H, Albrooks,S, Amin,A, Angiano,D,
    Anyalebechi,V, Ayoyagi,A, Ayodeji,M, Baca,E, Baden,H,
    Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
    Biewald,K, Blair,D, Blankenburg,K, Blyth,P, Brown,M,
    Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
    Cardenas,V, Carter,K, Cavazos,I, Cessari,H, Centner,A,
    Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
    Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
    Davis,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
    Delgado,O, Denison,S, Deramo,C, Ding,Y, Dinh,H, DiVya,K,
    Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Eaves,K,
    Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
    Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
    Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
    Gebregeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W,
    Gunaratne,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,K,
    Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J,
    Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
    Hollins,B, Howells,S, Huliyk,S, Hume,J, Idlebird,D, Jackson,A,
    Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Joliver,A,

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Karpachy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C,
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Lorenshuwa,L, Louisedge,H, Lozano,R,J, Lu,X, Ma,J,
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Mangun,B, Mapua,P, Martin,K, Martin,R, Martinez,E,
Mawhinney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
Milosavljevic,A, Miner,G, Minia,E, Montemayor,J, Moore,S,
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Naokelameh,O, Okunolu,G, Olarunsaogun,A, Pal,S, Parks,K,
Paternak,S, Paul,H, Perez,A, Perez,L, Pfannkuch,C,
Pioppert,F, Polidexter,A, Popovic,D, Primus,E, Pu,L-L,
Puzos,M, Quiroz,J, Rachlin,E, Reeves,K, Regier,M,A, Reigh,R,
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Steinle,M, Strong,R, Sutton,A, Swatek,A, Taber,P, Taylor,C,
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Weinstock,G, and Gibbs,R.A.

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COMMENT

The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GCCR
Center clone name: CH230-7M3
----- Summary Statistics
Assembly program: Atlas;
Consensus quality: 241903 bases at least Q40
Consensus quality: 247369 bases at least Q30
Estimated insert size: 268229; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)

```

\* NOTE: This sequence may represent more than one clone.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 6 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 6190: contig of 6190 bp in length  
 \* 6191 6290: gap of unknown length  
 \* 6291 10708: contig of 4418 bp in length  
 \* 10709 10808: gap of unknown length  
 \* 10809 255931: contig of 246123 bp in length  
 \* 255932 257031: gap of unknown length  
 \* 257032 272937: contig of 15906 bp in length  
 \* 272938 273038: gap of unknown length  
 \* 273038 276081: contig of 3044 bp in length  
 \* 276082 276181: gap of unknown length  
 \* 276182 278311: contig of 2130 bp in length.

## FEATURES

## SOURCE

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## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 278311;  
 Best Local Similarity 85.7%; Pred. No. 99;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNNNN 18  
 Db 212784 TCCTGAGANNNNNN 212771

RESULT 115  
 AC132498 292735 bp DNA linear HTG 20-NOV-2002  
 LOCUS AC132498  
 DEFINITION Rattus norvegicus clone CH230-12L9, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 2 unordered places.  
 AC132498  
 VERSION AC132498.3 GI:25139047  
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

## REFERENCE

## AUTHORS

Rattus.  
 1 (bases 1 to 292735)

Muzny,D,Marier, Metzker,M, Lee, Abramson,S, Adams,C, Alder,J, Allen,C, Allen,H, Alsbrooks,S, Amin,A, Anguiano,D, Anyalebechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H, Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benhmed,F, Bissalio,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M, Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E, Cardenas,V, Carter,K, Cavazos,I, Caesar,H, Center,A, Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J, Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cre,A, D'Souza,L, Davila,M,L, Davis,C, Davy-Carroll,L, De Ande,C, Dederich,D, Delgado,O, Denison,S, Deramo,C, Ding,Y, Din,H, Divya,K, Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Evans,K, Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G, Fernandez,S, Finley,M, Flaggy,N, Forbes,L, Foster,M, Foster,P, Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M, Gebregergis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,M, Gunaratne,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,K, Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J, Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M, Hollins,B, Howells,S, Hui,Y,S, Hume,J, Idlebird,D, Jackson,A, Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolyet,A, Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C, Kowals,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J, Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J, Lorensuhewa,L, Louisedge,H, Lozado,R,J, Lu,X, Ma,D, Maheshwari,M, Mahindaratne,M, Mahmoud,M, Malloy,K, Mangum,A, Mangum,B, Mapa,P, Martin,K, Martin,R, Martinez,E, Mawhinney,S, McLeod,M,P, McNeill,T,Z, Meenen,E, Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S, Morgan,M, Morris,K, Morris,S, Mundaas,M, Murphy,M, Nair,L, Nankervyls,C, Neal,D, Newton,N, Nyuyen,N, Norris,S, Nwackelemehe,O, Okwoudu,G, Olarnuagsoon,A, Pal,S, Parks,K, Pasternak,S, Paul,H, Perez,A, Perez,L, Pfannkuch,C, Plopper,F, Poindexter,A, Popovic,D, Primus,E, Pu,L-L, Puazo,M, Quiroz,J, Rachlin,E, Reeves,K, Register,M,A, Reigh,R, Reilly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F, Rivers,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Rutz,S,J, Sanders,W, Savery,G, Scherer,S, Scott,G, Shatsman,S, Shen,H, Shetty,J, Shvartsbeyn,A, Sisson,I, Sitter,C,D, Smajd,D, Sneed,A, Sodergren,E, Song,X-Z, Sorelle,R, Soosa,J, Steimle,M, Strong,R, Sutou,A, Svetek,A, Taber,Z, Taylor,C, Taylor,T, Thomas,N, Thomas,S, Tingey,A, Tjofos,Z, Usmani,K, Vais,R, Vera,V, Villasana,D, Walston,L, Walker,B, Wang,J, Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,F, Williams,G, Willson,R, Wleczky,R, Wooden,H, Worley,K, Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V, Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von Niederhausern,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O, Meinstock,G, and Gibbs,R,A.

## TITLE

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## COMMENT

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Nov 20, 2002 this sequence version replaced gi:22855835.  
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

#### ----- Genome Center

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: KBXK  
Center clone name: CH230-12L9

#### ----- Summary Statistics

Assembly program: Phrap; version 0.990129  
Consensus quality: 247040 bases at least Q40  
Consensus quality: 249556 bases at least Q30  
Consensus quality: 251629 bases at least Q20  
Estimated insert size: 254147; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see <http://www.hgsc.bcm.tmc.edu/docs/genbankdraftdata.html>)  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 289860: contig of 289860 bp in length  
\* 289861 289860: gap of unknown length  
\* 289861 292735: contig of 2775 bp in length.  
Location/Qualifiers

1. 292735  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-12L9"  
1. 1218  
/notes="wgs contig"  
2438. 3924  
/note="wgs\_contig"  
288298. 289860  
/note="wgs\_contig"

#### ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 292735;  
Best Local Similarity 85.7%; Pred. NO. 98;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 UCCUGAGAGNNNNN 18  
Db 2445 TCCTGAGAGNNNNN 2432

RESULT 116  
AC097975/c  
LOCUS  
DEFINITION Rattus norvegicus clone CH230-29D22, \*\*\* SEQUENCING IN PROGRESS  
AC097975 303281 bp DNA linear HTG 10-MAY-2003  
AC097975  
\*\*\* 5 unordered pieces.  
AC097975  
VERSION AC097975.6 GI:30520737  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 303281)  
AUTHORS Muzny, D., Marie, M., Metzker, M., Lee, A., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alebrooks, S., Amin, A., Anguiano, D.,  
Ayalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
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Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,  
Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,  
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Mlosovljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S.,  
Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L.,  
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,  
Nsokeleleh, O., Okunolu, G., Olarunpasegun, A., Pal, S., Parks, K.,  
Pasternak, S., Paul, H., Perez, A., Perez, L., Plannoch, C.,  
Plopper, F., Podexter, A., Popovic, D., Primus, E., Pu, L.,  
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Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,  
Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,  
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,  
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhou, S., Dunn, D., von  
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
Weinstock, G. and Gibbs, R. A.  
Direct Submission  
TITLE  
JOURNAL  
AUTHORS  
REFERENCE  
2 (bases 1 to 303281)  
Worley, K. C.  
Direct Submission  
TITLE  
JOURNAL  
AUTHORS  
REFERENCE  
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 303281)  
Rat Genome Sequencing Consortium.  
Direct Submission  
TITLE  
JOURNAL  
AUTHORS  
REFERENCE  
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On May 10, 2003 this sequence version replaced gi:2306370.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome





Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,  
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,  
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,  
Williams, G., Wilson, R., Wleczek, R., Wood, H., Worley, K.,  
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,  
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von  
Niederhauser, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
Weinstock, G. and Gibbs, R. A.  
Direct Submission  
Unpublished  
2 (bases 1 to 303894)  
Worley, K. C.  
Direct Submission  
Submitted (10-JAN-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 303894)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Oct 9, 2002 this sequence version replaced gi:21736956.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GNM7  
Center clone name: CH230-336G16  
----- Summary Statistics  
Assembly program: Phrap, version 0.990329  
Consensus quality: 228462 bases at least Q40  
Consensus quality: 234940 bases at least Q30  
Consensus quality: 239424 bases at least Q20  
Estimated insert size: 232995; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
(see http://www.hgsc.bcm.tmc.edu/docs/genbank\_difft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 16 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 13303: contig of 13303 bp in length  
\* 13304 13403: gap of unknown length  
\* 13404 28005: contig of 14602 bp in length  
\* 28006 28106: gap of unknown length  
\* 28106 54260: contig of 26155 bp in length  
\* 54261 54360: gap of unknown length  
\* 54361 66354: contig of 11994 bp in length  
\* 66355 66454: gap of unknown length  
\* 66455 74904: contig of 8450 bp in length  
\* 74905 90386: contig of 15382 bp in length  
\* 90387 90486: gap of unknown length

90487 291741: contig of 201255 bp in length  
\* 291742 291841: gap of unknown length  
\* 291842 292873: contig of 1032 bp in length  
\* 292874 292973: gap of unknown length  
\* 292974 294062: contig of 1089 bp in length  
\* 294063 294162: gap of unknown length  
\* 294163 295422: contig of 1260 bp in length  
\* 295423 295522: gap of unknown length  
\* 295523 296705: contig of 1183 bp in length  
\* 296706 296805: gap of unknown length  
\* 296806 297824: contig of 1019 bp in length  
\* 297825 297924: gap of unknown length  
\* 297925 299158: contig of 1234 bp in length  
\* 299159 299258: gap of unknown length  
\* 299259 300609: contig of 1351 bp in length  
\* 300610 300709: gap of unknown length  
\* 300710 302210: contig of 1501 bp in length  
\* 302211 302310: gap of unknown length  
\* 302311 303894: contig of 1584 bp in length.

FEATURES  
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1. .303894  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-336G16"  
1. .1129  
/note="wgs\_end\_extension  
clone\_end:T7"  
8025. .8867  
/note="clone\_boundary  
clone\_end:T7  
site:Mbol  
end\_sequence:RXAPV44TV"  
13404. .16741  
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42706. .45474  
/note="wgs\_contig"  
48415. .50766  
/note="wgs\_contig"  
54361. .56464  
/note="wgs\_contig"  
66455. .68048  
/note="wgs\_contig"  
75005. .76092  
/note="wgs\_contig"  
76641. .78149  
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90487. .91649  
/note="wgs\_contig"  
91700. .93465  
/note="wgs\_contig"  
/complement(199710. .200620)  
/note="clone\_boundary  
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site:Mbol  
end\_sequence:RXAPV44TV"

ORIGIN  
Query Match 77.8%; Score 14; DB 2; Length 303894;  
Best Local Similarity 85.7%; Pred. No. 98;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNNNN 18  
:|||||  
Db 229336 TCCTGAGANNNNNN 229349

RESULT 118  
AX555067/c AX555067 20 bp DNA linear PAT 27-NOV-2002  
LOCUS Sequence 30 from Patent WO0233128.  
DEFINITION AX555067  
ACCESSION AX555067.1 GI:25898622  
VERSION

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. .20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="labeled oligonucleotide (probe) used to detect HCV viral load"  
misc\_feature  
1  
/note="n=FAM modified cytosine"  
misc\_feature  
20  
/note="n=TMRA modified cytosine"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 20;  
Best Local Similarity 84.6%; Pred. No. 6e+02;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAGN 13  
Db 13 GGGGCTCTGGAGN 1  
RESULT 119  
AX037216/c  
LOCUS AX037216 21 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 128 from Patent WO0056923.  
ACCESSION AX037216  
VERSION AX037216.1 GI:11226641  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 21;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGNNNNNN 18  
Db 21 CCTGGAGNNNNNN 9  
RESULT 120  
AX037233/c  
LOCUS AX037233 21 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 145 from Patent WO0056923.  
ACCESSION AX037233  
VERSION AX037233.1 GI:11226658  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/note="replacement plasmid sequence"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 21;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGNNNNNN 18  
Db 20 CCTGGAGNNNNNN 8  
RESULT 121  
AX037217  
LOCUS AX037217 27 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 129 from Patent WO0056923.  
ACCESSION AX037217  
VERSION AX037217.1 GI:11226642  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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source  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGNNNNNN 18  
Db 6 CCTGGAGNNNNNN 18  
RESULT 122  
AX037218  
LOCUS AX037218 27 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 130 from Patent WO0056923.  
ACCESSION AX037218  
VERSION AX037218.1 GI:11226643  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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source  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/note="replacement plasmid sequence"

ORIGIN

/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

## RESULT 123

LOCUS AX037219 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 131 from Patent WO0056923.  
ACCESSION AX037219  
VERSION AX037219.1 GI:11226644  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 131 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)

FEATURES  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

RESULT 124  
LOCUS AX037220 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 132 from Patent WO0056923.  
ACCESSION AX037220  
VERSION AX037220.1 GI:11226645  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 132 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)

FEATURES  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18

Db ||:|||||  
6 CCTGAGAGNNNNNN 18

RESULT 125  
LOCUS AX037221 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 133 from Patent WO0056923.  
ACCESSION AX037221  
VERSION AX037221.1 GI:11226646  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 133 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)

FEATURES  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

RESULT 126  
LOCUS AX037222 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 134 from Patent WO0056923.  
ACCESSION AX037222  
VERSION AX037222.1 GI:11226647  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 134 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)

FEATURES  
source 1..27  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

RESULT 127  
LOCUS AX037223 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 135 from Patent WO0056923.  
ACCESSION AX037223

VERSION AX037223.1 GI:11226648  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Patent: WO 0056923-A 135 28-SEP-2000;  
JOURNAL SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source  
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/note="replacement plasmid sequence"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Gaps 0;  
Matches 12; Conservative 1; Indels 0;  
QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18  
Db  
RESULT 128  
AX037224 27 bp DNA linear PAT 16-NOV-2000  
LOCUS AX037224  
DEFINITION Sequence 136 from Patent WO0056923.  
ACCESSION AX037224  
VERSION AX037224.1 GI:11226649  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 136 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
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/note="replacement plasmid sequence"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Gaps 0;  
Matches 12; Conservative 1; Indels 0;  
QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18  
Db  
RESULT 129  
AX037225 27 bp DNA linear PAT 16-NOV-2000  
LOCUS AX037225  
DEFINITION Sequence 137 from Patent WO0056923.  
ACCESSION AX037225  
VERSION AX037225.1 GI:11226650  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 137 28-SEP-2000;

FEATURES  
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/organism="synthetic construct"  
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ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Gaps 0;  
Matches 12; Conservative 1; Indels 0;  
QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18  
Db  
RESULT 130  
AX037226 27 bp DNA linear PAT 16-NOV-2000  
LOCUS AX037226  
DEFINITION Sequence 138 from Patent WO0056923.  
ACCESSION AX037226  
VERSION AX037226.1 GI:11226651  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 138 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
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/note="replacement plasmid sequence"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Gaps 0;  
Matches 12; Conservative 1; Indels 0;  
QY 6 CCUGAGAGNNNNNN 18  
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6 CCTGAGAGNNNNNN 18  
Db  
RESULT 131  
AX037227 27 bp DNA linear PAT 16-NOV-2000  
LOCUS AX037227  
DEFINITION Sequence 139 from Patent WO0056923.  
ACCESSION AX037227  
VERSION AX037227.1 GI:11226652  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 139 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source  
1. .27  
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/note="replacement plasmid sequence"  
ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db

RESULT 132  
AX037228 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 140 from Patent WO0056923.  
AX037228  
ACCESSION  
VERSION AX037228.1 GI:11226653  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db

RESULT 133  
AX037229 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 141 from Patent WO0056923.  
AX037229  
ACCESSION  
VERSION AX037229.1 GI:11226654  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db

RESULT 134  
AX037230 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 142 from Patent WO0056923.  
AX037230  
ACCESSION  
VERSION AX037230.1 GI:11226655  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db

RESULT 135  
AX037231 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 143 from Patent WO0056923.  
AX037231  
ACCESSION  
VERSION AX037231.1 GI:11226656  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
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/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db

RESULT 136  
AX037232 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 144 from Patent WO0056923.  
AX037232  
ACCESSION  
VERSION AX037232.1 GI:11226657  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db

RESULT 137  
AX037233 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 145 from Patent WO0056923.  
AX037233  
ACCESSION  
VERSION AX037233.1 GI:11226658  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db

REFERENCE 1 other sequences; artificial sequences.

AUTHORS Sibson, R.

TITLE Genetic analysis

JOURNAL Patent: WO 0056923-A 144 28-SEP-2000;

FEATURES

source

1. .27

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;

Best Local Similarity 92.3%; Pred. No. 6e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNNN 18

Db 6 CCTGAGAGNNNNNN 18

RESULT 137

LOCUS G06767

DEFINITION human STS WI-7926, sequence tagged site.

ACCESSION G06767

VERSION G06767.1 GI:860012

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 761)

AUTHORS Hudson, T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically

JOURNAL Mapped ESTs

COMMENT Unpublished (1995)

Contact: Thomas Hudson

Whitehead Institute/MIT Center for Genome Research

Whitehead Institute for Biomedical Research

9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: CATTCGCATCTGTCACCG

Primer B: CCTCCCTCAAAATGAAACCG

STS size: 347

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from U09368 -- UniGene.

Location/Qualifiers

source

1. .761

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/map="745\_H\_9; 782\_H\_9; 903\_F\_7; 807\_G\_12"

STS 364. .710

primer\_bind 364. .382

primer\_bind complement(690. .710)

ORIGIN

Query Match 72.2%; Score 13; DB 11; Length 761;

Best Local Similarity 92.3%; Pred. No. 5.3e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNNN 18

Db 142 CCTGAGAGNNNNNN 154

RESULT 138

LOCUS BD021433/c

DEFINITION Novel gene and novel gene fragment cloned in human neuroblastoma.

ACCESSION BD021433

VERSION BD021433.1 GI:22562656

KEYWORDS JP 2001245671-A/3671.

SOURCE JP 2001245671-A/3671.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 784)

AUTHORS Nakagawara, A.

TITLE Novel gene and novel gene fragment cloned in human neuroblastoma

JOURNAL Patent: JP 2001245671-A 3671 11-SEP-2001;

CHIBA PREP. HISAMITSU PHARMACEUTICAL CO INC

COMMENT OS Homo sapiens (human)

PN JP 2001245671-A/3671

PD 11-SEP-2001

PF 07-MAR-2000 JP 2000159195

PI AKIRA NAKAGAWARA

PC C12N15/09, C12Q1/68, G01N33/53, G01N33/566//C12Q1/68, C12R1:91,

PC C12N15/00

CC Novel gene and novel gene fragment cloned in human CC

neuroblastoma

FN Key

FT source

Location/Qualifiers

1. .784

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/db\_xref="taxon:9606"

FEATURES

source

Location/Qualifiers

1. .784

/organism="Homo sapiens (human)"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 784;

Best Local Similarity 84.6%; Pred. No. 5.3e+02;

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGAGAGN 13

Db 570 GGGGTCCTGAGAGN 558

RESULT 139

LOCUS BD101371/c

DEFINITION Novel genes cloned in humanneuroblastoma and fragments thereof.

ACCESSION BD101371

VERSION BD101371.1 GI:22646945

KEYWORDS WO 0166719-A/3671.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 784)  
 AUTHORS Nakagawara, A.  
 TITLE Novel genes cloned in humanneuroblastoma and fragments thereof  
 JOURNAL Patent: WO 0166719-A 3671 13-SEP-2001;  
 COMMENT CHIBA PREF, HISAMITSU PHARMACEUTICAL CO INC, AKIRA NAKAGAWARA  
 OS Homo sapiens (human)  
 PN WO 0166719-A/3671  
 PD 13-SEP-2001  
 PF 02-MAR-2001 WO 2001JP001629  
 PR 07-MAR-2000 JP 00P 159195  
 PI AKIRA NAKAGAWARA  
 PC C12N15/11.C1201/68.G01N33/53.G01N33/566  
 CC Novel genes cloned in humanneuroblastoma and fragments thereof  
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ORIGIN  
 Query Match 72.2% Score 13; DB 6; Length 784;  
 Best Local Similarity 84.6%; Pred. No. 5.3e+02;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAGN 13  
 |||||  
 570 GGGGCTCTGGAGN 558

Db

RESULT 140  
 LOCUS AC015491 30040 bp DNA linear HTG 13-JUL-2000  
 DEFINITION Homo sapiens clone RP11-20L18, LOW-PASS SEQUENCE SAMPLING.  
 AC015491  
 AC015491.2 GI:9123963  
 VERSION  
 KEYWORDS HTG; HTGS\_PHASE0.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 30040)  
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 Homo sapiens, clone RP11-20L18  
 Unpublished  
 2 (bases 1 to 30040)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baldwin, J., Barina, N., Becker, R., Boguslavsky, L., Boukhalter, B.,  
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
 Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
 Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,  
 Galagan, J., Gardina, S., Grant, G., Hago, B., Headford, A., Horton, L.,  
 Howland, J., Johnson, R., Jones, C., Kann, L., Karst, A., Klein, J.,  
 Lebeck, J., Liu, C., Locke, K., Macdonald, P., Marquis, N.,  
 McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
 Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Tesfaye, S., Tirelli, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
 Wyman, D., Ye, W., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jul 13, 2000 this sequence version replaced gi:6437626.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WtBR

Web site: <http://www-geq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 Project Information  
 Center Project name: L3925  
 Center clone name: 20\_L\_18

NOTE: This record contains 33 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.

1 824 823: contig of 823 bp in length  
 924 923: gap of 100 bp  
 1774 1773: contig of 850 bp in length  
 1874 1873: gap of 100 bp  
 2677 2677: contig of 804 bp in length  
 2678 2777: gap of 100 bp  
 2778 3578: contig of 801 bp in length  
 3579 3678: gap of 100 bp  
 3679 4455: contig of 778 bp in length  
 4457 4556: gap of 100 bp  
 4557 5338: contig of 782 bp in length  
 5339 5438: gap of 100 bp  
 5439 6230: contig of 792 bp in length  
 6231 6330: gap of 100 bp  
 6331 7128: contig of 793 bp in length  
 7130 7229: gap of 100 bp  
 7230 8035: contig of 806 bp in length  
 8036 8135: gap of 100 bp  
 8136 8973: contig of 838 bp in length  
 8974 9073: gap of 100 bp  
 9074 9888: contig of 816 bp in length  
 9890 9989: gap of 100 bp  
 9990 10826: contig of 837 bp in length  
 10827 10926: gap of 100 bp  
 10927 11716: contig of 790 bp in length  
 11717 11816: gap of 100 bp  
 11817 12671: contig of 855 bp in length  
 12672 12771: gap of 100 bp  
 12772 13593: contig of 822 bp in length  
 13594 13693: gap of 100 bp  
 13694 14493: contig of 800 bp in length  
 14494 14593: gap of 100 bp  
 14594 15387: contig of 794 bp in length  
 15388 15487: gap of 100 bp  
 15488 16316: contig of 829 bp in length  
 16317 16416: gap of 100 bp  
 16417 17235: contig of 819 bp in length  
 17236 17335: gap of 100 bp  
 17336 18142: contig of 807 bp in length  
 18143 18242: gap of 100 bp  
 18243 19042: contig of 800 bp in length  
 19043 19142: gap of 100 bp  
 19143 19934: contig of 792 bp in length  
 19935 20034: gap of 100 bp  
 20035 20880: contig of 846 bp in length  
 20881 20980: gap of 100 bp  
 20981 21835: contig of 855 bp in length  
 21836 21935: gap of 100 bp  
 21936 22747: contig of 812 bp in length  
 22748 22847: gap of 100 bp  
 22848 23670: contig of 823 bp in length  
 23671 23770: gap of 100 bp  
 23771 24552: contig of 782 bp in length  
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 25484 25583: gap of 100 bp

```

* 25584 26411: contig of 828 bp in length
* 26412 26511: gap of 100 bp
* 26512 27324: contig of 813 bp in length
* 27325 27424: gap of 100 bp
* 27425 28242: contig of 818 bp in length
* 28243 28343: gap of 100 bp
* 28343 29183: contig of 841 bp in length
* 29184 29283: gap of 100 bp
* 29284 30040: contig of 757 bp in length.
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        source          1. 30040
        organism="Homo sapiens"
        mol_type="genomic DNA"
        db_xref="taxon:9606"
        clone="RP11-20L18"
        clone_11b="RP11-11 Human Male BAC"

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ORIGIN
Query Match      72.2%; Score 13; DB 2; Length 30040;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      6 CCUGAGAGNNNNNN 18
      ||:|||||
Db      24546 CCTGAGAGNNNNNN 24558

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RESULT 141
AC025943/c      41107 bp DNA linear HTG 17-MAR-2000
LOCUS
DEFINITION
Homo sapiens chromosome 19 clone RP11-747B8 map 19, LOW-PASS
SEQUENCE SAMPLING.
AC025943
AC025943.1 GI:7259784
HTG; HTGS_PHASE0.

```

```

KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

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REFERENCE
1 (bases 1 to 41107)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Boguslavsky,L., Bouckgealter,B., Brown,A., Burkett,G.,
Campiano,A., Castle,A., Choquet,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goylete,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczký,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Margus,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mienna,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pletzer,N.,
Pisanu,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wymann,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

```

```

TITLE
JOURNAL
COMMENT
Submitted (17-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research

```

```

Center code: W1B8
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: 18601
Center clone name: 747_B_8

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* NOTE: This record contains 46 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

```

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1 794 793: contig of 793 bp in length
* 794 893: gap of 100 bp
* 894 1694: contig of 801 bp in length
* 1695 1794: gap of 100 bp
* 1795 2585: contig of 791 bp in length
* 2586 2686: gap of 100 bp
* 2686 3498: contig of 813 bp in length
* 3499 3598: gap of 100 bp
* 3599 4391: contig of 793 bp in length
* 4392 4491: gap of 100 bp
* 4492 5285: contig of 794 bp in length
* 5286 5385: gap of 100 bp
* 5386 6184: contig of 799 bp in length
* 6185 6284: gap of 100 bp
* 6285 7082: contig of 798 bp in length
* 7083 7182: gap of 100 bp
* 7183 7974: contig of 792 bp in length
* 7975 8074: gap of 100 bp
* 8075 8875: contig of 801 bp in length
* 8876 8975: gap of 100 bp
* 8976 9771: contig of 796 bp in length
* 9772 9871: gap of 100 bp
* 9872 10651: contig of 780 bp in length
* 10652 10751: gap of 100 bp
* 10752 11525: contig of 774 bp in length
* 11526 11625: gap of 100 bp
* 11626 12423: contig of 798 bp in length
* 12424 12523: gap of 100 bp
* 12524 13340: contig of 817 bp in length
* 13341 13441: gap of 100 bp
* 13441 14247: contig of 807 bp in length
* 14248 14347: gap of 100 bp
* 14348 15153: contig of 806 bp in length
* 15154 15253: gap of 100 bp
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* 16061 16160: gap of 100 bp
* 16161 16960: contig of 800 bp in length
* 16961 17060: gap of 100 bp
* 17061 17860: contig of 800 bp in length
* 17861 17960: gap of 100 bp
* 17961 18723: contig of 763 bp in length
* 18724 18823: gap of 100 bp
* 18824 19616: contig of 793 bp in length
* 19617 19716: gap of 100 bp
* 19717 20503: contig of 787 bp in length
* 20504 20603: gap of 100 bp
* 20604 21404: contig of 801 bp in length
* 21405 21504: gap of 100 bp
* 21505 22295: contig of 791 bp in length
* 22296 22395: gap of 100 bp
* 22396 23187: contig of 792 bp in length
* 23188 23287: gap of 100 bp
* 23288 24072: contig of 785 bp in length
* 24073 24172: gap of 100 bp
* 24173 24975: contig of 803 bp in length

```



```

* 24976 25075: gap of 100 bp
* 25076 25075: contig of 779 bp in length
* 25855 25954: gap of 100 bp
* 25955 26764: contig of 810 bp in length
* 26765 26864: gap of 100 bp
* 26865 27657: contig of 793 bp in length
* 27658 27757: gap of 100 bp
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* 30330 30429: gap of 100 bp
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* 32122 32222: gap of 100 bp
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* 33111 33906: contig of 796 bp in length
* 33907 34006: gap of 100 bp
* 34007 34810: contig of 804 bp in length
* 34811 34910: gap of 100 bp
* 34911 35696: contig of 786 bp in length
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* 35797 36594: contig of 798 bp in length
* 36595 36694: gap of 100 bp
* 36695 37498: contig of 804 bp in length
* 37499 37598: gap of 100 bp
* 37599 38406: contig of 807 bp in length
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* 39403 40197: contig of 797 bp in length
* 40198 40297: gap of 100 bp
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FEATURES  
source

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## ORIGIN

Query Match 72.2%; Score 13; DB 2; Length 41107;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
Db 17967 CCTGAGAGNNNNNN 17955

RESULT 142  
AC087168  
LOCUS  
DEFINITION Homo sapiens chromosome 8 clone RP11-235A15 map 8, LOW-PASS  
SEQUENCE SAMPLING.  
AC087168 45685 bp DNA linear HTG 11-DEC-2000  
AC087168  
VERSION  
KEYWORDS  
SOURCE HTG; HTGS\_PHASED.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 45685)  
AUTHORS Birren,B., Lincon,L., Nusbaum,C. and Lander,E.  
TITLE Homo sapiens chromosome 8, clone RP11-235A15  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 45685)

## AUTHORS

## COMMENT

Birren,B., Lincon,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,  
Barna,N., Bastien,V., Boguslavsky,L., Bouhagalter,B., Brown,A.,  
Camarta,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,  
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J.,  
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-pretre,N.,  
Hagos,B., Haefford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
Jones,C., Karatas,A., Labocque,K., Lamaszates,R., Landere,T.,  
Lenocky,J., Levine,R., Liu,G., Maclean,C., Macdonald,P.,  
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,  
McPheters,R., Meldrim,J., Meneses,L., Mihova,T., Mlenga,V.,  
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,  
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,  
Phunhkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,  
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetli,M.,  
Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P.,  
Sougnuez,C., Spencer,B., Strange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Teffaye,S., Theodore,J.,  
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,  
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,  
Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (11-DEC-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L11603  
Center clone name: 235\_A\_15  
-----  
\* NOTE: This record contains 59 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\* 1 646: contig of 646 bp in length  
\* 647 746: gap of 100 bp  
\* 747 1427: contig of 681 bp in length  
\* 1428 1527: gap of 100 bp  
\* 1528 2207: contig of 680 bp in length  
\* 2208 2307: gap of 100 bp  
\* 2308 2967: contig of 660 bp in length  
\* 2968 3067: gap of 100 bp  
\* 3068 3733: contig of 666 bp in length  
\* 3734 3833: gap of 100 bp  
\* 3834 4516: contig of 683 bp in length  
\* 4517 4616: gap of 100 bp  
\* 4617 5302: contig of 686 bp in length  
\* 5303 5403: gap of 100 bp  
\* 5403 6078: contig of 676 bp in length  
\* 6079 6178: gap of 100 bp  
\* 6179 6833: contig of 655 bp in length  
\* 6834 6933: gap of 100 bp  
\* 6934 7611: contig of 678 bp in length  
\* 7612 7711: gap of 100 bp  
\* 7712 8394: contig of 683 bp in length  
\* 8395 8494: gap of 100 bp  
\* 8495 9173: contig of 679 bp in length  
\* 9174 9273: gap of 100 bp  
\* 9274 9953: contig of 680 bp in length  
\* 9954 10053: gap of 100 bp

```

* 10054 10696: contig of 643 bp in length
* 10697 10796: gap of 100 bp
* 10797 11481: contig of 685 bp in length
* 11482 11581: gap of 100 bp
* 11582 12248: contig of 667 bp in length
* 12249 12348: gap of 100 bp
* 12349 13016: contig of 668 bp in length
* 13017 13116: gap of 100 bp
* 13117 13797: contig of 681 bp in length
* 13798 13897: gap of 100 bp
* 13898 14562: contig of 665 bp in length
* 14563 15346: contig of 684 bp in length
* 15347 15446: gap of 100 bp
* 15447 16107: contig of 661 bp in length
* 16108 16207: gap of 100 bp
* 16208 16903: contig of 696 bp in length
* 16904 17003: gap of 100 bp
* 17004 17692: contig of 689 bp in length
* 17693 17793: gap of 100 bp
* 17793 18457: contig of 665 bp in length
* 18458 18557: gap of 100 bp
* 18558 19228: contig of 671 bp in length
* 19229 19328: gap of 100 bp
* 19329 19996: contig of 668 bp in length
* 19997 20096: gap of 100 bp
* 20097 20764: contig of 668 bp in length
* 20765 20864: gap of 100 bp
* 20865 21545: contig of 681 bp in length
* 21546 21645: gap of 100 bp
* 21646 22342: contig of 697 bp in length
* 22343 22442: gap of 100 bp
* 22443 23098: contig of 656 bp in length
* 23099 23198: gap of 100 bp
* 23199 23903: contig of 705 bp in length
* 23904 24003: gap of 100 bp
* 24004 24661: contig of 658 bp in length
* 24662 25441: gap of 100 bp
* 25442 25541: gap of 100 bp
* 25542 26208: contig of 667 bp in length
* 26209 26308: gap of 100 bp
* 26309 26979: contig of 671 bp in length
* 26980 27079: gap of 100 bp
* 27080 27759: contig of 680 bp in length
* 27760 27859: gap of 100 bp
* 27860 28558: contig of 699 bp in length
* 28559 28658: gap of 100 bp
* 28659 29326: contig of 668 bp in length
* 29327 29426: gap of 100 bp
* 29427 30122: contig of 696 bp in length
* 30123 30223: gap of 100 bp
* 30223 30886: contig of 664 bp in length
* 30887 30986: gap of 100 bp
* 30987 31662: contig of 676 bp in length
* 31663 31762: gap of 100 bp
* 31763 32453: contig of 691 bp in length
* 32454 32553: gap of 100 bp
* 32554 33238: contig of 685 bp in length
* 33239 33338: gap of 100 bp
* 33339 34006: contig of 668 bp in length
* 34007 34106: gap of 100 bp
* 34107 34807: contig of 701 bp in length
* 34808 34907: gap of 100 bp
* 34908 35556: contig of 649 bp in length
* 35557 35656: gap of 100 bp
* 35657 36343: contig of 687 bp in length
* 36344 36443: gap of 100 bp
* 36444 37080: contig of 637 bp in length
* 37081 37180: gap of 100 bp
* 37181 37854: contig of 674 bp in length
* 37855 37954: gap of 100 bp
* 37955 38646: contig of 692 bp in length

```

## FEATURES

## Source

```

* 38647 38746: gap of 100 bp
* 38747 39458: contig of 712 bp in length
* 39459 39558: gap of 100 bp
* 39559 40253: contig of 695 bp in length
* 40254 40353: gap of 100 bp
* 40354 41023: contig of 670 bp in length
* 41024 41123: gap of 100 bp
* 41124 41790: contig of 667 bp in length
* 41791 41890: gap of 100 bp
* 41891 42558: contig of 668 bp in length
* 42559 42658: gap of 100 bp
* 42659 43331: contig of 673 bp in length
* 43332 43431: gap of 100 bp
* 43432 44126: contig of 695 bp in length
* 44127 44226: gap of 100 bp
* 44227 44892: contig of 666 bp in length
* 44893 44992: gap of 100 bp
* 44993 45685: contig of 693 bp in length.

```

Location/Qualifiers

## ORIGIN

## Query Match

Best local similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## QY

## Db

6 CCUGAGANNNNN 18  
1421 CCTGAGANNNNN 1433

## RESULT 143

## CER08A5

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

CER08A5 51920 bp DNA linear HTG 14-OCT-1998  
Caenorhabditis elegans chromosome V clone ROB45, \*\*\* SEQUENCING IN  
PROGRESS \*\*\*, 15 unordered pieces.  
282281  
282281.1 GI:3377979  
HTG; HTGS PHASE1.  
Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida;  
Rhabdilitida; Rhabdilitidae; Peioderinae; Caenorhabditis.  
1 (bases 1 to 51920)  
Sulston, J.  
Direct Submission  
Submitted (14-OCT-1998) Nematode Sequencing Project, Sanger Centre,  
Hinxton, Cambridge CB10 1RO, UK and Department of Genetics,  
Washington University, St. Louis, MO 63110, USA. E-mail:  
jesse.sanger@wustl.edu  
On Aug 3, 1998 this sequence version replaced gi:166615.  
IMPORTANT: This sequence is unfinished and does not necessarily  
represent the correct sequence. Work on the sequence is in progress  
and the release of this data is based on the understanding that the  
sequence may change as work continues. The sequence may be  
contaminated with foreign sequence from E.coli, yeast, vector,  
phage etc. Order of segments is not known; 800 n's separate  
segments.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 15 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 2711: contig of 2711 bp in length  
\* 2712 3511: gap of 800 bp  
\* 3512 6616: contig of 3105 bp in length  
\* 6617 7416: gap of 800 bp  
\* 7417 11750: contig of 4334 bp in length  
\* 11751 12550: gap of 800 bp  
\* 12551 13852: contig of 1302 bp in length  
\* 13853 14652: gap of 800 bp  
\* 14653 16018: contig of 1366 bp in length  
\* 16019 16818: gap of 800 bp  
\* 16819 21109: contig of 4291 bp in length  
\* 21110 21909: gap of 800 bp  
\* 21910 23528: contig of 1619 bp in length  
\* 23529 24328: gap of 800 bp  
\* 24329 27047: contig of 2719 bp in length  
\* 27048 27847: gap of 800 bp  
\* 27848 31484: contig of 3637 bp in length  
\* 31485 32285: gap of 800 bp  
\* 32285 34192: contig of 1908 bp in length  
\* 34193 34992: gap of 800 bp  
\* 34993 36387: contig of 1395 bp in length  
\* 36388 37187: gap of 800 bp  
\* 37188 42955: contig of 5768 bp in length  
\* 42956 43755: gap of 800 bp  
\* 43756 46806: contig of 3051 bp in length  
\* 46807 47607: gap of 800 bp  
\* 47607 49371: contig of 1764 bp in length  
\* 49371 50170: gap of 800 bp  
\* 50171 51920: contig of 1750 bp in length.  
\* Location/Qualifiers  
1. 51920  
/organism="Caenorhabditis elegans"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:6239"  
/chromosome="V"  
/clone="R08A5"

ORIGIN  
Query Match 72.2%; Score 13; DB 2; Length 51920;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGNNNNNN 18  
DB 11744 CCTGAGNNNNNN 11756

RESULT 144  
AC021293 52867 bp DNA linear HTG 13-JUL-2000  
LOCUS AC021293  
DEFINITION Homo sapiens clone RP11-22P22, LOW-PASS SEQUENCE SAMPLING.  
AC021293  
AC021293.2 GI:9124425  
VERSION HTG: HTGS PHASED.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 52867)  
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
TITLE Homo sapiens clone RP11-22P22  
JOURNAL Unpublished  
2 (bases 1 to 52867)  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,  
Boguslavsky, J., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,  
Chenopel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
DeArtilano, K., Dewar, K., Domino, M., Doyle, M., Fenescor, J.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,  
Gardyna, S., Grant, G., Hagos, B., Heatford, A., Horton, L.,  
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,  
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,

TITLE  
JOURNAL  
COMMENT  
McPheters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,  
Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,  
Pierie, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,  
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Subramanian, A., Talamas, J., Teeffaye, S., Theodore, J.,  
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,  
Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6705813.  
All repeats were identified using RepeatMasker:  
Smit, A. F. A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: U4158  
Center clone name: 22\_P\_22  
-----  
\* NOTE: This record contains 52 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1 889: contig of 889 bp in length  
\* 890 989: gap of 100 bp  
\* 990 1904: contig of 915 bp in length  
\* 1905 2004: gap of 100 bp  
\* 2005 2937: contig of 933 bp in length  
\* 2938 3037: gap of 100 bp  
\* 3038 3968: contig of 931 bp in length  
\* 3969 4068: gap of 100 bp  
\* 4069 4973: contig of 905 bp in length  
\* 4974 5073: gap of 100 bp  
\* 5074 5952: contig of 879 bp in length  
\* 5953 6052: gap of 100 bp  
\* 6053 6964: contig of 912 bp in length  
\* 6965 7064: gap of 100 bp  
\* 7065 7950: contig of 886 bp in length  
\* 7951 8050: gap of 100 bp  
\* 8051 8972: contig of 922 bp in length  
\* 8973 9072: gap of 100 bp  
\* 9073 9990: contig of 918 bp in length  
\* 9991 10090: gap of 100 bp  
\* 10091 11026: contig of 936 bp in length  
\* 11027 11126: gap of 100 bp  
\* 11127 12048: contig of 922 bp in length  
\* 12049 12148: gap of 100 bp  
\* 12149 13075: contig of 927 bp in length  
\* 13076 13175: gap of 100 bp  
\* 13176 14102: contig of 927 bp in length  
\* 14103 14202: gap of 100 bp  
\* 14203 15114: contig of 912 bp in length  
\* 15115 15214: gap of 100 bp  
\* 15215 16129: contig of 915 bp in length  
\* 16130 16229: gap of 100 bp  
\* 16230 17164: contig of 935 bp in length  
\* 17165 17264: gap of 100 bp  
\* 17265 18204: contig of 940 bp in length  
\* 18205 18304: gap of 100 bp  
\* 18305 19263: contig of 959 bp in length  
\* 19264 19363: gap of 100 bp  
\* 19364 20281: contig of 918 bp in length

```

* 20282 20381: gap of 100 bp
* 20382 21319: contig of 938 bp in length
* 21320 21419: gap of 100 bp
* 21420 22349: contig of 930 bp in length
* 22350 22449: gap of 100 bp
* 22450 23345: contig of 896 bp in length
* 23346 23445: gap of 100 bp
* 23446 24328: contig of 883 bp in length
* 24329 24428: gap of 100 bp
* 24429 25347: contig of 919 bp in length
* 25348 25447: gap of 100 bp
* 25448 26374: contig of 927 bp in length
* 26375 26475: gap of 100 bp
* 26476 27388: contig of 914 bp in length
* 27389 27488: gap of 100 bp
* 27489 28387: contig of 899 bp in length
* 28388 28487: gap of 100 bp
* 28488 29423: contig of 936 bp in length
* 29424 29523: gap of 100 bp
* 29524 30436: contig of 913 bp in length
* 30437 30536: gap of 100 bp
* 30537 31494: contig of 958 bp in length
* 31495 31594: gap of 100 bp
* 31595 32508: contig of 914 bp in length
* 32509 32608: gap of 100 bp
* 32609 33513: contig of 905 bp in length
* 33514 33613: gap of 100 bp
* 33614 34564: contig of 951 bp in length
* 34565 34664: gap of 100 bp
* 34665 35573: contig of 909 bp in length
* 35574 35673: gap of 100 bp
* 35674 36594: contig of 921 bp in length
* 36595 36694: gap of 100 bp
* 36695 37703: contig of 1009 bp in length
* 37704 37803: gap of 100 bp
* 37804 38708: contig of 905 bp in length
* 38709 38808: gap of 100 bp
* 38809 39716: contig of 908 bp in length
* 39717 39816: gap of 100 bp
* 39817 40706: contig of 890 bp in length
* 40707 40806: gap of 100 bp
* 40807 41719: contig of 913 bp in length
* 41720 41819: gap of 100 bp
* 41820 42728: contig of 909 bp in length
* 42729 42828: gap of 100 bp
* 42830 43735: contig of 908 bp in length
* 43737 43836: gap of 100 bp
* 43837 44736: contig of 900 bp in length
* 44737 44836: gap of 100 bp
* 44837 45735: contig of 899 bp in length
* 45736 45835: gap of 100 bp
* 45836 46756: contig of 921 bp in length
* 46757 46856: gap of 100 bp
* 46857 47772: contig of 916 bp in length
* 47773 47872: gap of 100 bp
* 47873 48791: contig of 919 bp in length
* 48792 48891: gap of 100 bp
* 48892 49773: contig of 882 bp in length
* 49774 49873: gap of 100 bp
* 49874 50784: contig of 911 bp in length
* 50785 50884: gap of 100 bp
* 50885 51843: contig of 959 bp in length
* 51844 51943: gap of 100 bp
* 51944 52867: contig of 924 bp in length.

```

## FEATURES

```

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  /db_xref="taxon:9606"
  /clone="RP11-22P22"
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## ORIGIN

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Query Match      72.2%; Score 13; DB 2; Length 52867;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      6 CCGGAGNNNNNN 18
Db      1898 CCGGAGNNNNNN 1910

RESULT 145
AC111183
LOCUS      Homo sapiens chromosome 17 clone RP11-958E8 map 17, LOW-PASS
DEFINITION
AC111183
VERSION    AC111183.1 GI:18699948
KEYWORDS   HTG; HTGS PHASE0.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
            1 (bases 1 to 56611)
REFERENCE  1
            Birren, B., Linton, L., Nussbaum, C. and Lander, E.
            Homo sapiens chromosome 17, clone RP11-958E8
            Unpublished
            2 (bases 1 to 56611)
REFERENCE  2
            Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
            Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,
            Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
            Choquel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,
            Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S.,
            Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S.,
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            Kamat, A., Karatas, A., Kelle, C., LaRoque, K., Lamazares, R.,
            Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
            MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,
            McEwan, P., McKernan, K., Melchior, J., Menus, L., Minova, T.,
            Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
            Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
            Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
            Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
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            Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
            Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J.,
            Topham, K., Travers, M., Travis, N., Triggillo, J., Vasiliiev, H.,
            Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
            Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
            Direct Submission
            Submitted (18-FEB-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            All repeats were identified using RepeatMasker:
            http://ftp.genome.washington.edu/RM/RepeatMasker.html

-- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L25445
Center clone name: 958_E_8

* NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will

```

\* be preserved.  
1 699: contig of 699 bp in length  
700 799: gap of 100 bp  
800 1487: contig of 688 bp in length  
1488 1587: gap of 100 bp  
1588 2276: contig of 689 bp in length  
2277 2376: gap of 100 bp  
2377 3084: contig of 708 bp in length  
3085 3184: gap of 100 bp  
3185 3890: contig of 706 bp in length  
3891 4696: contig of 706 bp in length  
4697 4796: gap of 100 bp  
4797 5508: contig of 712 bp in length  
5509 5608: gap of 100 bp  
5609 6307: contig of 699 bp in length  
6308 6407: gap of 100 bp  
6408 7111: contig of 704 bp in length  
7112 7211: gap of 100 bp  
7212 7923: contig of 712 bp in length  
7924 8023: gap of 100 bp  
8024 8725: contig of 702 bp in length  
8726 8825: gap of 100 bp  
8826 9534: contig of 709 bp in length  
9535 9634: gap of 100 bp  
9635 10350: contig of 716 bp in length  
10351 10450: gap of 100 bp  
10451 11147: contig of 697 bp in length  
11148 11247: gap of 100 bp  
11248 11947: contig of 700 bp in length  
11948 12047: gap of 100 bp  
12048 12725: contig of 678 bp in length  
12726 12825: gap of 100 bp  
12826 13545: contig of 720 bp in length  
13546 13645: gap of 100 bp  
13646 14346: contig of 701 bp in length  
14347 14446: gap of 100 bp  
14447 15146: contig of 700 bp in length  
15147 15246: gap of 100 bp  
15247 15945: contig of 699 bp in length  
15946 16045: gap of 100 bp  
16046 16731: contig of 686 bp in length  
16732 17536: contig of 705 bp in length  
17537 17636: gap of 100 bp  
17637 18336: contig of 700 bp in length  
18337 18436: gap of 100 bp  
18437 19114: contig of 678 bp in length  
19115 19214: gap of 100 bp  
19215 19913: contig of 695 bp in length  
19914 20013: gap of 100 bp  
20014 20686: contig of 673 bp in length  
20687 20786: gap of 100 bp  
20787 21497: contig of 711 bp in length  
21498 21597: gap of 100 bp  
21598 22267: contig of 670 bp in length  
22268 22367: gap of 100 bp  
22368 23059: contig of 692 bp in length  
23059 23159: gap of 100 bp  
23160 23864: contig of 705 bp in length  
23865 23964: gap of 100 bp  
23965 24667: contig of 703 bp in length  
24667 24767: gap of 100 bp  
24768 25484: contig of 717 bp in length  
25485 25584: gap of 100 bp  
25585 26272: contig of 688 bp in length  
26273 26372: gap of 100 bp  
26373 27068: contig of 696 bp in length  
27069 27168: gap of 100 bp  
27169 27870: contig of 702 bp in length  
27871 27970: gap of 100 bp  
27971 28677: contig of 707 bp in length  
28678 28777: gap of 100 bp

\* 28778 29479: contig of 702 bp in length  
29480 29579: gap of 100 bp  
29580 30274: contig of 695 bp in length  
30275 30374: gap of 100 bp  
30375 31083: contig of 709 bp in length  
31084 31183: gap of 100 bp  
31184 31884: contig of 701 bp in length  
31885 31984: gap of 100 bp  
31985 32686: contig of 702 bp in length  
32687 32786: gap of 100 bp  
32787 33501: contig of 714 bp in length  
33501 33601: gap of 100 bp  
33601 34307: contig of 707 bp in length  
34308 34407: gap of 100 bp  
34408 35097: contig of 690 bp in length  
35098 35197: gap of 100 bp  
35198 35899: contig of 702 bp in length  
35900 35999: gap of 100 bp  
36000 36692: contig of 693 bp in length  
36693 36792: gap of 100 bp  
36793 37491: contig of 699 bp in length  
37492 37591: gap of 100 bp  
37592 38278: contig of 687 bp in length  
38279 38378: gap of 100 bp  
38379 39078: contig of 700 bp in length  
39079 39178: gap of 100 bp  
39179 39869: contig of 691 bp in length  
39870 40668: contig of 699 bp in length  
40669 40768: gap of 100 bp  
40769 41473: contig of 705 bp in length  
41474 41573: gap of 100 bp  
41574 42247: contig of 674 bp in length  
42248 42347: gap of 100 bp  
42348 43052: contig of 705 bp in length  
43053 43152: gap of 100 bp  
43153 43850: contig of 698 bp in length  
43851 43950: gap of 100 bp  
43951 44650: contig of 700 bp in length  
44651 44750: gap of 100 bp  
44751 45440: contig of 690 bp in length  
45441 45540: gap of 100 bp  
45541 46250: contig of 710 bp in length  
46251 46350: gap of 100 bp  
46351 47056: contig of 706 bp in length  
47057 47156: gap of 100 bp  
47157 47860: contig of 704 bp in length  
47861 47960: gap of 100 bp  
47961 48657: contig of 697 bp in length  
48658 48757: gap of 100 bp  
48758 49457: contig of 700 bp in length  
49459 49557: gap of 100 bp  
49558 50267: contig of 710 bp in length  
50268 50367: gap of 100 bp  
50368 51067: contig of 700 bp in length  
51068 51167: gap of 100 bp  
51168 51861: contig of 694 bp in length  
51862 51961: gap of 100 bp  
51962 52644: contig of 683 bp in length  
52645 52744: gap of 100 bp  
52745 53426: contig of 682 bp in length  
53427 53526: gap of 100 bp  
53527 54224: contig of 698 bp in length  
54225 54324: gap of 100 bp  
54325 55019: contig of 695 bp in length

Query Match 6 CCUGAGAGNNNNNN 18  
Best Local Similarity 92.3%; Score 13; DB 2; Length 56611;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Cy 45433 CCUGAGAGNNNNNN 45445  
Db

RESULT 146  
AC101344  
LOCUS  
DEFINITION Mus musculus clone RP23-110N1, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC101344  
VERSION AC101344.1 GI:17060119  
KEYWORDS HTG; HTGS PHASEO.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 57736)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Mus musculus, clone RP23-110N1  
JOURNAL  
TITLE  
AUTHORS  
REFERENCE  
2 (bases 1 to 57736)  
Unpublished  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastian, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, T., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Harford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lenoczky, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J., Menais, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
COMMENT  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L16494  
Center clone name: 110\_N\_1

NOTE: This record contains 74 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
be preserved.

1 765: contig of 765 bp in length  
\* 766 865: gap of 100 bp  
\* 866 1545: contig of 680 bp in length  
\* 1546 1645: gap of 100 bp  
\* 1646 2332: contig of 687 bp in length  
\* 2333 2432: gap of 100 bp  
\* 2433 3120: contig of 688 bp in length

3121 3220: gap of 100 bp  
\* 3221 3891: contig of 671 bp in length  
\* 3892 3991: gap of 100 bp  
\* 3992 4682: contig of 691 bp in length  
\* 4683 4783: gap of 100 bp  
\* 4783 5426: contig of 644 bp in length  
\* 5427 5526: gap of 100 bp  
\* 5527 6206: contig of 680 bp in length  
\* 6207 6306: gap of 100 bp  
\* 6307 6967: contig of 661 bp in length  
\* 6968 7067: gap of 100 bp  
\* 7068 7652: contig of 695 bp in length  
\* 7653 7862: gap of 100 bp  
\* 7863 8542: contig of 680 bp in length  
\* 8543 8642: gap of 100 bp  
\* 8643 9345: contig of 703 bp in length  
\* 9346 9445: gap of 100 bp  
\* 9446 10116: contig of 671 bp in length  
\* 10117 10216: gap of 100 bp  
\* 10217 10907: contig of 691 bp in length  
\* 10908 11097: gap of 100 bp  
\* 11098 11697: contig of 690 bp in length  
\* 11698 11797: gap of 100 bp  
\* 11798 12480: contig of 683 bp in length  
\* 12481 12580: gap of 100 bp  
\* 12581 13251: contig of 671 bp in length  
\* 13252 13351: gap of 100 bp  
\* 13352 14007: contig of 656 bp in length  
\* 14008 14107: gap of 100 bp  
\* 14108 14768: contig of 661 bp in length  
\* 14769 15567: gap of 100 bp  
\* 15568 15657: contig of 689 bp in length  
\* 15658 16340: contig of 683 bp in length  
\* 16341 16440: gap of 100 bp  
\* 16441 17082: contig of 642 bp in length  
\* 17083 17182: gap of 100 bp  
\* 17183 17665: contig of 683 bp in length  
\* 17666 17965: gap of 100 bp  
\* 17966 18629: contig of 664 bp in length  
\* 18630 18729: gap of 100 bp  
\* 18730 19419: contig of 690 bp in length  
\* 19420 19519: gap of 100 bp  
\* 19520 20213: contig of 694 bp in length  
\* 20214 20314: gap of 100 bp  
\* 20314 20997: contig of 684 bp in length  
\* 20998 21097: gap of 100 bp  
\* 21098 21775: contig of 678 bp in length  
\* 21776 21875: gap of 100 bp  
\* 21876 22582: contig of 707 bp in length  
\* 22583 22682: gap of 100 bp  
\* 22683 23364: contig of 682 bp in length  
\* 23365 23464: gap of 100 bp  
\* 23465 24134: contig of 670 bp in length  
\* 24135 24234: gap of 100 bp  
\* 24235 24889: contig of 655 bp in length  
\* 24890 24989: gap of 100 bp  
\* 24990 25678: contig of 669 bp in length  
\* 25679 25778: gap of 100 bp  
\* 25779 26461: contig of 663 bp in length  
\* 26462 26561: gap of 100 bp  
\* 26562 27235: contig of 674 bp in length  
\* 27236 27335: gap of 100 bp  
\* 27336 28014: contig of 679 bp in length  
\* 28015 28114: gap of 100 bp  
\* 28115 28803: contig of 669 bp in length  
\* 28804 28903: gap of 100 bp  
\* 28904 29573: contig of 670 bp in length  
\* 29574 29673: gap of 100 bp  
\* 29674 30358: contig of 665 bp in length  
\* 30359 30458: gap of 100 bp  
\* 30459 31143: contig of 685 bp in length  
\* 31144 31243: gap of 100 bp

```

* 31244 31942: contig of 639 bp in length
* 31943 32042: gap of 100 bp
* 32043 32740: contig of 638 bp in length
* 32741 32840: gap of 100 bp
* 32841 33507: contig of 667 bp in length
* 33508 33607: gap of 100 bp
* 33608 34313: contig of 706 bp in length
* 34314 34413: gap of 100 bp
* 34414 35057: contig of 644 bp in length
* 35058 35157: gap of 100 bp
* 35158 35843: contig of 686 bp in length
* 35844 35943: gap of 100 bp
* 35944 36619: contig of 676 bp in length
* 36620 36719: gap of 100 bp
* 36720 37414: contig of 635 bp in length
* 37415 37514: gap of 100 bp
* 37515 38206: contig of 682 bp in length
* 38207 38306: gap of 100 bp
* 38307 38990: contig of 684 bp in length
* 38991 39090: gap of 100 bp
* 39091 39774: contig of 684 bp in length
* 39775 39874: gap of 100 bp
* 39875 40579: contig of 705 bp in length
* 40580 40679: gap of 100 bp
* 40680 41347: contig of 668 bp in length
* 41348 41447: gap of 100 bp
* 41448 42097: contig of 650 bp in length
* 42098 42197: gap of 100 bp
* 42198 42867: contig of 670 bp in length
* 42868 42967: gap of 100 bp
* 42968 43740: contig of 673 bp in length
* 43641 43740: gap of 100 bp
* 43741 44412: contig of 672 bp in length
* 44413 44512: gap of 100 bp
* 44513 45213: contig of 701 bp in length
* 45214 45313: gap of 100 bp
* 45314 45998: contig of 685 bp in length
* 45999 46098: gap of 100 bp
* 46099 46804: contig of 706 bp in length
* 46805 46904: gap of 100 bp
* 46905 47593: contig of 689 bp in length
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* 47694 48371: contig of 678 bp in length
* 48372 48471: gap of 100 bp
* 48472 49160: contig of 683 bp in length
* 49161 49260: gap of 100 bp
* 49261 49926: contig of 666 bp in length
* 49927 50026: gap of 100 bp
* 50027 50718: contig of 692 bp in length
* 50719 50818: gap of 100 bp
* 50819 51493: contig of 675 bp in length
* 51494 51593: gap of 100 bp
* 51594 52247: contig of 654 bp in length
* 52248 52347: gap of 100 bp
* 52348 53066: contig of 719 bp in length
* 53067 53167: gap of 100 bp
* 53167 53849: contig of 683 bp in length
* 53850 53949: gap of 100 bp

Query Match 72.2%: Score 13; DB 2; Length 57736;
Best Local Similarity 92.3%: Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 6 CCUGGAGNNNNN 18
Db 33501 CCTGGAGNNNNN 33513

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RESULT 147
AC127514 58456 bp DNA linear HTG 17-JUL-2002
LOCUS AC127514
DEFINITION Homo sapiens chromosome 17 clone RP11-246P6 map 17, LOW-PASS
SEQUENCE SAMPLING.

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ACCESSION AC127514
VERSION AC127514.1 GI:21886933
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 58456)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone RP11-246P6
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 58456)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Brestien,V., Bloom,T., Boguski,Y.L., Boukhalter,B.,
Camata,J., Chang,J., Chazaro,B., Choepel,Y., Collins,A.,
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McCarthy,M., Meldrum,U., Meneus,L., Minova,T., Mieng,A.V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Talamas,U.,
Tefaye,S., Theodore,J., Topnam,K., Travers,W., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
DIRECT SUBMISSION
Submitted (17-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Salt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27495
Center clone name: 246_P_6
-----
* NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
737 736: contig of 736 bp in length
837 836: gap of 100 bp
1578 1577: contig of 741 bp in length
1678 1677: gap of 100 bp
2388 2387: contig of 710 bp in length
2487 2487: gap of 100 bp
3212 3211: contig of 724 bp in length
3312 3311: gap of 100 bp
4041 4040: contig of 729 bp in length
4140 4140: gap of 100 bp
4141 4140: contig of 708 bp in length
4849 4848: gap of 100 bp
4949 4948: contig of 711 bp in length
5660 5659: gap of 100 bp
5760 5759: contig of 738 bp in length
6498 6497: gap of 100 bp
7325 7325: contig of 728 bp in length

```

```

* 7326 7425: gap of 100 bp
* 7426 8156: contig of 731 bp in length
* 8157 8256: gap of 100 bp
* 8257 8920: contig of 664 bp in length
* 8921 9020: gap of 100 bp
* 9021 9742: contig of 722 bp in length
* 9743 9842: gap of 100 bp
* 9843 10567: contig of 725 bp in length
* 10568 10667: gap of 100 bp
* 10668 11402: contig of 735 bp in length
* 11403 11502: gap of 100 bp
* 11503 12235: contig of 733 bp in length
* 12236 12335: gap of 100 bp
* 12336 13066: contig of 731 bp in length
* 13067 13166: gap of 100 bp
* 13167 13902: contig of 736 bp in length
* 13903 14002: gap of 100 bp
* 14003 14732: contig of 730 bp in length
* 14733 14832: gap of 100 bp
* 14833 15552: contig of 720 bp in length
* 15553 15652: gap of 100 bp
* 15653 16382: contig of 730 bp in length
* 16383 16482: gap of 100 bp
* 16483 17211: contig of 729 bp in length
* 17212 17311: gap of 100 bp
* 17312 18034: contig of 723 bp in length
* 18035 18134: gap of 100 bp
* 18135 18863: contig of 729 bp in length
* 18864 18963: gap of 100 bp
* 18964 19692: contig of 729 bp in length
* 19693 19792: gap of 100 bp
* 19793 20518: contig of 726 bp in length
* 20519 21351: gap of 100 bp
* 21352 21451: gap of 100 bp
* 21452 22180: contig of 729 bp in length
* 22181 22280: gap of 100 bp
* 22281 23013: contig of 733 bp in length
* 23014 23113: gap of 100 bp
* 23114 23830: contig of 717 bp in length
* 23831 23930: gap of 100 bp
* 23931 24646: contig of 716 bp in length
* 24647 24746: gap of 100 bp
* 24747 25482: contig of 736 bp in length
* 25483 25582: gap of 100 bp
* 25583 26308: contig of 726 bp in length
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* 26409 27125: contig of 717 bp in length
* 27126 27225: gap of 100 bp
* 27226 27954: contig of 729 bp in length
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* 28055 28780: contig of 726 bp in length
* 28781 28880: gap of 100 bp
* 28881 29603: contig of 723 bp in length
* 29604 29703: gap of 100 bp
* 29704 30427: contig of 724 bp in length
* 30428 30527: gap of 100 bp
* 30529 31250: contig of 723 bp in length
* 31251 31350: gap of 100 bp
* 31351 32061: contig of 711 bp in length
* 32062 32161: gap of 100 bp
* 32162 32889: contig of 728 bp in length
* 32890 32989: gap of 100 bp
* 32990 33695: contig of 706 bp in length
* 33696 33795: gap of 100 bp
* 33796 34510: contig of 715 bp in length
* 34511 34610: gap of 100 bp
* 34611 35333: contig of 723 bp in length
* 35334 35433: gap of 100 bp
* 35434 36165: contig of 732 bp in length
* 36166 36265: gap of 100 bp
* 36266 36997: contig of 732 bp in length
* 36998 37097: gap of 100 bp

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* 37098 37823: contig of 726 bp in length
* 37824 37923: gap of 100 bp
* 37924 38657: contig of 734 bp in length
* 38658 38757: gap of 100 bp
* 38758 39487: contig of 730 bp in length
* 39488 39587: gap of 100 bp
* 39588 40312: contig of 725 bp in length
* 40313 40412: gap of 100 bp
* 40413 41140: contig of 728 bp in length
* 41141 41240: gap of 100 bp
* 41241 41965: contig of 725 bp in length
* 41966 42065: gap of 100 bp
* 42066 42800: contig of 735 bp in length
* 42801 42900: gap of 100 bp
* 42901 43637: contig of 737 bp in length
* 43638 43737: gap of 100 bp
* 43738 44479: contig of 742 bp in length
* 44480 44579: gap of 100 bp
* 44580 45314: contig of 735 bp in length
* 45315 45414: gap of 100 bp
* 45415 46091: contig of 677 bp in length
* 46092 46192: gap of 100 bp
* 46192 46895: contig of 704 bp in length
* 46896 46995: gap of 100 bp
* 46996 47724: contig of 728 bp in length
* 47725 47824: gap of 100 bp
* 47825 48543: contig of 719 bp in length
* 48544 48643: gap of 100 bp
* 48644 49371: contig of 728 bp in length
* 49372 49471: gap of 100 bp
* 49472 50306: contig of 735 bp in length
* 50307 50306: gap of 100 bp
* 50307 51019: contig of 713 bp in length
* 51020 51119: gap of 100 bp
* 51120 51846: contig of 727 bp in length
* 51847 51946: gap of 100 bp
* 51947 52689: contig of 743 bp in length
* 52690 52789: gap of 100 bp
* 52790 53515: contig of 726 bp in length
* 53516 53616: gap of 100 bp
* 53616 54327: contig of 712 bp in length
* 54328 54427: gap of 100 bp
* 54428 55158: contig of 731 bp in length
* 55159 55258: gap of 100 bp
* 55259 55988: contig of 730 bp in length
* 55989 56088: gap of 100 bp
* 56089 56815: contig of 727 bp in length
* 56816 56915: gap of 100 bp
* 56916 57633: contig of 718 bp in length
* 57634 57733: gap of 100 bp
* 57734 58456: contig of 723 bp in length.

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Query Match Best Local Similarity 72.2%; Score 13; DB 2; Length 58456;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNN 18  
 Db 15546 CCTGGAGNNNNN 15558

## RESULT 148

AC100999 59550 bp DNA linear HTG 23-NOV-2001  
 LOCUS Mus musculus clone RP23-77A24, LOW-PASS SEQUENCE SAMPLING.  
 ACCESSION AC100999  
 VERSION AC100999.1 GI:17059773  
 KEYWORDS HTG; HTGS PHASED.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 59550)



AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Birtren,B., Linton,L., Nusbaum,C. and Lander,E.  
Mus musculus, clone Rp23-77A24  
Unpublished  
2 (bases 1 to 59550)

Birtren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Barina,N., Baetien,V., Boguslavsky,L., Boukhalter,B.,  
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,  
Chopel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
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Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,  
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
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Jones,C., Kamat,A., Karatae,A., Kelle,C., Labocque,K.,  
Lamarez,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,  
Maclean,C., Macdonald,P., Major,U., Margulis,N., Matthews,C.,  
McCarthy,M., McEwan,P., McKernan,K., McNeelers,R., Meldrum,J.,  
Menues,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,  
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Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
Roman,J., Rosetti,M., Roy,A., Santoe,R., Schauer,S., Schnupack,R.,  
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,  
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

Project Information  
Center project name: 77\_A\_24  
Center clone name: 77\_A\_24

\* NOTE: This record contains 73 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 687: contig of 687 bp in length  
\* 688 787: gap of 100 bp  
\* 788 1515: contig of 728 bp in length  
\* 1516 1616: gap of 100 bp  
\* 1616 2353: contig of 738 bp in length  
\* 2354 2453: gap of 100 bp  
\* 2454 3171: contig of 718 bp in length  
\* 3172 3271: gap of 100 bp  
\* 3272 3969: contig of 698 bp in length  
\* 3970 4069: gap of 100 bp  
\* 4070 4774: gap of 705 bp in length  
\* 4775 4874: gap of 100 bp  
\* 4875 5593: contig of 719 bp in length  
\* 5594 5693: gap of 100 bp  
\* 5694 6411: contig of 718 bp in length  
\* 6412 7228: gap of 100 bp  
\* 7229 7328: contig of 717 bp in length  
\* 7329 8053: contig of 725 bp in length  
\* 8054 8153: gap of 100 bp  
\* 8154 8875: contig of 722 bp in length

8876 8975: gap of 100 bp  
\* 8976 9681: contig of 706 bp in length  
\* 9682 9781: gap of 100 bp  
\* 9782 10484: contig of 703 bp in length  
\* 10485 10585: gap of 100 bp  
\* 10586 11283: contig of 698 bp in length  
\* 11283 11383: gap of 100 bp  
\* 11383 12089: contig of 706 bp in length  
\* 12089 12188: gap of 100 bp  
\* 12189 12890: contig of 702 bp in length  
\* 12891 12990: gap of 100 bp  
\* 12991 13716: contig of 726 bp in length  
\* 13717 13817: gap of 100 bp  
\* 13817 14547: contig of 731 bp in length  
\* 14548 14647: gap of 100 bp  
\* 14648 15367: contig of 720 bp in length  
\* 15368 15467: gap of 100 bp  
\* 15468 16206: contig of 739 bp in length  
\* 16207 16306: gap of 100 bp  
\* 16307 17046: contig of 740 bp in length  
\* 17047 17146: gap of 100 bp  
\* 17147 17838: contig of 692 bp in length  
\* 17839 17938: gap of 100 bp  
\* 17939 18639: contig of 701 bp in length  
\* 18640 18739: gap of 100 bp  
\* 18740 19444: contig of 705 bp in length  
\* 19445 19544: gap of 100 bp  
\* 19545 20261: contig of 717 bp in length  
\* 20262 20361: gap of 100 bp  
\* 20362 21087: contig of 725 bp in length  
\* 21087 21187: gap of 100 bp  
\* 21187 21918: contig of 731 bp in length  
\* 21918 22017: gap of 100 bp  
\* 22018 22754: contig of 736 bp in length  
\* 22754 22853: gap of 100 bp  
\* 22854 23560: contig of 707 bp in length  
\* 23561 23660: gap of 100 bp  
\* 23660 24405: contig of 745 bp in length  
\* 24406 24505: gap of 100 bp  
\* 24506 25235: contig of 730 bp in length  
\* 25236 25335: gap of 100 bp  
\* 25336 26069: contig of 734 bp in length  
\* 26070 26169: gap of 100 bp  
\* 26170 26872: contig of 703 bp in length  
\* 26873 26972: gap of 100 bp  
\* 26973 27680: contig of 708 bp in length  
\* 27681 27780: gap of 100 bp  
\* 27781 28496: contig of 716 bp in length  
\* 28497 28596: gap of 100 bp  
\* 28597 29328: contig of 732 bp in length  
\* 29329 29428: gap of 100 bp  
\* 29429 30157: contig of 729 bp in length  
\* 30158 30257: gap of 100 bp  
\* 30258 30994: contig of 737 bp in length  
\* 30995 31094: gap of 100 bp  
\* 31095 31834: contig of 740 bp in length  
\* 31835 31934: gap of 100 bp  
\* 31935 32578: contig of 644 bp in length  
\* 32579 32678: gap of 100 bp  
\* 32679 33406: contig of 728 bp in length  
\* 33407 33506: gap of 100 bp  
\* 33507 34225: contig of 719 bp in length  
\* 34226 34325: gap of 100 bp  
\* 34326 35030: contig of 705 bp in length  
\* 35031 35130: gap of 100 bp  
\* 35131 35831: contig of 701 bp in length  
\* 35832 35931: gap of 100 bp  
\* 35932 36637: contig of 706 bp in length  
\* 36638 36737: gap of 100 bp  
\* 36738 37451: contig of 714 bp in length  
\* 37452 37551: gap of 100 bp  
\* 37552 38271: contig of 720 bp in length  
\* 38272 38371: gap of 100 bp

```

* 38372 39116: contig of 745 bp in length
* 39117 39216: gap of 100 bp
* 39910 39910: contig of 694 bp in length
* 39911 40010: gap of 100 bp
* 40011 40725: contig of 715 bp in length
* 40726 40825: gap of 100 bp
* 40826 41534: contig of 709 bp in length
* 41535 41634: gap of 100 bp
* 42321 42421: contig of 687 bp in length
* 42322 42422: gap of 100 bp
* 43147 43247: contig of 726 bp in length
* 43148 43248: gap of 100 bp
* 43248 43975: contig of 728 bp in length
* 43976 44075: gap of 100 bp
* 44076 44821: contig of 746 bp in length
* 44822 44921: gap of 100 bp
* 44922 45648: contig of 727 bp in length
* 45649 45749: gap of 100 bp
* 45749 46490: contig of 742 bp in length
* 46491 46591: gap of 100 bp
* 47328 47428: contig of 738 bp in length
* 47329 47429: gap of 100 bp
* 47429 48143: contig of 714 bp in length
* 48143 48243: gap of 100 bp
* 48243 48936: contig of 694 bp in length
* 48937 49035: gap of 100 bp
* 49037 49748: contig of 712 bp in length
* 49749 49849: gap of 100 bp
* 49849 50559: contig of 711 bp in length
* 50560 51384: contig of 725 bp in length
* 51385 51485: gap of 100 bp
* 51485 52217: contig of 733 bp in length
* 52218 52317: gap of 100 bp
* 52317 53048: contig of 731 bp in length
* 53049 53149: gap of 100 bp
* 53149 53833: contig of 684 bp in length
* 53833 53933: gap of 100 bp
* 53933 54641: contig of 709 bp in length
* 54641 54741: gap of 100 bp
* 54742 55432: contig of 691 bp in length
* 55433 55533: gap of 100 bp
* 55533 56242: contig of 710 bp in length
* 56242 56342: gap of 100 bp

```

```

Query Match      72.2%  Score 13; DB 2; Length 59550;
Best Local Similarity 92.3%  Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      6 CCUGAGNNNNNN 18
Db      27674 CCTGAGNNNNNN 27686

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RESULT 149
AC087334      60323 bp   DNA      1linear   HTG 30-DEC-2001
LOCUS      AC087334
DEFINITION      Homo sapiens chromosome 17 clone RP11-73H6 map 17, LOW-PASS
SEQUENCE SAMPLING.
AC087334
VERSION      AC087334.3 GI:17998705
KEYWORDS      HTG; HTGS PHASE0.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 60323)
  Birren, B., Linton, L., Nuebaum, C. and Lander, E.
  Homo sapiens chromosome 17, clone RP11-73H6
  Unpublished
  2 (bases 1 to 60323)
  Birren, B., Linton, L., Nuebaum, C., Lander, E., Allen, N., Anderson, S.,
  Barina, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A.,

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# TITLE JOURNAL COMMENT

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Camrara, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J.,
Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagoe, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Karatas, A., Lakoque, K., Lamazares, R., Landers, T.,
Lehoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P.,
Marquis, N., Matthews, C., McCarthy, J., McEwan, P., McKernan, K.,
McPheters, R., Meldrum, J., Menus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunhthang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P.,
Strausz, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-DEC-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 30, 2001 this sequence version replaced gi:12658045.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10327
Center clone name: 73_H_5
-----
* NOTE: This record contains 72 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1
* 723 722: contig of 722 bp in length
* 823 822: gap of 100 bp
* 1576 1575: contig of 753 bp in length
* 1676 1675: gap of 100 bp
* 2435 2434: contig of 759 bp in length
* 2535 2534: gap of 100 bp
* 3263 3262: contig of 728 bp in length
* 3363 3362: gap of 100 bp
* 4098 4097: contig of 735 bp in length
* 4198 4197: gap of 100 bp
* 4952 4951: contig of 754 bp in length
* 5052 5051: gap of 100 bp
* 5810 5810: contig of 759 bp in length
* 5910 5910: gap of 100 bp
* 5911 6680: contig of 770 bp in length
* 6681 6780: gap of 100 bp
* 6781 7511: contig of 731 bp in length
* 7512 7611: gap of 100 bp
* 7612 8341: contig of 730 bp in length
* 8342 8441: gap of 100 bp
* 8442 9174: contig of 733 bp in length
* 9175 9274: gap of 100 bp
* 9275 10016: contig of 742 bp in length
* 10017 10116: gap of 100 bp
* 10117 10860: contig of 744 bp in length
* 10861 10960: gap of 100 bp
* 10961 11709: contig of 749 bp in length

```

```

* 11710 11809: gap of 100 bp
* 11810 12383: contig of 574 bp in length
* 12384 12483: gap of 100 bp
* 12484 13244: contig of 761 bp in length
* 13245 13344: gap of 100 bp
* 13345 14041: contig of 697 bp in length
* 14042 14141: gap of 100 bp
* 14142 14894: contig of 753 bp in length
* 14895 14994: gap of 100 bp
* 14995 15751: contig of 757 bp in length
* 15752 15851: gap of 100 bp
* 15852 16575: contig of 724 bp in length
* 16576 16766: gap of 100 bp
* 16767 17401: contig of 726 bp in length
* 17402 17501: gap of 100 bp
* 17502 18237: contig of 736 bp in length
* 18238 18337: gap of 100 bp
* 18338 19073: contig of 736 bp in length
* 19074 19173: gap of 100 bp
* 19174 19907: contig of 734 bp in length
* 19908 20007: gap of 100 bp
* 20008 20762: contig of 755 bp in length
* 20763 20862: gap of 100 bp
* 20863 21569: contig of 707 bp in length
* 21570 21669: gap of 100 bp
* 21670 22380: contig of 711 bp in length
* 22381 22480: gap of 100 bp
* 22481 23231: contig of 751 bp in length
* 23232 23331: gap of 100 bp
* 23332 24101: contig of 770 bp in length
* 24102 24201: gap of 100 bp
* 24202 24959: contig of 758 bp in length
* 24960 25059: gap of 100 bp
* 25060 25780: contig of 721 bp in length
* 25781 25880: gap of 100 bp
* 25881 26614: contig of 734 bp in length
* 26615 26714: gap of 100 bp
* 26715 27436: contig of 722 bp in length
* 27437 27536: gap of 100 bp
* 27537 28277: contig of 741 bp in length
* 28278 28377: gap of 100 bp
* 28378 29108: contig of 731 bp in length
* 29109 29208: gap of 100 bp
* 29209 29963: contig of 755 bp in length
* 29964 30063: gap of 100 bp
* 30064 30831: contig of 768 bp in length
* 30832 30931: gap of 100 bp
* 30932 31641: contig of 710 bp in length
* 31642 31741: gap of 100 bp
* 31742 32490: contig of 749 bp in length
* 32491 32590: gap of 100 bp
* 32591 33338: contig of 748 bp in length
* 33339 33438: gap of 100 bp
* 33439 34170: contig of 732 bp in length
* 34171 34270: gap of 100 bp
* 34271 35010: contig of 740 bp in length
* 35011 35110: gap of 100 bp
* 35111 35936: contig of 826 bp in length
* 35937 36036: gap of 100 bp
* 36037 36800: contig of 764 bp in length
* 36801 36900: gap of 100 bp
* 36901 37632: contig of 732 bp in length
* 37633 37732: gap of 100 bp
* 37733 38436: contig of 704 bp in length
* 38437 38536: gap of 100 bp
* 38537 39309: contig of 773 bp in length
* 39310 39409: gap of 100 bp
* 39410 40153: contig of 744 bp in length
* 40154 40253: gap of 100 bp
* 40254 40981: contig of 728 bp in length
* 40982 41081: gap of 100 bp
* 41082 41819: contig of 738 bp in length
* 41819: gap of 100 bp
* 41820

```

```

* 41920 42646: contig of 727 bp in length
* 42647 42746: gap of 100 bp
* 42747 43477: contig of 731 bp in length
* 43478 43577: gap of 100 bp
* 43578 44310: contig of 733 bp in length
* 44311 44410: gap of 100 bp
* 44411 45176: contig of 766 bp in length
* 45177 45276: gap of 100 bp
* 45277 46043: contig of 767 bp in length
* 46044 46143: gap of 100 bp
* 46144 46849: contig of 706 bp in length
* 46850 46949: gap of 100 bp
* 46950 47701: contig of 752 bp in length
* 47702 47801: gap of 100 bp
* 47802 48543: contig of 742 bp in length
* 48544 48643: gap of 100 bp
* 48644 49411: contig of 768 bp in length
* 49412 49511: gap of 100 bp
* 49512 50236: contig of 725 bp in length
* 50237 50336: gap of 100 bp
* 50337 51067: contig of 731 bp in length
* 51068 51167: gap of 100 bp
* 51168 51895: contig of 728 bp in length
* 51896 51995: gap of 100 bp
* 51996 52703: contig of 708 bp in length
* 52704 52803: gap of 100 bp
* 52804 53550: contig of 747 bp in length
* 53551 53650: gap of 100 bp
* 53651 54364: contig of 714 bp in length
* 54365 54464: gap of 100 bp
* 54465 55227: contig of 763 bp in length
* 55228 55327: gap of 100 bp
* 55328 56118: contig of 791 bp in length
* 56119 56218: gap of 100 bp
* 56219 56961: contig of 743 bp in length
* 56962 57062: gap of 100 bp
* 57062 57773: contig of 712 bp in length

Query Match      72.2%: Score 13; DB 2; Length 60323;
Best Local Similarity 92.3%: Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCUGAGNNNNNN 18
Db      46037 CCTGGAGNNNNNN 46049

RESULT 150
RN499P20/c
LOCUS
DEFINITION
Rattus norvegicus clone RPCI-31-499P20 strain Brown Norway, WORKING
DRAFT SEQUENCE, 25 unordered pieces.
AL603720
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGNANISM
Rattus norvegicus (Norway rat)
REFERENCE
AUTHORS
Sudbrak, R., Borzym, K., Mueller, I., Klages, S., Kosiura, A.,
Walter, U., Guenther, E., Hurt, P., Lehrach, H., Himmelbauer, H. and
Reinhardt, R.
JOURNAL
REFERENCE
Unpublished
TITLE
MOLGENR.
2 (bases 1 to 61582)
JOURNAL
Submitted (10-AUG-2001) MPMG, Abt. Lehrach, Max Planck Institut
Fuer Molekulare Genetik, Ihnestr. 73, Berlin, 14195 Germany
COMMENT
On Nov 29, 2001 this sequence version replaced gi:15149582.
contig 01 1.171
contig 02 272..495

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contig 03      596. .853
contig 04      954. .1040
contig 05      1141. .1441
contig 06      1542. .1682
contig 07      1783. .2107
contig 08      2208. .2576
contig 09      2677. .2776
contig 10      2877. .12941
contig 11      13042. .14190
contig 12      14291. .14828
contig 13      14929. .15502
contig 14      15603. .21365
contig 15      21466. .26703
contig 16      26804. .32901
contig 17      33002. .40856
contig 18      40957. .49047
contig 19      49148. .50018
contig 20      50119. .50909
contig 21      51010. .51922
contig 22      52023. .53560
contig 23      53661. .54827
contig 24      54928. .58361
contig 25      58462. .61582.

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\* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1 171: contig of 171 bp in length
2 271: gap of 100 bp
3 495: contig of 224 bp in length
4 595: gap of 100 bp
5 853: contig of 258 bp in length
6 953: gap of 100 bp
7 1040: contig of 87 bp in length
8 1041: gap of 100 bp
9 1141: contig of 301 bp in length
10 1442: gap of 100 bp
11 1541: gap of 100 bp
12 1682: contig of 141 bp in length
13 1782: gap of 100 bp
14 2107: contig of 325 bp in length
15 2207: gap of 100 bp
16 2576: contig of 369 bp in length
17 2676: gap of 100 bp
18 2776: contig of 100 bp in length
19 2876: gap of 100 bp
20 12941: contig of 10065 bp in length
21 12942: gap of 100 bp
22 13042: contig of 1149 bp in length
23 14190: gap of 100 bp
24 14291: gap of 100 bp
25 14828: contig of 538 bp in length
26 14829: gap of 100 bp
27 14928: gap of 100 bp
28 15502: contig of 574 bp in length
29 15603: gap of 100 bp
30 21365: contig of 5763 bp in length
31 21466: gap of 100 bp
32 26703: contig of 5238 bp in length
33 26804: gap of 100 bp
34 32901: contig of 6098 bp in length
35 33002: gap of 100 bp
36 40856: contig of 7855 bp in length
37 40957: gap of 100 bp
38 49047: contig of 8091 bp in length
39 49148: gap of 100 bp
40 50018: contig of 871 bp in length
41 50119: gap of 100 bp
42 50909: contig of 791 bp in length
43 51010: gap of 100 bp
44 51922: contig of 913 bp in length
45 52023: gap of 100 bp

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FEATURES
  source
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      /mol_type="genomic DNA"
      /strain="Brown Norway"
      /DB_xref="taxon:10116"
      /clone="RPCT-31-49920"
      /clone_1fb="RPCT-31"
      /note="Rfl region on chromosome 20"

ORIGIN
Query Match      72.2%; Score 13; DB 2; Length 61582;
Best Local Similarity 92.3%; Pred. No. 4,6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCUGAGNNNNN 18
Db      602 CCTGAGNNNNN 590

RESULT 151
AC100819
LOCUS
DEFINITION
  Homo sapiens chromosome 8 clone RP11-94F15 map 8, LOW-PASS SEQUENCE
  SAMPLING.
AC100819
AC100819.1 GI:17048189
VERSION
  HTG; HTGS PHASE0.
KEYWORDS
  SOURCE
  Homo sapiens (human)
  ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  1 (bases 1 to 61837)
  Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  Homo sapiens chromosome 8, clone RP11-94F15
  Unpublished
  2 (bases 1 to 61837)
  Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
  Anderson,S., Barina,N., Bastian,V., Boguslavsky,L., Boukhalter,B.,
  Brown,A., Camarata,J., Campolano,A., Chang,J., Chazaro,B.,
  Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
  Cooke,P., Deatellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
  Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
  Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
  Hages,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
  Jones,C., Kamat,A., Karatas,A., Kells,C., Laroque,K.,
  Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
  Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
  McCarthy,M., McEwan,P., McKernan,K., McNetters,R., Meldrum,J.,
  Menais,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
  Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
  Oliver,J., Peterson,K., Phunhthang,P., Pierre,N., Pollara,V.,
  Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
  Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
  Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
  Strauss,N., Subramanian,A., Talama,J., Tesfaye,S., Theodore,J.,
  Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
  Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
  Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.
  Direct Submission
  Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  All repeats were identified using RepeatMasker:
  Smit,A.F.A. & Green, P. (1996-1997)
  http://ftp.genome.washington.edu/RM/RepeatMasker.html
  ----- Genome Center

```

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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L21504
Center clone name: 94_F_15

* NOTE: This record contains 76 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
* 677 776: contig of 676 bp in length
* 777 1489: contig of 713 bp in length
* 1490 1589: gap of 100 bp
* 1590 2284: contig of 695 bp in length
* 2285 2384: gap of 100 bp
* 2385 3067: contig of 683 bp in length
* 3068 3167: gap of 100 bp
* 3168 3913: contig of 746 bp in length
* 3914 4013: gap of 100 bp
* 4014 4722: contig of 709 bp in length
* 4723 4822: gap of 100 bp
* 4823 5557: contig of 735 bp in length
* 5558 5657: gap of 100 bp
* 5659 6394: contig of 737 bp in length
* 6395 6494: gap of 100 bp
* 6495 7191: contig of 697 bp in length
* 7192 7291: gap of 100 bp
* 7292 8000: contig of 709 bp in length
* 8001 8100: gap of 100 bp
* 8101 8820: contig of 720 bp in length
* 8821 8920: gap of 100 bp
* 8921 9606: contig of 686 bp in length
* 9607 9706: gap of 100 bp
* 9707 10420: contig of 714 bp in length
* 10421 10520: gap of 100 bp
* 10521 11257: contig of 736 bp in length
* 11257 11356: gap of 100 bp
* 11357 12072: contig of 716 bp in length
* 12073 12172: gap of 100 bp
* 12173 12895: contig of 723 bp in length
* 12896 12995: gap of 100 bp
* 12996 13723: contig of 728 bp in length
* 13724 13823: gap of 100 bp
* 13824 14540: contig of 717 bp in length
* 14541 14640: gap of 100 bp
* 14641 15354: contig of 714 bp in length
* 15355 15454: gap of 100 bp
* 15455 16162: contig of 708 bp in length
* 16163 16262: gap of 100 bp
* 16263 17043: contig of 781 bp in length
* 17044 17143: gap of 100 bp
* 17144 17851: contig of 708 bp in length
* 17852 17951: gap of 100 bp
* 17952 18660: contig of 709 bp in length
* 18661 18760: gap of 100 bp
* 18761 19454: contig of 694 bp in length
* 19455 19554: gap of 100 bp
* 19555 20289: contig of 735 bp in length
* 20290 20389: gap of 100 bp
* 20390 21125: contig of 736 bp in length
* 21126 21225: gap of 100 bp
* 21226 21962: contig of 737 bp in length
* 21963 22062: gap of 100 bp

22063 22786: contig of 724 bp in length
22787 22887: gap of 100 bp
22887 23601: contig of 715 bp in length
23602 23701: gap of 100 bp
23702 24411: contig of 710 bp in length
24412 24511: gap of 100 bp
24512 25223: contig of 712 bp in length
25224 25323: gap of 100 bp
25324 26011: contig of 688 bp in length
26012 26111: gap of 100 bp
26112 26848: contig of 737 bp in length
26849 26948: gap of 100 bp
26949 27678: contig of 730 bp in length
27679 27778: gap of 100 bp
27779 28501: contig of 723 bp in length
28502 28601: gap of 100 bp
28602 29322: contig of 721 bp in length
29323 29422: gap of 100 bp
29423 30128: contig of 706 bp in length
30129 30228: gap of 100 bp
30229 30897: contig of 669 bp in length
30898 30997: gap of 100 bp
30998 31701: contig of 704 bp in length
31702 31801: gap of 100 bp
31802 32527: contig of 726 bp in length
32528 32627: gap of 100 bp
32628 33329: contig of 702 bp in length
33330 33429: gap of 100 bp
33430 34085: contig of 656 bp in length
34086 34185: gap of 100 bp
34186 34920: contig of 735 bp in length
34921 35020: gap of 100 bp
35021 35744: contig of 724 bp in length
35745 35844: gap of 100 bp
35845 36577: contig of 733 bp in length
36578 36677: gap of 100 bp
36678 37377: contig of 700 bp in length
37378 37477: gap of 100 bp
37478 38201: contig of 724 bp in length
38202 38301: gap of 100 bp
38302 39034: contig of 733 bp in length
39035 39134: gap of 100 bp
39135 39829: contig of 695 bp in length
39830 39929: gap of 100 bp
39930 40634: contig of 705 bp in length
40635 40734: gap of 100 bp
40735 41449: contig of 715 bp in length
41450 41549: gap of 100 bp
41550 42260: contig of 711 bp in length
42261 42360: gap of 100 bp
42361 43048: contig of 688 bp in length
43049 43148: gap of 100 bp
43149 43869: contig of 721 bp in length
43870 43969: gap of 100 bp
43970 44697: contig of 728 bp in length
44698 44797: gap of 100 bp
44798 45523: contig of 726 bp in length
45524 45623: gap of 100 bp
45624 46335: contig of 712 bp in length
46336 46435: gap of 100 bp
46436 47097: contig of 662 bp in length
47098 47197: gap of 100 bp
47198 47922: contig of 725 bp in length
47923 48022: gap of 100 bp
48023 48732: contig of 710 bp in length
48733 48832: gap of 100 bp
48833 49557: contig of 725 bp in length
49558 49657: gap of 100 bp
49658 50350: contig of 693 bp in length
50351 50450: gap of 100 bp
50451 51198: contig of 748 bp in length
51199 51298: gap of 100 bp
51299 52015: contig of 717 bp in length
```

```

*      52016      52115: gap of 100 bp
*      52116      52860: contig of 745 bp in length
*      52861      52960: gap of 100 bp
*      52961      53676: contig of 716 bp in length
*      53677      53776: gap of 100 bp
*      53777      54500: contig of 724 bp in length
*      54501      54600: gap of 100 bp
*      54601      55328: contig of 728 bp in length
*      55329      55428: gap of 100 bp
*      55429      56132: contig of 704 bp in length

Query Match      72.2%: Score 13: DB 2: Length 61837;
Best Local Similarity 92.3%: Pred. No. 4.6e+02;
Matches 12: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      6      CCTGGAGAGNNNNNN 18
Db      52009      CCTGGAGAGNNNNNN 52021

RESULT 152
AC100831
LOCUS
DEFINITION
Homo sapiens chromosome 17 clone RP11-157J7 map 17, LOW-PASS
SEQUENCE SAMPLING.
AC100831.2      GI:22004503
HTG: HTGS_PHASED.
KEYWORDS
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 62138)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-157J7
Unpublished
2 (bases 1 to 62138)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B.,
Brown,A., Camarata,J., Campiano,A., Chang,U., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Lacroque,K.,
Lamarez,R., Landers,T., Lenockzy,J., Levine,R., Liu,G.,
Maclean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuppback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 62138)
Birren,B., Bastien,V., Bloom,T., Boguslavsky,L., Bouckgalter,B.,
Camarata,J., Chang,U., Chazaro,B., Choepe,Y., Collamore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., MacDonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,

```

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TITLE
JOURNAL
COMMENT
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuppback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 30, 2002 this sequence version replaced gi:17048201.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center Project name: L21547
Center Clone name: 157_J_7
-----
* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
737      836: gap of 100 bp
837      1575: contig of 739 bp in length
1576      1675: gap of 100 bp
1676      2427: contig of 752 bp in length
2428      2527: gap of 100 bp
2528      3267: contig of 740 bp in length
3268      3367: gap of 100 bp
3368      4113: contig of 746 bp in length
4114      4213: gap of 100 bp
4214      4963: contig of 750 bp in length
4964      5063: gap of 100 bp
5064      5810: contig of 747 bp in length
5811      5911: gap of 100 bp
5911      6612: contig of 702 bp in length
6613      6713: gap of 100 bp
6713      7469: contig of 757 bp in length
7470      7569: gap of 100 bp
7570      8309: contig of 740 bp in length
8310      8409: gap of 100 bp
8410      9171: contig of 762 bp in length
9172      9271: gap of 100 bp
9272      10034: contig of 763 bp in length
10035      10134: gap of 100 bp
10135      10882: contig of 748 bp in length
10883      10982: gap of 100 bp
10983      11723: contig of 741 bp in length
11724      11823: gap of 100 bp
11824      12540: contig of 717 bp in length
12541      12640: gap of 100 bp
12641      13363: contig of 723 bp in length
13364      13463: gap of 100 bp
13464      14214: contig of 751 bp in length
14215      14314: gap of 100 bp
14315      15078: contig of 764 bp in length
15079      15178: gap of 100 bp
15179      15930: contig of 752 bp in length
15931      16030: gap of 100 bp

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* 16031 16759: contig of 729 bp in length
* 16760 16859: gap of 100 bp
* 16860 17620: contig of 761 bp in length
* 17621 17720: gap of 100 bp
* 17721 18458: contig of 738 bp in length
* 18459 18558: gap of 100 bp
* 18559 19293: contig of 735 bp in length
* 19294 19393: gap of 100 bp
* 19394 20139: contig of 746 bp in length
* 20140 20239: gap of 100 bp
* 20240 20973: contig of 734 bp in length
* 20974 21073: gap of 100 bp
* 21074 21796: contig of 723 bp in length
* 21797 21896: gap of 100 bp
* 21897 22648: contig of 752 bp in length
* 22649 22748: gap of 100 bp
* 22749 23483: contig of 735 bp in length
* 23484 23583: gap of 100 bp
* 23584 24312: contig of 729 bp in length
* 24313 24412: gap of 100 bp
* 24413 25153: contig of 741 bp in length
* 25154 25253: gap of 100 bp
* 25254 25991: contig of 738 bp in length
* 25992 26091: gap of 100 bp
* 26092 26828: contig of 737 bp in length
* 26829 26928: gap of 100 bp
* 26929 27688: contig of 760 bp in length
* 27689 28528: contig of 740 bp in length
* 28529 28628: gap of 100 bp
* 28629 29352: contig of 724 bp in length
* 29353 29452: gap of 100 bp
* 29453 30195: contig of 743 bp in length
* 30196 30295: gap of 100 bp
* 30296 31036: contig of 741 bp in length
* 31037 31136: gap of 100 bp
* 31137 31881: contig of 745 bp in length
* 31882 31981: gap of 100 bp
* 31982 32718: contig of 737 bp in length
* 32719 32818: gap of 100 bp
* 32819 33563: contig of 745 bp in length
* 33564 33663: gap of 100 bp
* 33664 34388: contig of 725 bp in length
* 34389 34488: gap of 100 bp
* 34489 35232: contig of 744 bp in length
* 35233 35332: gap of 100 bp
* 35333 36070: contig of 738 bp in length
* 36071 36170: gap of 100 bp
* 36171 36897: contig of 727 bp in length
* 36898 36997: gap of 100 bp
* 36998 37745: contig of 748 bp in length
* 37746 37845: gap of 100 bp
* 37846 38612: contig of 767 bp in length
* 38613 38712: gap of 100 bp
* 38713 39450: contig of 738 bp in length
* 39451 39550: gap of 100 bp
* 39551 40305: contig of 755 bp in length
* 40306 40405: gap of 100 bp
* 40406 41142: contig of 737 bp in length
* 41143 41242: gap of 100 bp
* 41243 41993: contig of 751 bp in length
* 41994 42093: gap of 100 bp
* 42094 42831: contig of 738 bp in length
* 42832 42931: gap of 100 bp
* 42932 43666: contig of 735 bp in length
* 43667 43766: gap of 100 bp
* 43767 44518: contig of 752 bp in length
* 44519 44618: gap of 100 bp
* 44619 45365: contig of 747 bp in length
* 45366 45465: gap of 100 bp
* 45466 46213: contig of 748 bp in length
* 46214 46313: gap of 100 bp
* 46314 47080: contig of 767 bp in length

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```

* 47081 47180: gap of 100 bp
* 47181 47911: contig of 731 bp in length
* 47912 48011: gap of 100 bp

Query Match
Best Local Similarity 92.24; Score 13; DB 2; Length 62138;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCTGAGAGNNNNN 18
||:|||||
Db 27682 CCTGAGAGNNNNN 27694

RESULT 153
AC099931
LOCUS 63831 bp DNA linear HTG 22-NOV-2001
DEFINITION Mus musculus clone RP23-17C18, LOW-PASS SEQUENCE SAMPLING.
AC099931
VERSION AC099931.1 GI:17047297
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 63831)
Birren, B., Linton, L., Nuebaum, C. and Lander, E.
TITLE Mus musculus, clone RP23-17C18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 63831)
Birren, B., Linton, L., Nuebaum, C., Lander, E., Ali, A., Allen, N.,
AUTHORS Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,
Brown, A., Camarata, J., Campiano, A., Chang, J., Chararo, B.,
Choepe, Y., Colangelo, M., Collins, S., Collins, A., Cook, A.,
COOKE, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N.,
Hagoe, B., Hatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K.,
Lamarez, R., Landers, T., Lenockzy, J., Levine, R., Liu, G.,
Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Melidim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retter, R., Riedack, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talama, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
----- Project Information
Center project name: L15577
Center clone name: 17_C_18

```

```

* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.

```

\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1  
672 771: contig of 671 bp in length  
772 771: gap of 100 bp  
1489 1489: contig of 718 bp in length  
1589 1589: gap of 100 bp  
2277 2277: contig of 688 bp in length  
2377 2377: gap of 100 bp  
3081 3081: contig of 704 bp in length  
3181 3181: gap of 100 bp  
3897 3897: contig of 716 bp in length  
3997 3997: gap of 100 bp  
4714 4714: contig of 717 bp in length  
4814 4814: gap of 100 bp  
5525 5525: contig of 711 bp in length  
5625 5625: gap of 100 bp  
6335 6335: contig of 710 bp in length  
6435 6435: gap of 100 bp  
7151 7151: contig of 716 bp in length  
7251 7251: gap of 100 bp  
7958 7958: contig of 707 bp in length  
8058 8058: gap of 100 bp  
8771 8771: contig of 713 bp in length  
8872 8872: gap of 100 bp  
9555 9555: contig of 684 bp in length  
9655 9655: gap of 100 bp  
10361 10361: contig of 705 bp in length  
10460 10460: gap of 100 bp  
11163 11163: contig of 703 bp in length  
11263 11263: gap of 100 bp  
11962 11962: contig of 699 bp in length  
12062 12062: gap of 100 bp  
12774 12774: contig of 712 bp in length  
12874 12874: gap of 100 bp  
13575 13575: contig of 701 bp in length  
13675 13675: gap of 100 bp  
14383 14383: contig of 708 bp in length  
14483 14483: gap of 100 bp  
15197 15197: contig of 714 bp in length  
15297 15297: gap of 100 bp  
16007 16007: contig of 710 bp in length  
16107 16107: gap of 100 bp  
16818 16818: contig of 711 bp in length  
16918 16918: gap of 100 bp  
17634 17634: contig of 716 bp in length  
17734 17734: gap of 100 bp  
18455 18455: contig of 721 bp in length  
18555 18555: gap of 100 bp  
19269 19269: contig of 714 bp in length  
19369 19369: gap of 100 bp  
20066 20066: contig of 697 bp in length  
20166 20166: gap of 100 bp  
20872 20872: contig of 706 bp in length  
20972 20972: gap of 100 bp  
21688 21688: contig of 716 bp in length  
21788 21788: gap of 100 bp  
22504 22504: contig of 716 bp in length  
22604 22604: gap of 100 bp  
23318 23318: contig of 714 bp in length  
23418 23418: gap of 100 bp  
24139 24139: contig of 721 bp in length  
24239 24239: gap of 100 bp  
24953 24953: contig of 714 bp in length  
25053 25053: gap of 100 bp  
25759 25759: contig of 706 bp in length  
25859 25859: gap of 100 bp  
26583 26583: contig of 724 bp in length  
26683 26683: gap of 100 bp  
27370 27370: contig of 687 bp in length  
27470 27470: gap of 100 bp  
28184 28184: contig of 714 bp in length

\* 28185 28284: gap of 100 bp  
\* 28285 28990: contig of 706 bp in length  
\* 28991 29090: gap of 100 bp  
\* 29091 29789: contig of 699 bp in length  
\* 29790 29890: gap of 100 bp  
\* 29890 30605: contig of 716 bp in length  
\* 30606 30705: gap of 100 bp  
\* 30706 31423: contig of 718 bp in length  
\* 31424 32236: contig of 713 bp in length  
\* 32237 32336: gap of 100 bp  
\* 32337 33041: contig of 705 bp in length  
\* 33042 33141: gap of 100 bp  
\* 33142 33833: contig of 692 bp in length  
\* 33834 33933: gap of 100 bp  
\* 33934 34654: contig of 721 bp in length  
\* 34655 34754: gap of 100 bp  
\* 34755 35467: contig of 713 bp in length  
\* 35468 35567: gap of 100 bp  
\* 35568 36263: contig of 696 bp in length  
\* 36264 36363: gap of 100 bp  
\* 36364 37073: contig of 710 bp in length  
\* 37074 37173: gap of 100 bp  
\* 37174 37894: contig of 721 bp in length  
\* 37895 37994: gap of 100 bp  
\* 37995 38709: contig of 715 bp in length  
\* 38710 38809: gap of 100 bp  
\* 38810 39532: contig of 723 bp in length  
\* 39533 39632: gap of 100 bp  
\* 39633 40342: contig of 710 bp in length  
\* 40343 40442: gap of 100 bp  
\* 40443 41115: contig of 673 bp in length  
\* 41116 41215: gap of 100 bp  
\* 41216 41938: contig of 723 bp in length  
\* 41939 42038: gap of 100 bp  
\* 42039 42747: contig of 703 bp in length  
\* 42748 42847: gap of 100 bp  
\* 42848 43551: contig of 704 bp in length  
\* 43552 43651: gap of 100 bp  
\* 43652 44361: contig of 710 bp in length  
\* 44362 44462: gap of 100 bp  
\* 44462 45138: contig of 677 bp in length  
\* 45139 45238: gap of 100 bp  
\* 45239 45943: contig of 705 bp in length  
\* 45944 46043: gap of 100 bp  
\* 46044 46758: contig of 715 bp in length  
\* 46759 46858: gap of 100 bp  
\* 46859 47594: contig of 736 bp in length  
\* 47595 47694: gap of 100 bp  
\* 47695 48410: contig of 716 bp in length  
\* 48411 48510: gap of 100 bp  
\* 48511 49202: contig of 692 bp in length  
\* 49202 49302: gap of 100 bp  
\* 49303 50100: contig of 708 bp in length  
\* 50110 50110: gap of 100 bp  
\* 50111 50801: contig of 691 bp in length  
\* 50802 50901: gap of 100 bp  
\* 50902 51622: contig of 721 bp in length  
\* 51623 51722: gap of 100 bp  
\* 51723 52429: contig of 707 bp in length  
\* 52430 52529: gap of 100 bp  
\* 52530 53348: contig of 719 bp in length  
\* 53349 53448: gap of 100 bp  
\* 53449 54065: contig of 717 bp in length  
\* 54066 54165: gap of 100 bp  
\* 54166 54891: contig of 726 bp in length  
\* 54892 54991: gap of 100 bp  
\* 54992 55704: contig of 713 bp in length  
\* 55705 55804: gap of 100 bp

Query Match 72.2%; Score 13; DB 2; Length 63831;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



Oy 6 CCUGAGNNNNNN 18  
 Db 58969 CCTGGAGNNNNNN 58981

# RESULT 154

AC100902

LOCUS AC100902 64919 bp DNA linear HTG 23-NOV-2001

DEFINITION Mus musculus clone RP23-70E20, LOW-PASS SEQUENCE SAMPLING.

AC100902

AC100902.1 GI:17059676

HTG: HTGS PHASED.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 64919)

Unpublished

2 (bases 1 to 64919)

Unpublished

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

1529 1628: gap of 100 bp  
 1529 1628: contig of 735 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 744 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 695 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 685 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 701 bp in length  
 1529 1628: gap of 100 bp  
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 1529 1628: gap of 100 bp  
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 1529 1628: gap of 100 bp  
 1529 1628: contig of 712 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 704 bp in length  
 1529 1628: gap of 100 bp  
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 1529 1628: gap of 100 bp  
 1529 1628: contig of 745 bp in length  
 1529 1628: gap of 100 bp  
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 1529 1628: gap of 100 bp  
 1529 1628: contig of 632 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 686 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 720 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 738 bp in length  
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 1529 1628: gap of 100 bp  
 1529 1628: contig of 737 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 733 bp in length  
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 1529 1628: contig of 716 bp in length  
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 1529 1628: gap of 100 bp  
 1529 1628: contig of 741 bp in length  
 1529 1628: gap of 100 bp  
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 1529 1628: gap of 100 bp  
 1529 1628: contig of 692 bp in length  
 1529 1628: gap of 100 bp  
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 1529 1628: gap of 100 bp  
 1529 1628: contig of 715 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 702 bp in length  
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 1529 1628: contig of 695 bp in length  
 1529 1628: gap of 100 bp  
 1529 1628: contig of 702 bp in length  
 1529 1628: gap of 100 bp

NOTE: This record contains 80 individual  
 sequencing reads that have not been assembled into  
 contigs. Runs of N are used to separate the reads  
 and the order in which they appear is completely  
 arbitrary. Low-pass sequence sampling is useful for  
 identifying clones that may be gene-rich and allows  
 overlap relationships among clones to be deduced.  
 However, it should not be assumed that this clone  
 will be sequenced to completion. In the event that  
 the record is updated, the accession number will  
 be preserved.

1 696: contig of 696 bp in length  
 697 796: gap of 100 bp  
 797 1528: contig of 732 bp in length

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* 30816 31519: contig of 704 bp in length
* 31520 31619: gap of 100 bp
* 32352 32352: contig of 733 bp in length
* 32353 32452: gap of 100 bp
* 32453 32453: contig of 717 bp in length
* 33170 33269: gap of 100 bp
* 33270 33960: contig of 691 bp in length
* 33961 34060: gap of 100 bp
* 34061 34731: contig of 671 bp in length
* 34732 34831: gap of 100 bp
* 34832 35572: contig of 741 bp in length
* 35573 35672: gap of 100 bp
* 35673 36416: contig of 744 bp in length
* 36417 36516: gap of 100 bp
* 36517 37214: contig of 698 bp in length
* 37215 37314: gap of 100 bp
* 37315 37993: contig of 679 bp in length
* 37994 38093: gap of 100 bp
* 38094 38790: contig of 697 bp in length
* 38791 38890: gap of 100 bp
* 38891 39590: contig of 700 bp in length
* 39591 39690: gap of 100 bp
* 39691 40416: contig of 726 bp in length
* 40417 40516: gap of 100 bp
* 40517 41256: contig of 740 bp in length
* 41257 41356: gap of 100 bp
* 41357 42053: contig of 697 bp in length
* 42054 42153: gap of 100 bp
* 42154 42886: contig of 733 bp in length
* 42887 42987: gap of 100 bp
* 42987 43734: contig of 748 bp in length
* 43735 43834: gap of 100 bp
* 43835 44579: contig of 745 bp in length
* 44580 44679: gap of 100 bp
* 44680 45385: contig of 706 bp in length
* 45386 45485: gap of 100 bp
* 45486 46179: contig of 694 bp in length
* 46180 46279: gap of 100 bp
* 46280 46974: contig of 695 bp in length
* 46975 47074: gap of 100 bp
* 47075 47796: contig of 722 bp in length
* 47797 47896: gap of 100 bp
* 47897 48604: contig of 708 bp in length
* 48605 48704: gap of 100 bp
* 48705 49434: contig of 730 bp in length
* 49435 49534: gap of 100 bp
* 49535 50252: contig of 718 bp in length
* 50253 50352: gap of 100 bp
* 50353 51027: contig of 675 bp in length
* 51028 51127: gap of 100 bp
* 51128 51847: contig of 720 bp in length
* 51848 51947: gap of 100 bp
* 51948 52682: contig of 735 bp in length
* 52683 52782: gap of 100 bp
* 52783 53476: contig of 694 bp in length
* 53477 53576: gap of 100 bp
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* 55058 55157: gap of 100 bp
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* 55875 55974: gap of 100 bp

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Query Match 72.2% Score 13; DB 2; Length 64919;  
 Best Local Similarity 92.3% Pred. NO. 4.6e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
 |||:|||||  
 Db 45379 CCTGAGANNNNNN 45391

RESULT 155

AC124644  
 LOCUS 64962 bp DNA linear HTG 27-NOV-2002  
 AC124644  
 DEFINITION Mus musculus clone RP23-135G22, LOW-PASS SEQUENCE SAMPLING.  
 AC124644  
 VERSION AC124644.2 GI:25705772  
 KEYWORDS HTG; HTGS PHASE0.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 64962)  
 Birren, B., Nusbaum, C., and Lander, E.  
 Mus musculus, clone RP23-135G22  
 Unpublished  
 2 (bases 1 to 64962)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,  
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,  
 Boukhgalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,  
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,  
 Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S.,  
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 Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larcocque, K.,  
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 Theodore, J., Topham, K., Travars, M., Travls, N., Trigillo, J.,  
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
 Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

TITLE  
 JOURNAL  
 AUTHORS  
 REFERENCES  
 Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 64962)  
 Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S.,  
 Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collamore, A.,  
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 Travars, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,  
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TITLE  
 JOURNAL  
 COMMENT  
 Submitted (27-NOV-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA.  
 On Nov 27, 2002 this sequence version replaced gi:21427876.  
 ALL repeats were identified using RepeatMasker:  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIRB  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L26856

Center clone name: 135\_G\_22

NOTE: This record contains 79 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 709: contig of 709 bp in length  
710 809: gap of 100 bp  
810 1531: contig of 722 bp in length  
1532 1631: gap of 100 bp  
1632 2343: contig of 712 bp in length  
2344 2443: gap of 100 bp  
2444 3150: contig of 707 bp in length  
3151 3250: gap of 100 bp  
3251 3972: contig of 722 bp in length  
3973 4072: gap of 100 bp  
4073 4807: contig of 735 bp in length  
4808 4907: gap of 100 bp  
4908 5629: contig of 722 bp in length  
5630 5729: gap of 100 bp  
5730 6451: contig of 722 bp in length  
6452 6551: gap of 100 bp  
6552 7281: contig of 730 bp in length  
7282 7382: gap of 100 bp  
7382 8104: contig of 723 bp in length  
8105 8204: gap of 100 bp  
8205 8922: contig of 718 bp in length  
8923 9022: gap of 100 bp  
9023 9736: contig of 714 bp in length  
9737 9836: gap of 100 bp  
9837 10569: contig of 733 bp in length  
10570 10669: gap of 100 bp  
10670 11388: contig of 719 bp in length  
11389 11488: gap of 100 bp  
11489 12217: contig of 729 bp in length  
12218 12317: gap of 100 bp  
12318 13054: contig of 737 bp in length  
13055 13154: gap of 100 bp  
13155 13884: contig of 730 bp in length  
13885 13984: gap of 100 bp  
13985 14714: contig of 730 bp in length  
14715 14814: gap of 100 bp  
14815 15534: contig of 720 bp in length  
15535 15634: gap of 100 bp  
15636 16352: contig of 718 bp in length  
16353 16452: gap of 100 bp  
16453 17175: contig of 723 bp in length  
17176 17275: gap of 100 bp  
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17999 18098: gap of 100 bp  
18099 18835: contig of 737 bp in length  
18836 18935: gap of 100 bp  
18936 19656: contig of 721 bp in length  
19657 19756: gap of 100 bp  
19757 20481: contig of 725 bp in length  
20482 20581: gap of 100 bp  
20582 21299: contig of 718 bp in length  
21299 21399: gap of 100 bp  
21300 22130: contig of 731 bp in length  
22131 22230: gap of 100 bp  
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23069 23786: contig of 717 bp in length  
23787 23886: gap of 100 bp  
23887 24605: contig of 719 bp in length  
24606 24705: gap of 100 bp

24706 25426: contig of 721 bp in length  
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27190 27911: contig of 722 bp in length  
27912 28011: gap of 100 bp  
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28740 28839: gap of 100 bp  
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32961 33673: contig of 713 bp in length  
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34604 35317: contig of 714 bp in length  
35318 35417: gap of 100 bp  
35418 36144: contig of 727 bp in length  
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36245 36957: contig of 713 bp in length  
36958 37057: gap of 100 bp  
37058 37779: contig of 722 bp in length  
37780 37879: gap of 100 bp  
37880 38594: contig of 715 bp in length  
38595 38694: gap of 100 bp  
38695 39417: contig of 723 bp in length  
39418 39517: gap of 100 bp  
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40246 40345: gap of 100 bp  
40346 41072: contig of 727 bp in length  
41073 41172: gap of 100 bp  
41173 41891: contig of 719 bp in length  
41892 41991: gap of 100 bp  
41992 42714: contig of 723 bp in length  
42715 42814: gap of 100 bp  
42815 43539: contig of 725 bp in length  
43540 43639: gap of 100 bp  
43640 44373: contig of 734 bp in length  
44374 44473: gap of 100 bp  
44474 45192: contig of 719 bp in length  
45193 45292: gap of 100 bp  
45293 46003: contig of 711 bp in length  
46004 46103: gap of 100 bp  
46104 46833: contig of 730 bp in length  
46834 46933: gap of 100 bp  
46934 47658: contig of 725 bp in length

Query Match 72.2% Score 13; DB 2; Length 64962;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGNNNNNN 18  
Db 22962 CCGGAGNNNNNN 22974

RESULT 156  
AC100429  
LOCUS AC100429 6518 bp DNA linear HTG 22-NOV-2001  
DEFINITION Mus musculus clone RP23-136W7, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC100429  
VERSION AC100429.1 GI:17047795  
KEYWORDS HTG; HTGS PHASEO.  
SOURCE Mus musculus (house mouse)

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ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 65158)
AUTHORS
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE
Mus musculus, clone RP23-136M7
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 65158)
AUTHORS
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barina, N., Baetjen, V., Boguslavsky, L., Boukhalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
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Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
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Jones, C., Kamat, A., Karatas, A., Kellis, C., Labrecque, K.,
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L15320
Center clone name: 136_M_7
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* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
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* 710: contig of 710 bp in length
* 711 810: gap of 100 bp
* 811 1502: contig of 692 bp in length
* 1503 1602: gap of 100 bp
* 1603 2321: contig of 719 bp in length
* 2322 2421: gap of 100 bp
* 2422 3121: contig of 700 bp in length
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* 3222 3914: contig of 693 bp in length
* 3915 4014: gap of 100 bp
* 4015 4707: contig of 693 bp in length
* 4708 4807: gap of 100 bp
* 4808 5489: contig of 682 bp in length
* 5490 5590: gap of 100 bp
* 5590 6302: contig of 712 bp in length
* 6302 6401: gap of 100 bp
* 6401 7109: contig of 708 bp in length
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* 7209: gap of 100 bp
* 7210 7928: contig of 719 bp in length
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* 8029 8731: contig of 703 bp in length
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* 8832 9557: contig of 726 bp in length
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* 9658 10389: contig of 732 bp in length
* 10390 10489: gap of 100 bp
* 10490 11185: contig of 696 bp in length
* 11186 11285: gap of 100 bp
* 11286 11989: contig of 704 bp in length
* 11990 12089: gap of 100 bp
* 12090 12796: contig of 707 bp in length
* 12797 12896: gap of 100 bp
* 12897 13599: contig of 703 bp in length
* 13600 13699: gap of 100 bp
* 13700 14381: contig of 682 bp in length
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* 14482 15199: contig of 718 bp in length
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* 15300 16004: contig of 705 bp in length
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* 16105 16811: contig of 707 bp in length
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* 17703 18417: contig of 715 bp in length
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* 19389 20105: contig of 718 bp in length
* 20106 20205: gap of 100 bp
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* 20900 21694: contig of 695 bp in length
* 21695 21794: gap of 100 bp
* 21795 22477: contig of 683 bp in length
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* 24181 24894: contig of 714 bp in length
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* 24995 25701: contig of 707 bp in length
* 25702 25801: gap of 100 bp
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* 26503 26602: gap of 100 bp
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* 27294 27393: gap of 100 bp
* 27394 28098: contig of 705 bp in length
* 28099 28198: gap of 100 bp
* 28199 28914: contig of 716 bp in length
* 28915 29014: gap of 100 bp
* 29015 29705: contig of 691 bp in length
* 29706 29805: gap of 100 bp
* 29806 30494: contig of 689 bp in length
* 30495 30594: gap of 100 bp
* 30595 31291: contig of 697 bp in length
* 31292 31391: gap of 100 bp
* 31392 32092: contig of 701 bp in length
* 32093 32192: gap of 100 bp
* 32193 32801: contig of 709 bp in length
* 32802 33001: gap of 100 bp
* 33002 33699: contig of 698 bp in length
* 33700 33799: gap of 100 bp
* 33800 34501: contig of 702 bp in length
* 34502 34601: gap of 100 bp
* 34602 35325: contig of 724 bp in length
* 35326 35425: gap of 100 bp
* 35426 36137: contig of 712 bp in length
* 36138 36237: gap of 100 bp

```

```

* 36238 36942: contig of 705 bp in length
* 36943 37042: gap of 100 bp in length
* 37043 37748: contig of 706 bp in length
* 37749 37848: gap of 100 bp in length
* 37849 38571: contig of 723 bp in length
* 38572 38671: gap of 100 bp in length
* 38672 39367: contig of 696 bp in length
* 39368 39467: gap of 100 bp in length
* 39468 40185: contig of 718 bp in length
* 40186 40286: gap of 100 bp in length
* 40287 41009: contig of 724 bp in length
* 41010 41110: gap of 100 bp in length
* 41111 41817: contig of 708 bp in length
* 41818 41917: gap of 100 bp in length
* 41918 42620: contig of 703 bp in length
* 42621 42720: gap of 100 bp in length
* 42721 43424: contig of 704 bp in length
* 43425 43524: gap of 100 bp in length
* 43525 44243: contig of 719 bp in length
* 44244 44343: gap of 100 bp in length
* 44344 45039: contig of 696 bp in length
* 45040 45139: gap of 100 bp in length
* 45140 45827: contig of 688 bp in length
* 45828 45927: gap of 100 bp in length
* 45928 46616: contig of 689 bp in length
* 46617 46716: gap of 100 bp in length
* 46717 47424: contig of 708 bp in length
* 47425 47524: gap of 100 bp in length
* 47525 48232: contig of 708 bp in length
* 48233 48332: gap of 100 bp in length
* 48333 48053: contig of 721 bp in length
* 48054 49153: gap of 100 bp in length
* 49154 49842: contig of 689 bp in length
* 49843 49942: gap of 100 bp in length
* 49943 50632: contig of 690 bp in length
* 50633 50732: gap of 100 bp in length
* 50733 51435: contig of 703 bp in length
* 51436 51535: gap of 100 bp in length
* 51536 52247: contig of 712 bp in length
* 52248 52347: gap of 100 bp in length
* 52348 53048: contig of 700 bp in length
* 53049 53147: gap of 100 bp in length
* 53148 53837: contig of 690 bp in length
* 53838 53937: gap of 100 bp in length
* 53938 54640: contig of 703 bp in length
* 54641 54740: gap of 100 bp in length
* 54741 55439: contig of 699 bp in length
* 55440 55539: gap of 100 bp in length

```

Query Match 72.2% Score 13; DB 2; Length 65158;  
 Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 DB 15193 CCTGAGNNNNNN 15205

RESULT 157  
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 LOCUS AC100675 65199 bp DNA linear HTG 22-NOV-2001  
 DEFINITION Mus musculus clone RP23-167M2; LOW-PASS SEQUENCE SAMPLING.  
 AC100675  
 VERSION AC100675.1 GI:17048041  
 KEYWORDS HTG; HTGS PHASED.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 65199)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 TITLE Mus musculus, clone RP23-167M2  
 JOURNAL Unpublished

## REFERENCE

2 (bases 1 to 65199)  
 AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,J., Baxendale,V., Boguski,M.S., Boulton,A.,  
 Brown,A., Camarata,J., Campione,A., Chang,U., Chazaro,B.,  
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 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
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 Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,  
 Veli,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.

## TITLE

Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

## COMMENT

All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIRB  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu

Project Information  
 Center project name: L15933  
 Center clone name: 167\_M2

NOTE: This record contains 77 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.

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1 701: contig of 701 bp in length
702 801: gap of 100 bp
802 1544: contig of 743 bp in length
1545 1644: gap of 100 bp
1645 2398: contig of 754 bp in length
2399 2498: gap of 100 bp
2499 3238: contig of 740 bp in length
3239 3338: gap of 100 bp
3339 4087: contig of 749 bp in length
4088 4187: gap of 100 bp
4188 4932: contig of 745 bp in length
4933 5032: gap of 100 bp
5033 5748: contig of 716 bp in length
5749 5848: gap of 100 bp
5849 6698: contig of 750 bp in length
6699 7411: contig of 713 bp in length
7412 7511: gap of 100 bp
7512 8274: contig of 763 bp in length
8275 8374: gap of 100 bp
8375 9129: contig of 755 bp in length
9130 9229: gap of 100 bp
9230 9946: contig of 717 bp in length
9947 10046: gap of 100 bp

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* 10047 10772: contig of 726 bp in length
* 10773 10872: gap of 100 bp
* 10873 11633: contig of 761 bp in length
* 11634 11733: gap of 100 bp
* 11734 12485: contig of 752 bp in length
* 12486 12586: gap of 100 bp
* 12587 13348: contig of 763 bp in length
* 13349 13449: gap of 100 bp
* 13450 14183: contig of 735 bp in length
* 14184 14283: gap of 100 bp
* 14284 15071: contig of 788 bp in length
* 15072 15171: gap of 100 bp
* 15172 15944: contig of 773 bp in length
* 15945 16044: gap of 100 bp
* 16045 16809: contig of 765 bp in length
* 16810 16909: gap of 100 bp
* 16910 17661: contig of 752 bp in length
* 17662 18494: contig of 733 bp in length
* 18495 18594: gap of 100 bp
* 18595 19353: contig of 759 bp in length
* 19354 19453: gap of 100 bp
* 19454 20168: contig of 715 bp in length
* 20169 20268: gap of 100 bp
* 20269 21014: contig of 746 bp in length
* 21015 21114: gap of 100 bp
* 21115 21850: contig of 736 bp in length
* 21851 21950: gap of 100 bp
* 21951 22714: contig of 764 bp in length
* 22715 22814: gap of 100 bp
* 22815 23562: contig of 748 bp in length
* 23563 23662: gap of 100 bp
* 23663 24428: contig of 766 bp in length
* 24429 24528: gap of 100 bp
* 24530 25275: contig of 747 bp in length
* 25276 25375: gap of 100 bp
* 25376 26115: contig of 740 bp in length
* 26116 26215: gap of 100 bp
* 26216 26973: contig of 758 bp in length
* 26974 27073: gap of 100 bp
* 27074 27825: contig of 752 bp in length
* 27826 27925: gap of 100 bp
* 27926 28666: contig of 741 bp in length
* 28667 28766: gap of 100 bp
* 28767 29500: contig of 734 bp in length
* 29501 29600: gap of 100 bp
* 29601 30342: contig of 742 bp in length
* 30343 30442: gap of 100 bp
* 30443 31237: contig of 795 bp in length
* 31238 31337: gap of 100 bp
* 31338 32076: contig of 739 bp in length
* 32077 32176: gap of 100 bp
* 32177 32933: contig of 757 bp in length
* 32934 33033: gap of 100 bp
* 33034 33801: contig of 768 bp in length
* 33802 33901: gap of 100 bp
* 33902 34647: contig of 746 bp in length
* 34648 34747: gap of 100 bp
* 34748 35477: contig of 730 bp in length
* 35478 35577: gap of 100 bp
* 35578 36322: contig of 745 bp in length
* 36323 36422: gap of 100 bp
* 36423 37155: contig of 733 bp in length
* 37156 37255: gap of 100 bp
* 37256 37987: contig of 732 bp in length
* 37988 38087: gap of 100 bp
* 38088 38835: contig of 748 bp in length
* 38836 39690: contig of 755 bp in length
* 39691 39790: gap of 100 bp
* 39791 40533: contig of 743 bp in length
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* 41404: contig of 771 bp in length
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* 41405 41504: gap of 100 bp
* 41505 42215: contig of 711 bp in length
* 42216 42316: gap of 100 bp
* 42317 43074: contig of 758 bp in length
* 43075 43174: gap of 100 bp
* 43175 43925: contig of 751 bp in length
* 43926 44024: gap of 100 bp
* 44025 44771: contig of 747 bp in length
* 44772 45599: contig of 728 bp in length
* 45600 45699: gap of 100 bp
* 45700 46459: contig of 760 bp in length
* 46460 46560: gap of 100 bp
* 46561 47275: contig of 716 bp in length
* 47276 47375: gap of 100 bp
* 47376 48099: contig of 724 bp in length
* 48100 48199: gap of 100 bp
* 48200 48964: contig of 765 bp in length
* 48965 49064: gap of 100 bp
* 49066 49824: contig of 760 bp in length
* 49825 49924: gap of 100 bp
* 49925 50673: contig of 749 bp in length
* 50674 50773: gap of 100 bp
* 50774 51516: contig of 743 bp in length
* 51517 51616: gap of 100 bp
* 51617 52339: contig of 723 bp in length
* 52340 52439: gap of 100 bp
* 52440 53187: contig of 748 bp in length
* 53188 53288: gap of 100 bp
* 53289 54048: contig of 761 bp in length
* 54049 54149: gap of 100 bp
* 54150 54901: contig of 753 bp in length
* 54902 55001: gap of 100 bp
* 55002 55712: contig of 711 bp in length
* 55713 55812: gap of 100 bp
* 55813 56604: contig of 792 bp in length
* 56605 56704: gap of 100 bp
* 56705 57465: contig of 761 bp in length
* 57466 57565: gap of 100 bp
* 57566 58314: contig of 749 bp in length
* 58315 58414: gap of 100 bp

Query Match
Best Local Similarity 72.2% Score 13; DB 2; Length 65199;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCGGAGNNNNNN 18
Db 38829 CCGGAGNNNNNN 38841

RESULT 158
AC090157
LOCUS Homo sapiens chromosome 11 clone RP11-223K12 map 11, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
ACCESSION AC090157.2 GI:13431020
VERSION 1
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 65259)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Baclen,V., Boguslavsky,L., Boukhalter,B., Brown,A.,
Camataia,J., Campoliano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Faro,S., Ferreira,F., Fitzhugh,W., Gage,D., Galagan,J.,
```

TITLE  
JOURNAL  
COMMENT

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagos, B., Heatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
Jones, C., Karatas, A., Lacroix, K., Lamazares, R., Landers, T.,  
Lencock, J., Levine, R., Liu, G., Maclean, C., MacDonald, P.,  
Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K.,  
McNeeters, R., Meldrum, J., Meneu, L., Mohova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H.,  
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,  
Phunkiang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,  
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,  
Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P.,  
Strausz, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Sugan, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,  
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,  
Zembek, L., Zimmer, A. and Zody, M.

Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 22, 2001 this sequence version replaced gi:1257786.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: W1BR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L11791  
Center clone name: 223\_K\_12

\* NOTE: This record contains 81 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allow  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 682: contig of 682 bp in length  
\* 683 782: gap of 100 bp  
\* 783 1487: contig of 705 bp in length  
\* 1488 1587: gap of 100 bp  
\* 1588 2310: contig of 723 bp in length  
\* 2311 2410: gap of 100 bp  
\* 2411 3102: contig of 692 bp in length  
\* 3103 3202: gap of 100 bp  
\* 3203 3906: contig of 704 bp in length  
\* 3907 4006: gap of 100 bp  
\* 4007 4705: contig of 699 bp in length  
\* 4706 4805: gap of 100 bp  
\* 4806 5499: contig of 694 bp in length  
\* 5500 5599: gap of 100 bp  
\* 5600 6293: contig of 694 bp in length  
\* 6294 6393: gap of 100 bp  
\* 6394 7101: contig of 708 bp in length  
\* 7102 7201: gap of 100 bp  
\* 7202 7913: contig of 712 bp in length  
\* 7914 8013: gap of 100 bp  
\* 8014 8730: contig of 717 bp in length  
\* 8731 8830: gap of 100 bp  
\* 8831 9543: contig of 713 bp in length  
\* 9544 9644: gap of 100 bp  
\* 9645 10358: contig of 715 bp in length  
\* 10359 10458: gap of 100 bp  
\* 10459 11146: contig of 688 bp in length  
\* 11147 11246: gap of 100 bp  
\* 11247 11960: contig of 714 bp in length  
\* 11961 12060: gap of 100 bp

\* 12061 12767: contig of 707 bp in length  
\* 12768 12867: gap of 100 bp  
\* 12868 13567: contig of 700 bp in length  
\* 13568 13667: gap of 100 bp  
\* 13668 14369: contig of 702 bp in length  
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\* 16107 16829: contig of 723 bp in length  
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\* 16930 17633: contig of 704 bp in length  
\* 17634 17733: gap of 100 bp  
\* 17734 18450: contig of 717 bp in length  
\* 18451 18550: gap of 100 bp  
\* 18551 19275: contig of 725 bp in length  
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\* 19376 20078: contig of 703 bp in length  
\* 20079 20178: gap of 100 bp  
\* 20179 20878: contig of 700 bp in length  
\* 20879 21670: contig of 692 bp in length  
\* 21671 21770: gap of 100 bp  
\* 21771 22459: contig of 689 bp in length  
\* 22460 22559: gap of 100 bp  
\* 22560 23278: contig of 719 bp in length  
\* 23279 23378: gap of 100 bp  
\* 23379 24085: contig of 707 bp in length  
\* 24086 24185: gap of 100 bp  
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\* 24885 24984: gap of 100 bp  
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\* 26587 27350: contig of 764 bp in length  
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\* 30545 30644: gap of 100 bp  
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\* 32298 32984: contig of 687 bp in length  
\* 32985 33084: gap of 100 bp  
\* 33085 33770: contig of 686 bp in length  
\* 33771 33870: gap of 100 bp  
\* 33871 34620: contig of 750 bp in length  
\* 34621 34720: gap of 100 bp  
\* 34721 35430: contig of 710 bp in length  
\* 35431 35530: gap of 100 bp  
\* 35531 36223: contig of 693 bp in length  
\* 36224 36323: gap of 100 bp  
\* 36324 37013: contig of 690 bp in length  
\* 37014 37113: gap of 100 bp  
\* 37114 37786: contig of 673 bp in length  
\* 37787 37886: gap of 100 bp  
\* 37887 38596: contig of 710 bp in length  
\* 38597 38696: gap of 100 bp  
\* 38697 39400: contig of 704 bp in length  
\* 39401 39500: gap of 100 bp  
\* 39501 40224: contig of 724 bp in length  
\* 40225 40324: gap of 100 bp  
\* 40325 41025: contig of 701 bp in length  
\* 41026 41125: gap of 100 bp  
\* 41126 41875: contig of 750 bp in length

```

* 41876 41975: gap of 100 bp
* 41976 42703: contig of 734 bp in length
* 42710 42809: gap of 100 bp
* 42810 43526: contig of 717 bp in length
* 43527 43626: gap of 100 bp
* 43627 44329: contig of 703 bp in length
* 44330 44429: gap of 100 bp
* 44430 45130 45229: contig of 700 bp in length
* 45130 45230 45913: contig of 684 bp in length
* 45913 46013: gap of 100 bp
* 46014 46700: contig of 687 bp in length
* 46701 46800: gap of 100 bp
* 46801 47505: contig of 705 bp in length
* 47506 47605: gap of 100 bp
* 47606 48303: contig of 698 bp in length
* 48304 48403: gap of 100 bp
* 48404 49121: contig of 718 bp in length
* 49122 49221: gap of 100 bp
* 49222 49899: contig of 678 bp in length
* 49900 49999: gap of 100 bp
* 50000 50750: contig of 751 bp in length
* 50751 50850: gap of 100 bp
* 50851 51574: contig of 724 bp in length
* 51575 51674: gap of 100 bp
* 51675 52381: contig of 707 bp in length
* 52382 52481: gap of 100 bp
* 52482 53183: contig of 702 bp in length
* 53184 53283: gap of 100 bp
* 53284 53961: contig of 678 bp in length
* 53962 54061: gap of 100 bp
* 54062 54789: contig of 728 bp in length
* 54790 54889: gap of 100 bp
* 54890 55571: contig of 682 bp in length

```

Query Match 72.2% Score 13; DB 2; Length 65259;  
 Best Local Similarity 92.3% Pred. No. 4.6e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCGAGAGNNNNNN 18  
 Db 60406 CCTGAGAGNNNNNN 60418

```

RESULT 159
AC012249
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

```

AC012249 66086 bp DNA linear HTG 13-JUL-2000  
 Homo sapiens clone RP11-16N23, LOW-PASS SEQUENCE SAMPLING.  
 AC012249 GI:7144955  
 HTG: HTGS PHASE0.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 66086)  
 Birren, B., Linton, L., Nuebaum, C. and Lander, E.  
 Homo sapiens, clone RP11-16N23  
 Unpublished  
 2 (bases 1 to 66086)  
 Birren, B., Linton, L., Nuebaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baldwin, J., Barta, N., Becker, R., Boguslavsky, L., Bouckgalter, B.,  
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
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 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
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 Testaye, S., Tirrell, A., Vasilev, H., Vo, A., Wheeler, J., Wu, X.,

# TITLE JOURNAL COMMENT

Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
 Direct Submision  
 Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 3, 2000 this sequence version replaced gi:6091795.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: MIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L3591  
 Center clone name: 16\_N23  
 -----  
 \* NOTE: This record contains 78 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.  
 1  
 800 799: contig of 799 bp in length  
 900 899: gap of 100 bp  
 1637 1736: contig of 737 bp in length  
 1737 2465: gap of 100 bp  
 2466 3372: contig of 729 bp in length  
 3373 3372: contig of 707 bp in length  
 3373 4125: gap of 100 bp  
 4126 4225: contig of 753 bp in length  
 4226 4225: gap of 100 bp  
 4226 4975: contig of 750 bp in length  
 4976 5075: gap of 100 bp  
 5076 5847: contig of 772 bp in length  
 5848 5947: gap of 100 bp  
 5948 6692: contig of 745 bp in length  
 6693 7530: gap of 100 bp  
 6793 7530: contig of 738 bp in length  
 7531 7630: gap of 100 bp  
 7631 8374: contig of 744 bp in length  
 8375 8474: gap of 100 bp  
 8475 9210: contig of 736 bp in length  
 9211 9310: gap of 100 bp  
 9311 10028: contig of 718 bp in length  
 10029 10128: gap of 100 bp  
 10129 10840: contig of 712 bp in length  
 10841 10940: gap of 100 bp  
 10941 11687: contig of 747 bp in length  
 11688 11787: gap of 100 bp  
 11788 12520: contig of 733 bp in length  
 12521 12620: gap of 100 bp  
 12621 13379: contig of 759 bp in length  
 13380 13479: gap of 100 bp  
 13480 14248: contig of 769 bp in length  
 14249 15148: gap of 100 bp  
 15149 15241: contig of 793 bp in length  
 15242 16000: gap of 100 bp  
 16001 16100: contig of 759 bp in length  
 16101 16836: contig of 736 bp in length  
 16837 16936: gap of 100 bp  
 16937 17720: contig of 784 bp in length  
 17721 17820: gap of 100 bp  
 17821 18504: contig of 684 bp in length  
 18505 18604: gap of 100 bp  
 18605 19321: contig of 717 bp in length



```

* 19322 19421: gap of 100 bp
* 19422 20147: contig of 726 bp in length
* 20148 20247: gap of 100 bp
* 20248 21001: contig of 754 bp in length
* 21002 21101: gap of 100 bp
* 21102 21816: contig of 715 bp in length
* 21817 21916: gap of 100 bp
* 21917 22658: contig of 742 bp in length
* 22659 22758: gap of 100 bp
* 22759 23487: contig of 729 bp in length
* 23488 23587: gap of 100 bp
* 23588 24318: contig of 731 bp in length
* 24319 24418: gap of 100 bp
* 24419 25154: contig of 736 bp in length
* 25155 25254: gap of 100 bp
* 25255 26015: contig of 761 bp in length
* 26016 26115: gap of 100 bp
* 26116 26837: contig of 722 bp in length
* 26838 26937: gap of 100 bp
* 26938 27653: contig of 716 bp in length
* 27654 27753: gap of 100 bp
* 27754 28482: contig of 729 bp in length
* 28483 28582: gap of 100 bp
* 28583 29337: contig of 755 bp in length
* 29338 29437: gap of 100 bp
* 29438 30183: contig of 746 bp in length
* 30184 30283: gap of 100 bp
* 30284 31031: contig of 748 bp in length
* 31032 31131: gap of 100 bp
* 31132 31879: contig of 748 bp in length
* 31880 31979: gap of 100 bp
* 31980 32741: contig of 762 bp in length
* 32742 32841: gap of 100 bp
* 32842 33567: contig of 726 bp in length
* 33568 33667: gap of 100 bp
* 33668 34386: contig of 719 bp in length
* 34387 34486: gap of 100 bp
* 34487 35205: contig of 719 bp in length
* 35206 35305: gap of 100 bp
* 35306 36089: contig of 784 bp in length
* 36090 36189: gap of 100 bp
* 36190 36943: contig of 754 bp in length
* 36944 37043: gap of 100 bp
* 37044 37823: contig of 779 bp in length
* 37823 37922: gap of 100 bp
* 37923 38669: contig of 747 bp in length
* 38670 38769: gap of 100 bp
* 38770 39501: contig of 732 bp in length
* 39502 39601: gap of 100 bp
* 39602 40343: contig of 742 bp in length
* 40344 40443: gap of 100 bp
* 40444 41203: contig of 760 bp in length
* 41204 41303: gap of 100 bp
* 41304 42019: contig of 716 bp in length
* 42020 42119: gap of 100 bp
* 42120 42831: contig of 712 bp in length
* 42832 42931: gap of 100 bp
* 42932 43655: contig of 724 bp in length
* 43656 43755: gap of 100 bp
* 43756 44532: contig of 777 bp in length
* 44533 44632: gap of 100 bp
* 44633 45430: contig of 798 bp in length
* 45431 45530: gap of 100 bp
* 45531 46291: contig of 761 bp in length
* 46292 46391: gap of 100 bp
* 46392 47129: contig of 738 bp in length
* 47130 47229: gap of 100 bp
* 47230 47972: contig of 743 bp in length
* 47973 48072: gap of 100 bp
* 48073 48856: contig of 784 bp in length
* 48857 48956: gap of 100 bp
* 48957 49689: contig of 733 bp in length
* 49690 49789: gap of 100 bp

```

```

* 49790 50510: contig of 721 bp in length
* 50511 50611: gap of 100 bp
* 50612 51411: contig of 801 bp in length
* 51412 51511: gap of 100 bp
* 51512 52277: contig of 766 bp in length
* 52278 52377: gap of 100 bp
* 52378 53140: contig of 763 bp in length
* 53141 53240: gap of 100 bp
* 53241 54011: contig of 771 bp in length
* 54012 54111: gap of 100 bp
* 54112 54862: contig of 751 bp in length
* 54863 54962: gap of 100 bp
* 54963 55758: contig of 796 bp in length
* 55759 55858: gap of 100 bp
* 55859 56604: contig of 746 bp in length
* 56605 56704: gap of 100 bp
* 56705 57481: contig of 777 bp in length
* 57482 57581: gap of 100 bp
* 57582 58287: contig of 706 bp in length
* 58288 58387: gap of 100 bp
* 58388 59099: contig of 712 bp in length
* 59100 59199: gap of 100 bp
* 59200 59928: contig of 729 bp in length
* 59929 60028: gap of 100 bp
* 60029 60836: contig of 808 bp in length
* 60837 60936: gap of 100 bp
* 60937 61747: contig of 811 bp in length

Query Match      72.2%; Score 13; DB 2; Length 66086;
Best Local Similarity 92.3%; Pred. No. 4,6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY      6 CCTGAGAGNNNNNN 18
Db      11681 CCTGAGAGNNNNNN 11693

RESULT 160
AC120428
LOCUS      M18 musculus clone RP24-542F4, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC120428
ACCESSION  AC120428.1 GI:20455762
VERSION    AC120428.1
KEYWORDS   HTG; HTGS PHASE0.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 67572)
AUTHORS    Birren, B., Linton, L., Nuebaum, C., Lander, E., Ali, A., Allen, N.,
            Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
            Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
            Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
            Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
            Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
            Gange, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
            Hinds, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
            Kamat, A., Karakas, A., Kells, C., Labrecque, K., Lamazates, R.,
            Landers, T., Lenoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
            Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,
            McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menene, L.,
            Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
            Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
            Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
            Raymond, C., Recta, R., Rieback, W., Riley, R., Rise, C., Rogov, P.,
            Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Schuppach, R.,
            Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
            Strauss, N., Subramanian, A., Talama, J., Tesfaye, S., Theodore, J.,
            Topham, K., Travers, M., Travis, N., Trifoglio, J., Vassiliev, H.,

```

TITLE  
JOURNAL

## COMMENT

Viel.R., Vo.A., Wilson.B., Wu.X., Wyman.D., Ye.W.J., Young.G.,  
Zainoun.J., Zemek.L., Zimmer.A. and Zody.M.

TITLE  
JOURNAL

## COMMENT

Submitted (06-May-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

Project Information  
Center project name: L26045  
Center clone name: 542\_F\_4

\* NOTE: This record contains 81 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 737: contig of 737 bp in length  
\* 738 837: gap of 100 bp  
\* 838 1583: contig of 746 bp in length  
\* 1584 1683: gap of 100 bp  
\* 1684 2434: contig of 751 bp in length  
\* 2435 2534: gap of 100 bp  
\* 2535 3271: contig of 737 bp in length  
\* 3272 3371: gap of 100 bp  
\* 3372 4120: contig of 749 bp in length  
\* 4121 4220: gap of 100 bp  
\* 4221 4959: contig of 739 bp in length  
\* 4960 5059: gap of 100 bp  
\* 5060 5803: contig of 744 bp in length  
\* 5804 5903: gap of 100 bp  
\* 5904 6629: contig of 726 bp in length  
\* 6630 6729: gap of 100 bp  
\* 6730 7468: contig of 739 bp in length  
\* 7469 7568: gap of 100 bp  
\* 7569 8294: contig of 726 bp in length  
\* 8295 8394: gap of 100 bp  
\* 8395 9156: contig of 762 bp in length  
\* 9157 9256: gap of 100 bp  
\* 9257 10002: contig of 746 bp in length  
\* 10003 10102: gap of 100 bp  
\* 10103 10850: contig of 748 bp in length  
\* 10851 10950: gap of 100 bp  
\* 10951 11682: contig of 732 bp in length  
\* 11683 11782: gap of 100 bp  
\* 11783 12522: contig of 740 bp in length  
\* 12523 12622: gap of 100 bp  
\* 12623 13323: contig of 701 bp in length  
\* 13324 13424: gap of 100 bp  
\* 13425 14147: contig of 724 bp in length  
\* 14148 14247: gap of 100 bp  
\* 14249 14974: contig of 727 bp in length  
\* 14975 15074: gap of 100 bp  
\* 15075 15804: contig of 730 bp in length  
\* 15805 15904: gap of 100 bp  
\* 15905 16646: contig of 742 bp in length  
\* 16647 16746: gap of 100 bp  
\* 16747 17497: contig of 751 bp in length  
\* 17498 17597: gap of 100 bp  
\* 17598 18332: contig of 735 bp in length  
\* 18333 18432: gap of 100 bp  
\* 18433 19165: contig of 733 bp in length

\* 19166 19265: gap of 100 bp  
\* 19266 20012: contig of 747 bp in length  
\* 20013 20112: gap of 100 bp  
\* 20113 20821: contig of 709 bp in length  
\* 20822 20921: gap of 100 bp  
\* 20922 21652: contig of 731 bp in length  
\* 21653 21752: gap of 100 bp  
\* 21753 22467: contig of 715 bp in length  
\* 22468 22567: gap of 100 bp  
\* 22568 23295: contig of 728 bp in length  
\* 23296 23395: gap of 100 bp  
\* 23396 24120: contig of 725 bp in length  
\* 24121 24220: gap of 100 bp  
\* 24221 24955: contig of 735 bp in length  
\* 24956 25055: gap of 100 bp  
\* 25056 25815: contig of 760 bp in length  
\* 25816 25915: gap of 100 bp  
\* 25916 26671: contig of 756 bp in length  
\* 26672 26771: gap of 100 bp  
\* 26772 27510: contig of 739 bp in length  
\* 27511 27610: gap of 100 bp  
\* 27611 28353: contig of 743 bp in length  
\* 28354 28453: gap of 100 bp  
\* 28454 29188: contig of 735 bp in length  
\* 29189 29288: gap of 100 bp  
\* 29289 30030: contig of 742 bp in length  
\* 30031 30130: gap of 100 bp  
\* 30131 30858: contig of 728 bp in length  
\* 30859 30958: gap of 100 bp  
\* 30959 31677: contig of 719 bp in length  
\* 31678 31777: gap of 100 bp  
\* 31778 32500: contig of 723 bp in length  
\* 32501 32600: gap of 100 bp  
\* 32601 33328: contig of 728 bp in length  
\* 33329 33428: gap of 100 bp  
\* 33429 34172: contig of 744 bp in length  
\* 34173 34272: gap of 100 bp  
\* 34273 35029: contig of 757 bp in length  
\* 35030 35129: gap of 100 bp  
\* 35130 35865: contig of 736 bp in length  
\* 35866 35965: gap of 100 bp  
\* 35966 36710: contig of 745 bp in length  
\* 36711 36810: gap of 100 bp  
\* 36811 37668: contig of 758 bp in length  
\* 37669 37668: gap of 100 bp  
\* 37669 38364: contig of 696 bp in length  
\* 38365 38464: gap of 100 bp  
\* 38465 39196: contig of 732 bp in length  
\* 39197 39296: gap of 100 bp  
\* 39297 39993: contig of 697 bp in length  
\* 39994 40093: gap of 100 bp  
\* 40094 40824: contig of 731 bp in length  
\* 40825 40924: gap of 100 bp  
\* 40925 41652: contig of 728 bp in length  
\* 41653 41752: gap of 100 bp  
\* 41753 42485: contig of 733 bp in length  
\* 42486 42585: gap of 100 bp  
\* 42586 43313: contig of 728 bp in length  
\* 43314 43413: gap of 100 bp  
\* 43414 44176: contig of 763 bp in length  
\* 44177 44276: gap of 100 bp  
\* 44277 45024: contig of 748 bp in length  
\* 45025 45124: gap of 100 bp  
\* 45125 45851: contig of 727 bp in length  
\* 45852 45951: gap of 100 bp  
\* 45952 46678: contig of 727 bp in length  
\* 46679 46778: gap of 100 bp  
\* 46779 47516: contig of 738 bp in length  
\* 47517 47616: gap of 100 bp  
\* 47617 48344: contig of 728 bp in length  
\* 48345 48444: gap of 100 bp  
\* 48445 49177: contig of 733 bp in length  
\* 49178 49277: gap of 100 bp



```

* 12371 12470: gap of 100 bp
* 12471 13194: contig of 724 bp in length
* 13195 13294: gap of 100 bp
* 13295 14031: contig of 737 bp in length
* 14032 14131: gap of 100 bp
* 14132 14850: contig of 719 bp in length
* 14851 14950: gap of 100 bp
* 14951 15695: contig of 745 bp in length
* 15696 15795: gap of 100 bp
* 15796 16539: contig of 744 bp in length
* 16540 17395: contig of 756 bp in length
* 17396 17495: gap of 100 bp
* 17496 18207: contig of 711 bp in length
* 18207 18306: gap of 100 bp
* 18307 19021: contig of 715 bp in length
* 19022 19121: gap of 100 bp
* 19122 19856: contig of 735 bp in length
* 19857 20664: contig of 708 bp in length
* 20665 20764: gap of 100 bp
* 20765 21514: contig of 750 bp in length
* 21515 22357: contig of 743 bp in length
* 22358 22457: gap of 100 bp
* 22458 23203: contig of 746 bp in length
* 23204 24031: gap of 100 bp
* 24032 24131: gap of 100 bp
* 24132 24870: contig of 739 bp in length
* 24871 25723: contig of 753 bp in length
* 25724 25823: gap of 100 bp
* 25824 26779: contig of 756 bp in length
* 26780 27406: contig of 727 bp in length
* 27407 27507: gap of 100 bp
* 27507 28233: contig of 727 bp in length
* 28234 29065: contig of 732 bp in length
* 29066 29165: gap of 100 bp
* 29166 29898: contig of 733 bp in length
* 29899 30735: contig of 737 bp in length
* 30736 30835: gap of 100 bp
* 30836 31561: contig of 726 bp in length
* 31562 31661: gap of 100 bp
* 31662 32380: contig of 719 bp in length
* 32381 32480: gap of 100 bp
* 32481 33226: contig of 746 bp in length
* 33227 33326: gap of 100 bp
* 33327 34072: contig of 746 bp in length
* 34073 34172: gap of 100 bp
* 34173 34922: contig of 750 bp in length
* 34923 35022: gap of 100 bp
* 35023 35736: contig of 714 bp in length
* 35737 35836: gap of 100 bp
* 35837 36562: contig of 726 bp in length
* 36563 37294: gap of 100 bp
* 37295 37494: gap of 100 bp
* 37495 38201: contig of 707 bp in length
* 38202 39021: contig of 720 bp in length
* 39022 39121: gap of 100 bp
* 39122 39860: contig of 733 bp in length
* 39861 39960: gap of 100 bp
* 39961 40702: contig of 742 bp in length
* 40703 40802: gap of 100 bp
* 40803 41542: contig of 740 bp in length
* 41543 41642: gap of 100 bp
* 41643 42394: contig of 752 bp in length
* 42395 42494: gap of 100 bp

```

```

Query Match      72.2%; Score 13; DB 2; Length 68315;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCGGAGGNNNNNN 18
Db      12364 CCGGAGNNNNNN 12376

```

```

RESULT 162
AC100130
LOCUS      AC100130      68536 bp      DNA      linear      HTG 22-NOV-2001
DEFINITION Mus musculus clone RP23-41A2, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC100130
VERSION    AC100130.1 GI:17047496
KEYWORDS   HTG; HTGS PHASE0.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

REFERENCE  1 (bases 1 to 68536)
AUTHORS   Birren, B., Linton, L., Nussbaum, C. and Lander, E.
TITLE     Mus musculus, clone RP23-41A2
JOURNAL   Unpublished
AUTHORS

```

```

2 (bases 1 to 68536)
Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barina, N., Bastian, V., Bogunlavsky, L., Boukhalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gadda, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., Laroque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J.,
Menues, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Notbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Pollard, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strause, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, D.,
Topham, K., Travers, M., Travie, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, M., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information

```

Center project name: L14000  
Center clone name: 41\_A\_2

NOTE: This record contains 66 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
\* 918 917: contig of 917 bp in length  
\* 1018 1017: gap of 100 bp  
\* 1972 1971: contig of 954 bp in length  
\* 2072 2071: gap of 100 bp  
\* 2985 2984: contig of 913 bp in length  
\* 3085 3084: gap of 100 bp  
\* 3989 3988: contig of 904 bp in length  
\* 4089 4088: gap of 100 bp  
\* 4991 4990: contig of 902 bp in length  
\* 5091 5090: gap of 100 bp  
\* 6122 6121: contig of 1031 bp in length  
\* 7176 7175: gap of 100 bp  
\* 7276 7275: contig of 955 bp in length  
\* 8204 8203: contig of 927 bp in length  
\* 9183 9182: gap of 100 bp  
\* 9283 9282: contig of 879 bp in length  
\* 10212 10211: contig of 930 bp in length  
\* 10213 10212: gap of 100 bp  
\* 11268 11267: contig of 955 bp in length  
\* 11368 11367: gap of 100 bp  
\* 12370 12369: contig of 1002 bp in length  
\* 12470 12469: gap of 100 bp  
\* 13387 13386: contig of 918 bp in length  
\* 13488 13487: gap of 100 bp  
\* 14478 14477: contig of 991 bp in length  
\* 14579 14578: gap of 100 bp  
\* 15493 15492: contig of 915 bp in length  
\* 15494 15493: gap of 100 bp  
\* 16398 16397: contig of 804 bp in length  
\* 16497 16496: gap of 100 bp  
\* 17420 17419: contig of 922 bp in length  
\* 17520 17519: gap of 100 bp  
\* 18462 18461: contig of 942 bp in length  
\* 18562 18561: gap of 100 bp  
\* 19478 19477: contig of 916 bp in length  
\* 19578 19577: gap of 100 bp  
\* 20525 20524: contig of 947 bp in length  
\* 20625 20624: gap of 100 bp  
\* 21537 21536: contig of 912 bp in length  
\* 21637 21636: gap of 100 bp  
\* 22572 22571: contig of 936 bp in length  
\* 22673 22672: gap of 100 bp  
\* 23644 23643: contig of 971 bp in length  
\* 23743 23742: gap of 100 bp  
\* 24721 24720: contig of 978 bp in length  
\* 24722 24721: gap of 100 bp  
\* 24822 24821: gap of 100 bp  
\* 25774 25773: contig of 953 bp in length  
\* 25875 25874: gap of 100 bp  
\* 26833 26832: contig of 959 bp in length  
\* 26933 26932: gap of 100 bp  
\* 27852 27851: contig of 919 bp in length  
\* 27953 27952: gap of 100 bp  
\* 28932 28931: contig of 980 bp in length  
\* 29033 29032: gap of 100 bp  
\* 29933 29932: contig of 901 bp in length  
\* 30034 30033: gap of 100 bp  
\* 30934 30933: contig of 906 bp in length

## FEATURES

\* 30940 31039: gap of 100 bp  
\* 31040 31953: contig of 914 bp in length  
\* 31954 32053: gap of 100 bp  
\* 32054 33021: contig of 968 bp in length  
\* 33022 33121: gap of 100 bp  
\* 33122 34030: contig of 909 bp in length  
\* 34031 34130: gap of 100 bp  
\* 34131 35105: contig of 976 bp in length  
\* 35107 35206: gap of 100 bp  
\* 35207 36123: contig of 917 bp in length  
\* 36124 36223: gap of 100 bp  
\* 36224 37138: contig of 915 bp in length  
\* 37139 37238: gap of 100 bp  
\* 37239 38209: contig of 971 bp in length  
\* 38210 38309: gap of 100 bp  
\* 38310 39381: contig of 1072 bp in length  
\* 39382 39481: gap of 100 bp  
\* 39482 40378: contig of 897 bp in length  
\* 40379 40478: gap of 100 bp  
\* 40479 41424: contig of 946 bp in length  
\* 41425 41524: gap of 100 bp  
\* 41525 42481: contig of 957 bp in length  
\* 42482 42581: gap of 100 bp  
\* 42582 43529: contig of 948 bp in length  
\* 43530 43629: gap of 100 bp  
\* 43630 44561: contig of 932 bp in length  
\* 44562 44661: gap of 100 bp  
\* 44662 45633: contig of 972 bp in length  
\* 45634 45733: gap of 100 bp  
\* 45734 46556: contig of 923 bp in length  
\* 46557 46756: gap of 100 bp  
\* 46757 47661: contig of 905 bp in length  
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\* 51959 52881: contig of 923 bp in length  
\* 52882 52981: gap of 100 bp  
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\* 58138 58237: gap of 100 bp  
\* 58238 59145: contig of 908 bp in length  
\* 59146 59245: gap of 100 bp  
\* 59246 60209: contig of 964 bp in length  
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\* 60310 61234: contig of 925 bp in length  
\* 61235 61334: gap of 100 bp  
\* 61335 62290: contig of 956 bp in length  
\* 62291 62391: gap of 100 bp  
\* 62391 63347: contig of 957 bp in length  
\* 63348 63447: gap of 100 bp  
\* 63448 64429: contig of 982 bp in length  
\* 64430 64529: gap of 100 bp  
\* 64530 65437: contig of 908 bp in length  
\* 65438 65537: gap of 100 bp  
\* 65538 66485: contig of 948 bp in length  
\* 66486 66585: gap of 100 bp  
\* 66586 67458: contig of 873 bp in length  
\* 67459 68536: gap of 100 bp  
\* 68536 68536: contig of 978 bp in length

Location/Qualifiers

source

1. 68536  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="RP23-41A2"  
/clone\_lib="RPCI-23 Female Mouse BAC"

Query Match 72.2%; Score 13; DB 2; Length 68536;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNN 18  
||:|||||||  
46650 CCTGAGAGNNNNN 46662

Db

RESULT 163  
AC091036  
LOCUS  
DEFINITION Homo sapiens chromosome 15 clone RP11-79J21 map 15, LOW-PASS  
SEQUENCE SAMPLING.  
AC091036 68732 bp DNA linear HTG 24-MAR-2001  
AC091036.1 GI:13443198  
HTG; HTGS PHASEO.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 68732)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens chromosome 15, clone RP11-79J21  
Unpublished  
2 (bases 1 to 68732)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barnes,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glende,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., Lacroque,K., Lamasares,R., Landers,T., Lenoczky,J., Levine,R., Liu,G., Maclean,C., MacDonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrum,J., Menus,L., Mihsya,T., Mlenga,V., Santos,R., Riese,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tefaye,S., Theodore,J., Travers,M., Travis,N., Trigglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (24-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L13156  
Center clone name: 79\_J\_21

TITLE  
JOURNAL  
COMMENT

arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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678 677: contig of 677 bp in length  
778 777: gap of 100 bp  
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1553 1552: gap of 100 bp  
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2365 2365: gap of 100 bp  
2465 2465: gap of 100 bp  
3177 3177: contig of 713 bp in length  
3277 3277: gap of 100 bp  
3378 3378: contig of 711 bp in length  
3989 3989: gap of 100 bp  
4089 4089: gap of 100 bp  
4791 4791: contig of 703 bp in length  
4792 4792: gap of 100 bp  
5599 5599: contig of 708 bp in length  
5600 5600: gap of 100 bp  
5700 5700: contig of 790 bp in length  
6489 6489: gap of 100 bp  
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7463 7463: contig of 775 bp in length  
8238 8238: gap of 100 bp  
8338 8338: contig of 712 bp in length  
9149 9149: gap of 100 bp  
9150 9150: contig of 749 bp in length  
9899 9899: gap of 100 bp  
9999 9999: gap of 100 bp  
10747 10746: contig of 748 bp in length  
10847 10846: gap of 100 bp  
11580 11580: contig of 734 bp in length  
11581 11580: gap of 100 bp  
11681 11680: gap of 100 bp  
12390 12390: contig of 710 bp in length  
12391 12390: gap of 100 bp  
12491 12490: contig of 707 bp in length  
13197 13197: gap of 100 bp  
13297 13297: gap of 100 bp  
13998 13998: contig of 709 bp in length  
14006 14006: gap of 100 bp  
14107 14106: gap of 100 bp  
14875 14875: contig of 769 bp in length  
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14975 14975: gap of 100 bp  
15743 15743: contig of 768 bp in length  
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16642 16642: contig of 799 bp in length  
16742 16742: gap of 100 bp  
16743 16743: contig of 731 bp in length  
17473 17473: gap of 100 bp  
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26851 26851: contig of 720 bp in length  
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27668 27668: contig of 717 bp in length  
27768 27768: gap of 100 bp

\* NOTE: This record contains 82 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely

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* 27769 28543: contig of 775 bp in length
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* 31200 31951: contig of 752 bp in length
* 31952 32051: gap of 100 bp
* 32052 32802: contig of 751 bp in length
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* 37858 38570: contig of 713 bp in length
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* 38671 39423: contig of 753 bp in length
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* 44577 45289: contig of 713 bp in length
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* 46239 46922: contig of 684 bp in length
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* 53889 54605: contig of 717 bp in length
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Db 5593 CCTGAGNNNNNN 5605

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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 68951)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-33F9
Unpublished
2 (bases 1 to 68951)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Anderson,S., Barna,N., Baetien,V., Boguslavsky,L., Boukngalter,B.,
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Coopel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
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Oliver,J., Peterson,K., Phunhahng,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
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Strauss,N., Subramanian,A., Talmas,J., Tesfaye,S., Theodore,J.,
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Viel,R., Vo,A., Wilson,D., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L13892
Center clone name: 33_F_9
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* NOTE: This record contains 86 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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4008 4695: contig of 688 bp in length  
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8034 8753: contig of 720 bp in length  
8754 8853: gap of 100 bp  
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9570 9669: gap of 100 bp  
9670 10363: contig of 694 bp in length  
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11152 11251: gap of 100 bp  
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11947 12046: gap of 100 bp  
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12740 12839: gap of 100 bp  
12840 13543: contig of 704 bp in length  
13544 13643: gap of 100 bp  
13644 14352: contig of 709 bp in length  
14353 14452: gap of 100 bp  
14453 15165: contig of 713 bp in length  
15166 15265: gap of 100 bp  
15266 15995: contig of 730 bp in length  
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16096 16830: contig of 735 bp in length  
16831 16930: gap of 100 bp  
16931 17624: contig of 694 bp in length  
17625 17725: gap of 100 bp  
17726 18448: contig of 724 bp in length  
18449 18548: gap of 100 bp  
18549 19238: contig of 690 bp in length  
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19339 20028: contig of 690 bp in length  
20029 20128: gap of 100 bp  
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20916 21731: contig of 816 bp in length  
21732 21831: gap of 100 bp  
21832 22542: contig of 691 bp in length  
22543 22642: gap of 100 bp  
22643 23329: contig of 707 bp in length  
23330 23429: gap of 100 bp  
23430 24156: contig of 727 bp in length  
24157 24256: gap of 100 bp  
24257 24931: contig of 675 bp in length  
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30537 30637 30636: gap of 100 bp  
30638 31342: contig of 706 bp in length  
31343 31443 31442: gap of 100 bp  
31444 32145: contig of 703 bp in length  
32146 32245 32245: gap of 100 bp  
32246 32944: contig of 699 bp in length  
32945 33044: gap of 100 bp  
33045 33772: contig of 728 bp in length  
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34556 34656 34655: gap of 100 bp  
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35366 35465: gap of 100 bp  
35466 36193: contig of 728 bp in length  
36194 36293: gap of 100 bp  
36294 37013: contig of 720 bp in length  
37014 37113: gap of 100 bp  
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37874 38568: contig of 695 bp in length  
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40141 40240: gap of 100 bp  
40241 40921: contig of 681 bp in length  
40922 41021: gap of 100 bp  
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41737 41836: gap of 100 bp  
41837 42552: contig of 716 bp in length  
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42653 43365: contig of 713 bp in length  
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Query Match 72.2%; Score 13; DB 2; Length 68951;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCGAGGNNNNNN 18  
DB 60965 CCGAGGNNNNNN 60977



RESULT 165  
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Homo sapiens (human)  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 70557)  
Barren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 8, clone RP11-263C6  
Unpublished  
2 (bases 1 to 70557)  
Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,  
Barna, N., Baetjen, V., Boguslavsky, L., Boukhalter, B., Brown, A.,  
Camaretta, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,  
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McIntosh, R., Meldrum, J., Meneus, L., Mhova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H.,  
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,  
Phunkiang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,  
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,  
Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P.,  
Sougnaz, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J.,  
Travers, M., Travis, N., Trigglio, J., Vasilev, H., Viel, R., Vo, A.,  
Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G., Zaitoun, J.,  
Zemke, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 22, 2001 this sequence version replaced gi:14029927.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIRB  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L1676  
Center clone name: 263\_C\_6  
-----  
\* NOTE: This record contains 90 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\* 1  
\* 638 737: contig of 637 bp in length  
\* 638 737: gap of 100 bp  
\* 738 1410: contig of 673 bp in length  
\* 1411 1510: gap of 100 bp  
\* 1511 2179: contig of 669 bp in length  
\* 2180 2279: gap of 100 bp

2280 2951: contig of 672 bp in length  
2952 3051: gap of 100 bp  
3052 3751: contig of 700 bp in length  
3752 3851: gap of 100 bp  
3852 4543: contig of 692 bp in length  
4544 4643: gap of 100 bp  
4644 5335: contig of 692 bp in length  
5336 5435: gap of 100 bp  
5436 6130: contig of 695 bp in length  
6131 6230: gap of 100 bp  
6231 6916: contig of 686 bp in length  
6917 7017: gap of 100 bp  
7017 7693: contig of 677 bp in length  
7694 7793: gap of 100 bp  
7794 8475: contig of 682 bp in length  
8476 8575: gap of 100 bp  
8576 9244: contig of 669 bp in length  
9245 9344: gap of 100 bp  
9345 10033: contig of 689 bp in length  
10034 10133: gap of 100 bp  
10134 10821: contig of 688 bp in length  
10822 10921: gap of 100 bp  
10922 11604: contig of 683 bp in length  
11605 11704: gap of 100 bp  
11705 12386: contig of 682 bp in length  
12387 12486: gap of 100 bp  
12487 13175: contig of 689 bp in length  
13176 13275: gap of 100 bp  
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13965 14064: gap of 100 bp  
14065 14761: contig of 697 bp in length  
14762 14861: gap of 100 bp  
14862 15557: contig of 696 bp in length  
15558 15657: gap of 100 bp  
15658 16342: contig of 685 bp in length  
16343 16442: gap of 100 bp  
16443 17135: contig of 693 bp in length  
17136 17235: gap of 100 bp  
17236 17894: contig of 659 bp in length  
17895 17994: gap of 100 bp  
17995 18680: contig of 686 bp in length  
18681 18780: gap of 100 bp  
18781 19469: contig of 689 bp in length  
19470 19569: gap of 100 bp  
19570 20257: contig of 688 bp in length  
20258 20357: gap of 100 bp  
20358 21033: contig of 676 bp in length  
21034 21133: gap of 100 bp  
21134 21840: contig of 707 bp in length  
21841 21940: gap of 100 bp  
21941 22625: contig of 685 bp in length  
22626 22725: gap of 100 bp  
22726 23415: contig of 690 bp in length  
23416 23515: gap of 100 bp  
23516 24186: contig of 671 bp in length  
24187 24286: gap of 100 bp  
24287 24976: contig of 690 bp in length  
24977 25076: gap of 100 bp  
25077 25766: contig of 690 bp in length  
25767 25866: gap of 100 bp  
25867 26550: contig of 684 bp in length  
26551 26650: gap of 100 bp  
26651 27317: contig of 667 bp in length  
27318 27417: gap of 100 bp  
27418 28106: contig of 689 bp in length  
28107 28206: gap of 100 bp  
28207 28897: contig of 691 bp in length  
28898 28997: gap of 100 bp  
28998 29691: contig of 694 bp in length  
29692 29791: gap of 100 bp  
29792 30469: contig of 678 bp in length  
30470 30569: gap of 100 bp  
30570 31234: contig of 665 bp in length

```

* 31235 31334: gap of 100 bp
* 31235 32019: contig of 685 bp in length
* 32020 32119: gap of 100 bp
* 32120 32809: contig of 690 bp in length
* 32810 32909: gap of 100 bp
* 32910 33576: contig of 667 bp in length
* 33577 33676: gap of 100 bp
* 33677 34370: contig of 694 bp in length
* 34371 34470: gap of 100 bp
* 34471 35139: contig of 669 bp in length
* 35140 35239: gap of 100 bp
* 35240 35935: contig of 696 bp in length
* 35936 36035: gap of 100 bp
* 36036 36706: contig of 671 bp in length
* 36707 37489: contig of 683 bp in length
* 37490 37589: gap of 100 bp
* 37590 38276: contig of 687 bp in length
* 38277 38376: gap of 100 bp
* 38377 39046: contig of 670 bp in length
* 39047 39146: gap of 100 bp
* 39147 39822: contig of 676 bp in length
* 39823 39923: gap of 100 bp
* 39923 40583: contig of 661 bp in length
* 40584 41381: contig of 698 bp in length
* 41382 41482: gap of 100 bp
* 41482 42179: contig of 698 bp in length
* 42180 42279: gap of 100 bp
* 42280 42971: contig of 692 bp in length
* 42972 43071: gap of 100 bp
* 43072 43768: contig of 697 bp in length
* 43769 43868: gap of 100 bp
* 43869 44559: contig of 691 bp in length
* 44560 44659: gap of 100 bp
* 44660 45328: contig of 669 bp in length
* 45329 45428: gap of 100 bp
* 45429 46121: contig of 693 bp in length
* 46122 46221: gap of 100 bp
* 46222 46911: contig of 690 bp in length
* 46912 47011: gap of 100 bp
* 47012 47704: contig of 693 bp in length
* 47705 47805: gap of 100 bp
* 47805 48487: contig of 683 bp in length
* 48488 48587: gap of 100 bp
* 48588 49280: contig of 693 bp in length
* 49281 49380: gap of 100 bp
* 49381 50070: contig of 690 bp in length
* 50071 50170: gap of 100 bp
* 50171 50866: contig of 696 bp in length
* 50867 50966: gap of 100 bp
* 50967 51654: contig of 688 bp in length
* 51655 51754: gap of 100 bp
* 51755 52441: contig of 687 bp in length
* 52442 52541: gap of 100 bp
* 52542 53220: contig of 679 bp in length
* 53221 53320: gap of 100 bp
* 53321 54016: contig of 696 bp in length

```

Query Match Best Local Similarity 92.3%; Score 13; DB 2; Length 70557; Pred. No. 4.6e+02; Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNN 18  
Db 44553 CCTGAGAGNNNNN 44565

RESULT 166  
AC100674  
LOCUS  
DEFINITION Mus musculus clone RP23-167K24, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC100674

# VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

AC100674.1 GI:117048040  
HTG; HTGS PHASE0.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 71396)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Mus musculus, clone RP23-167K24  
Unpublished  
2 (bases 1 to 71396)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bonkshaiter, B.,  
Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B.,  
Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,  
Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,  
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardina, S.,  
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Hagos, B., Heaford, A., Horton, L., Hulme, W., Illie, I., Johnson, R.,  
Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K.,  
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,  
McCarthy, M., McEwan, P., McKernan, K., McPeckers, R., Meldrum, J.,  
Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,  
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Triggilio, J., Vasiliiev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.D., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE JOURNAL COMMENT

Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www.seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: 167\_K\_24  
Center clone name: 167\_K\_24

\* NOTE: This record contains 71 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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1 789 888: gap of 100 bp
* 789 889 1702: contig of 814 bp in length
* 1703 1803 1802: gap of 100 bp
* 1803 2642: contig of 840 bp in length
* 2643 2743 2742: gap of 100 bp
* 2743 3637: contig of 895 bp in length
* 3638 3737: gap of 100 bp
* 3738 4635: contig of 898 bp in length
* 4636 4736 4735: gap of 100 bp
* 4736 5657: contig of 922 bp in length
* 5658 5757: gap of 100 bp
* 5758 6692: contig of 935 bp in length
* 6693 6792: gap of 100 bp

```

```
* 6793 7703: contig of 911 bp in length
* 7704 7803: gap of 100 bp in length
* 8743 8742: contig of 939 bp in length
* 8843 8842: gap of 100 bp in length
* 9788 9787: contig of 945 bp in length
* 9888 9887: gap of 100 bp in length
* 10820 10819: contig of 932 bp in length
* 10920 11808: contig of 889 bp in length
* 11809 11908: gap of 100 bp in length
* 11909 12830: contig of 922 bp in length
* 12831 12930: gap of 100 bp in length
* 12931 13847: contig of 917 bp in length
* 13848 13947: gap of 100 bp in length
* 13948 14886: contig of 939 bp in length
* 14887 14986: gap of 100 bp in length
* 14987 15911: contig of 925 bp in length
* 15912 16011: gap of 100 bp in length
* 16012 16903: contig of 892 bp in length
* 16904 17003: gap of 100 bp in length
* 17004 17906: contig of 903 bp in length
* 17907 18006: gap of 100 bp in length
* 18007 18931: contig of 925 bp in length
* 18932 19031: gap of 100 bp in length
* 19032 19945: contig of 914 bp in length
* 19946 20045: gap of 100 bp in length
* 20046 20951: contig of 906 bp in length
* 20952 21051: gap of 100 bp in length
* 21052 21949: contig of 898 bp in length
* 21950 22049: gap of 100 bp in length
* 22050 22950: contig of 901 bp in length
* 22951 23051: gap of 100 bp in length
* 23051 23945: contig of 895 bp in length
* 23946 24045: gap of 100 bp in length
* 24046 24955: contig of 910 bp in length
* 24956 25055: gap of 100 bp in length
* 25056 25981: contig of 925 bp in length
* 25981 26080: gap of 100 bp in length
* 26081 27052: contig of 972 bp in length
* 27053 27152: gap of 100 bp in length
* 27153 28067: contig of 915 bp in length
* 28068 28167: gap of 100 bp in length
* 28168 29076: contig of 909 bp in length
* 29077 29176: gap of 100 bp in length
* 29177 30093: contig of 917 bp in length
* 30094 30193: gap of 100 bp in length
* 30194 31099: contig of 906 bp in length
* 31100 31199: gap of 100 bp in length
* 31200 33097: contig of 898 bp in length
* 32098 32197: gap of 100 bp in length
* 32198 33113: contig of 916 bp in length
* 33114 33213: gap of 100 bp in length
* 33214 34125: contig of 912 bp in length
* 34126 34225: gap of 100 bp in length
* 34226 35133: contig of 908 bp in length
* 35134 35233: gap of 100 bp in length
* 35234 36150: contig of 917 bp in length
* 36151 36250: gap of 100 bp in length
* 36251 37171: contig of 921 bp in length
* 37172 37271: gap of 100 bp in length
* 37272 38159: contig of 888 bp in length
* 38160 38259: gap of 100 bp in length
* 38260 39156: contig of 897 bp in length
* 39157 39256: gap of 100 bp in length
* 39257 40188: contig of 932 bp in length
* 40189 40288: gap of 100 bp in length
* 40289 41210: contig of 922 bp in length
* 41211 41310: gap of 100 bp in length
* 41311 42222: contig of 912 bp in length
* 42223 42322: gap of 100 bp in length
* 42323 43218: contig of 896 bp in length
* 43219 43318: gap of 100 bp in length
* 44233: contig of 915 bp in length
```

```
* 44234 44333: gap of 100 bp in length
* 44334 45245: contig of 913 bp in length
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* 45347 46261: contig of 915 bp in length
* 46262 46361: gap of 100 bp in length
* 46362 47279: contig of 918 bp in length
* 47280 47379: gap of 100 bp in length
* 47380 48275: contig of 897 bp in length
* 48276 48376: gap of 100 bp in length
* 48377 49282: contig of 906 bp in length
* 49283 49382: gap of 100 bp in length
* 49383 50305: contig of 923 bp in length
* 50306 50405: gap of 100 bp in length
* 50406 51314: contig of 909 bp in length
* 51315 51414: gap of 100 bp in length
* 51415 52335: contig of 921 bp in length
* 52336 52435: gap of 100 bp in length
* 52436 53163: contig of 728 bp in length
* 53164 53263: gap of 100 bp in length
* 53264 54210: contig of 947 bp in length
* 54211 54310: gap of 100 bp in length
* 54311 55199: contig of 889 bp in length
* 55200 55299: gap of 100 bp in length
* 55300 56212: contig of 913 bp in length
* 56213 56312: gap of 100 bp in length
* 56313 57287: contig of 975 bp in length
* 57288 57387: gap of 100 bp in length
* 57388 58245: contig of 858 bp in length
* 58246 58345: gap of 100 bp in length
* 58346 59235: contig of 891 bp in length
* 59237 59336: gap of 100 bp in length
* 59337 60272: contig of 936 bp in length
* 60273 60372: gap of 100 bp in length
* 60373 61289: contig of 917 bp in length
* 61290 61389: gap of 100 bp in length
* 61390 62299: contig of 910 bp in length
* 62300 62399: gap of 100 bp in length
* 62400 63322: contig of 923 bp in length
* 63323 63422: gap of 100 bp in length
* 63423 64336: contig of 914 bp in length
* 64337 64436: gap of 100 bp in length
* 64437 65354: contig of 918 bp in length
* 65355 65454: gap of 100 bp in length
* 65455 66352: contig of 898 bp in length
* 66353 66452: gap of 100 bp in length
* 66453 67362: contig of 910 bp in length
* 67363 67462: gap of 100 bp in length
* 67463 68370: contig of 908 bp in length
* 68371 68470: gap of 100 bp in length
* 68471 69379: contig of 909 bp in length
* 69380 69479: gap of 100 bp in length

Query Match      72.2% Score 13; DB 2; Length 71396;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCTGAGAGNNNNNN 18
Db      68364 CCTGAGAGNNNNNN 68376

RESULT 167
AC026581      72969 bp      DNA      linear      HTG 22-MAR-2000
LOCUS      Homo sapiens clone RP11-67804, LOW-PASS SEQUENCE SAMPLING.
DEFINITION      AC026581
ACCESSION      AC026581
VERSION      AC026581.1 GI:7284166
KEYWORDS      HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 72969)
```

AUTHORS  
JOURNAL  
REFERENCE  
AUTHORSBirtren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens, clone RP11-67804

2 (bases 1 to 72969)

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,  
Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collamore, A., Cooke, P., DeRetellano, K., Dewar, K., Diaz, J.S.,  
Dodge, S., Domini, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,  
Galden, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
Klein, J., Labrecque, K., Lamazares, R., Landers, T., Lehotzky, J.,  
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,  
McCarthy, M., McEwan, P., McGuck, A., McKernan, K., McPheters, R.,  
Melidrim, J., Menus, L., Mihova, T., Miranda, C., Mlangi, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neil, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N., P.,  
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, F., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

## TITLE

## JOURNAL

## COMMENT

Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WITB

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L8363

Center clone name: 678\_O\_4

-----  
\* NOTE: This record contains 88 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 716: contig of 716 bp in length  
\* 717 816: gap of 100 bp  
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\* 2398 2497: gap of 100 bp  
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\* 4047 4146: gap of 100 bp  
\* 4147 4863: contig of 717 bp in length  
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\* 5695 5794: gap of 100 bp  
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\* 8180 8279: gap of 100 bp  
\* 8280 9017: contig of 738 bp in length  
\* 9018 9117: gap of 100 bp

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\* 11513 11612: gap of 100 bp  
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\* 18942 19042: gap of 100 bp  
\* 19042 19775: contig of 733 bp in length  
\* 19775 19875: gap of 100 bp  
\* 19875 20595: contig of 720 bp in length  
\* 20595 20695: gap of 100 bp  
\* 20695 21432: contig of 737 bp in length  
\* 21432 21532: gap of 100 bp  
\* 21532 22263: contig of 721 bp in length  
\* 22263 22363: gap of 100 bp  
\* 22363 23085: contig of 722 bp in length  
\* 23085 23185: gap of 100 bp  
\* 23185 23902: contig of 717 bp in length  
\* 23902 24002: gap of 100 bp  
\* 24002 24717: contig of 715 bp in length  
\* 24717 24817: gap of 100 bp  
\* 24817 25549: contig of 732 bp in length  
\* 25549 25649: gap of 100 bp  
\* 25649 26395: contig of 746 bp in length  
\* 26395 26495: gap of 100 bp  
\* 26495 27238: contig of 743 bp in length  
\* 27238 27338: gap of 100 bp  
\* 27338 28076: contig of 738 bp in length  
\* 28076 28176: gap of 100 bp  
\* 28176 28894: contig of 718 bp in length  
\* 28894 29735: contig of 741 bp in length  
\* 29735 29835: gap of 100 bp  
\* 29835 30573: contig of 728 bp in length  
\* 30573 30673: gap of 100 bp  
\* 30673 31492: contig of 719 bp in length  
\* 31492 32223: contig of 731 bp in length  
\* 32223 33046: contig of 723 bp in length  
\* 33046 33147: gap of 100 bp  
\* 33147 33853: contig of 707 bp in length  
\* 33853 33953: gap of 100 bp  
\* 33953 34691: contig of 738 bp in length  
\* 34691 34791: gap of 100 bp  
\* 34791 35522: contig of 721 bp in length  
\* 35522 35622: gap of 100 bp  
\* 35622 36364: contig of 742 bp in length  
\* 36364 37206: contig of 742 bp in length  
\* 37206 37306: gap of 100 bp  
\* 37306 38052: contig of 746 bp in length  
\* 38052 38152: gap of 100 bp  
\* 38152 38878: contig of 726 bp in length  
\* 38878 39707: gap of 100 bp  
\* 39707: contig of 729 bp in length

```

* 39708 39807: gap of 100 bp
* 39808 40529: contig of 722 bp in length
* 40530 40629: gap of 100 bp
* 40630 41363: contig of 734 bp in length
* 41364 41463: gap of 100 bp
* 41464 42185: contig of 722 bp in length
* 42186 42285: gap of 100 bp
* 42286 43013: contig of 728 bp in length
* 43014 43113: gap of 100 bp
* 43114 43823: contig of 710 bp in length
* 43824 43923: gap of 100 bp
* 43924 44657: contig of 734 bp in length
* 44658 44757: gap of 100 bp
* 44758 45502: contig of 745 bp in length
* 45503 45602: gap of 100 bp
* 45603 46323: contig of 721 bp in length
* 46324 46424: gap of 100 bp
* 46424 47167: contig of 744 bp in length
* 47168 47267: gap of 100 bp
* 47268 47993: contig of 726 bp in length
* 47994 48093: gap of 100 bp
* 48094 48810: contig of 717 bp in length
* 48811 48910: gap of 100 bp
* 48911 49639: contig of 729 bp in length
* 49640 49739: gap of 100 bp
* 49740 50468: contig of 729 bp in length
* 50469 50568: gap of 100 bp
* 50569 51284: contig of 716 bp in length
* 51285 51384: gap of 100 bp
* 51385 52109: contig of 725 bp in length
* 52110 52209: gap of 100 bp
* 52210 52945: contig of 736 bp in length
* 52946 53045: gap of 100 bp
* 53046 53783: contig of 738 bp in length
* 53784 53883: gap of 100 bp
* 53884 54621: contig of 738 bp in length
* 54622 54721: gap of 100 bp
* 54722 55447: contig of 726 bp in length
* 55448 55547: gap of 100 bp
* 55548 56291: contig of 744 bp in length
* 56292 56392: gap of 100 bp
* 56392 57110: contig of 719 bp in length
* 57111 57210: gap of 100 bp
* 57211 57938: contig of 728 bp in length

```

```

Query Match 72.2%; Score 13; DB 2; Length 72969;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 6 CCGGAGNNNNNN 18
Db 18936 CCGGAGNNNNNN 18948

```

```

RESULT 168
AC025146
LOCUS Homo sapiens chromosome 1 clone RP11-27H21 map 1, LOW-PASS SEQUENCE
DEFINITION AC025146.1 GI:7158957
ACCESSION AC025146
VERSION AC025146.1
KEYWORDS HTG, HTGS-PHASED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 73173)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 1, clone RP11-27H21
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 73173)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,

```

# TITLE JOURNAL COMMENT

Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,  
Campiano, A., Casle, A., Choe, Y., Colangelo, M., Collins, S.,  
Collins, A., Cooke, P., DeArle, K., Dewar, K., Diaz, J. S.,  
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,  
Galegani, J., Gardina, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hago, B., Heaford, A., Horton, L.,  
Howard, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
Klein, J., Larocque, K., Lamazara, R., Landers, T., Lehotzky, J.,  
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,  
McCarthy, M., McMan, P., McGurk, A., McKernan, K., McPeckers, R.,  
Meldrum, J., Meneses, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,  
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rotman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tessier, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,  
Vassiliev, H., Vael, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Submitted (05-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information -----  
Center project name: L7962  
Center clone name: 27\_H\_21

NOTE: This record contains 84 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
be preserved.

```

1 800: contig of 800 bp in length
* 801 900: gap of 100 bp
* 901 1680: contig of 780 bp in length
* 1681 1780: gap of 100 bp
* 1781 2570: contig of 790 bp in length
* 2571 2670: gap of 100 bp
* 2671 3445: contig of 775 bp in length
* 3446 3545: gap of 100 bp
* 3546 4328: contig of 783 bp in length
* 4329 4428: gap of 100 bp
* 4429 5197: contig of 769 bp in length
* 5198 5297: gap of 100 bp
* 5297 6047: contig of 750 bp in length
* 6048 6147: gap of 100 bp
* 6148 6927: contig of 780 bp in length
* 6928 7027: gap of 100 bp
* 7028 7806: contig of 779 bp in length
* 7807 7906: gap of 100 bp
* 7907 8702: contig of 796 bp in length
* 8703 8802: gap of 100 bp
* 8803 9572: contig of 770 bp in length
* 9573 9672: gap of 100 bp
* 9673 10454: contig of 782 bp in length
* 10455 10554: gap of 100 bp
* 10555 11340: contig of 786 bp in length
* 11341 11440: gap of 100 bp
* 11441 12218: contig of 778 bp in length
* 12219 12318: gap of 100 bp

```

```

* 12319 13100: contig of 782 bp in length
* 13101 13200: gap of 100 bp
* 13201 13969: contig of 769 bp in length
* 13970 14069: gap of 100 bp
* 14070 14797: contig of 728 bp in length
* 14798 14897: gap of 100 bp
* 14898 15664: contig of 767 bp in length
* 15665 15764: gap of 100 bp
* 15765 16525: contig of 761 bp in length
* 16526 17422: contig of 797 bp in length
* 17423 17522: gap of 100 bp
* 17523 18305: contig of 783 bp in length
* 18306 18405: gap of 100 bp
* 18406 19167: contig of 761 bp in length
* 19167 19266: gap of 100 bp
* 19267 20044: contig of 778 bp in length
* 20045 20144: gap of 100 bp
* 20145 20925: contig of 781 bp in length
* 20926 21025: gap of 100 bp
* 21026 21805: contig of 779 bp in length
* 21805 21905: gap of 100 bp
* 21905 22635: contig of 730 bp in length
* 22635 22735: gap of 100 bp
* 22735 23484: contig of 749 bp in length
* 23484 24345: gap of 100 bp
* 24346 24445: gap of 100 bp
* 24446 25194: contig of 749 bp in length
* 25195 25295: gap of 100 bp
* 25295 26059: contig of 764 bp in length
* 26059 26159: gap of 100 bp
* 26159 26925: contig of 767 bp in length
* 26926 27025: gap of 100 bp
* 27026 27783: contig of 758 bp in length
* 27784 27884: gap of 100 bp
* 27884 28664: contig of 781 bp in length
* 28665 28764: gap of 100 bp
* 28764 29545: contig of 781 bp in length
* 29546 30422: gap of 100 bp
* 30423 30522: contig of 777 bp in length
* 30523 31299: contig of 776 bp in length
* 31299 31398: gap of 100 bp
* 31398 32159: contig of 761 bp in length
* 32160 32259: gap of 100 bp
* 32259 33040: contig of 781 bp in length
* 33041 33140: gap of 100 bp
* 33141 33912: contig of 772 bp in length
* 33913 34012: gap of 100 bp
* 34013 34794: contig of 782 bp in length
* 34795 34894: gap of 100 bp
* 34895 35664: contig of 769 bp in length
* 35664 35763: gap of 100 bp
* 35764 36536: contig of 773 bp in length
* 36537 37409: contig of 773 bp in length
* 37410 37509: gap of 100 bp
* 37510 38248: contig of 739 bp in length
* 38249 38348: gap of 100 bp
* 38349 39153: contig of 805 bp in length
* 39154 39253: gap of 100 bp
* 39254 40034: contig of 781 bp in length
* 40035 40134: gap of 100 bp
* 40135 40918: contig of 784 bp in length
* 40919 41018: gap of 100 bp
* 41019 41803: contig of 784 bp in length
* 41803 42670: contig of 768 bp in length
* 42671 42770: gap of 100 bp
* 42771 43542: contig of 772 bp in length
* 43543 43642: gap of 100 bp
* 43643 44407: contig of 765 bp in length

```

```

* 44408 44507: gap of 100 bp
* 44508 45268: contig of 761 bp in length
* 45269 45368: gap of 100 bp
* 45369 46141: contig of 773 bp in length
* 46142 46241: gap of 100 bp
* 46242 47013: contig of 772 bp in length
* 47014 47113: gap of 100 bp
* 47114 47891: contig of 778 bp in length
* 47892 47991: gap of 100 bp
* 47992 48772: contig of 781 bp in length
* 48773 48872: gap of 100 bp
* 48873 49647: contig of 775 bp in length
* 49648 49747: gap of 100 bp
* 49748 50520: contig of 773 bp in length
* 50521 50620: gap of 100 bp
* 50621 51395: contig of 775 bp in length
* 51396 51495: gap of 100 bp
* 51496 52281: contig of 786 bp in length
* 52282 52381: gap of 100 bp
* 52382 53162: contig of 781 bp in length
* 53163 53262: gap of 100 bp
* 53263 54030: contig of 768 bp in length
* 54031 54130: gap of 100 bp
* 54131 54916: contig of 786 bp in length
* 54917 55016: gap of 100 bp
* 55017 55767: contig of 751 bp in length
* 55768 55867: gap of 100 bp
* 55868 56638: contig of 771 bp in length
* 56639 56738: gap of 100 bp
* 56739 57511: contig of 773 bp in length
* 57512 57611: gap of 100 bp
* 57612 58384: contig of 773 bp in length
* 58385 58484: gap of 100 bp
* 58485 59271: contig of 787 bp in length
* 59272 59371: gap of 100 bp
* 59372 60141: contig of 770 bp in length
* 60142 60241: gap of 100 bp

```

```

Query Match      72.2%; Score 13; DB 2; Length 73173;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      6 CCUGAGNNNNNN 18
Db      69671 CCTGAGNNNNNN 69683

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RESULT 169
AC090991
LOCUS      75974 bp      DNA      linear      HTG 22-MAR-2001
DEFINITION Homo sapiens chromosome 15 clone RP11-100A21 map 15, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC090991.1 GI:13431041
VERSION AC090991.1
KEYWORDS HTG; HTGS PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 75974)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Unpublished
JOURNAL 2 (bases 1 to 75974)
REFERENCE 2 (bases 1 to 75974)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Batra,N., Bastien,V., Boguslavsky,L., Bouckgalter,B., Brown,A.,
Cammarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K.,
Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,

```

TITLE  
JOURNAL  
COMMENT

MacLean, C., Macdonald, P., Marguis, N., Matthews, C., McCarthy, M.,  
McGowan, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, L.,  
Milnova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nordu, C.,  
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,  
Retta, R., Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,  
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,  
Severy, P., Sougniez, C., Spencer, B., Stange-Rhmann, N.,  
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,  
Theodore, J., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zannou, J., Zemdek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (22-MAR-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

## ----- Project Information

Center project name: 112420

Center clone name: 100\_A\_21

## ----- NOTE: This record contains 92 individual

\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
739: contig of 739 bp in length  
740  
839: gap of 100 bp  
840  
1561: contig of 722 bp in length  
1562  
1661: gap of 100 bp  
1662  
2385: contig of 724 bp in length  
2386  
2485: gap of 100 bp  
2486  
3207: contig of 722 bp in length  
3208  
3307: gap of 100 bp  
3308  
4035: contig of 728 bp in length  
4036  
4135: gap of 100 bp  
4136  
4880: contig of 745 bp in length  
4881  
4980: gap of 100 bp  
4981  
5707: contig of 727 bp in length  
5708  
5807: gap of 100 bp  
5808  
6534: contig of 727 bp in length  
6535  
6634: gap of 100 bp  
6636  
7374: contig of 740 bp in length  
7375  
7474: gap of 100 bp  
7475  
8179: contig of 705 bp in length  
8180  
8279: gap of 100 bp  
8280  
9015: contig of 736 bp in length  
9016  
9115: gap of 100 bp  
9116  
9832: contig of 717 bp in length  
9833  
9932: gap of 100 bp  
9934  
10672: contig of 740 bp in length  
10673  
10772: gap of 100 bp  
10773  
11493: contig of 721 bp in length  
11494  
11593: gap of 100 bp  
11594  
12319: contig of 726 bp in length  
12320  
12419: gap of 100 bp  
12420  
13148: contig of 729 bp in length  
13149  
13248: gap of 100 bp  
13249  
13955: contig of 707 bp in length  
13956  
14055: gap of 100 bp  
14056  
14796: contig of 741 bp in length

14797  
14896: gap of 100 bp  
14897  
15624: contig of 728 bp in length  
15625  
15724: gap of 100 bp  
15725  
16436: contig of 712 bp in length  
16437  
16536: gap of 100 bp  
16537  
17258: contig of 722 bp in length  
17259  
17358: gap of 100 bp  
17359  
18076  
18175: gap of 100 bp  
18176  
18913: contig of 738 bp in length  
18914  
19013: gap of 100 bp  
19014  
19724: contig of 711 bp in length  
19725  
19824: gap of 100 bp  
19825  
20541: contig of 717 bp in length  
20542  
20641: gap of 100 bp  
20642  
21378: contig of 737 bp in length  
21379  
21478: gap of 100 bp  
21479  
22226: contig of 748 bp in length  
22227  
22325: gap of 100 bp  
22327  
23062: contig of 736 bp in length  
23063  
23162: gap of 100 bp  
23163  
23897: contig of 735 bp in length  
23898  
23997: gap of 100 bp  
23998  
24728: contig of 731 bp in length  
24729  
24828: gap of 100 bp  
24829  
25555: contig of 728 bp in length  
25557  
25656: gap of 100 bp  
25657  
26385: contig of 729 bp in length  
26386  
26485: gap of 100 bp  
26486  
27210: contig of 725 bp in length  
27211  
27310: gap of 100 bp  
27311  
28029: contig of 719 bp in length  
28030  
28123: gap of 100 bp  
28124  
28858: contig of 729 bp in length  
28859  
28955: gap of 100 bp  
28956  
29672: contig of 714 bp in length  
29673  
29772: gap of 100 bp  
29773  
30497: contig of 725 bp in length  
30498  
30597: gap of 100 bp  
30598  
31314: contig of 717 bp in length  
31315  
31415: gap of 100 bp  
31416  
32154: contig of 740 bp in length  
32155  
32254: gap of 100 bp  
32255  
32980: contig of 726 bp in length  
32981  
33080: gap of 100 bp  
33081  
33814: contig of 734 bp in length  
33815  
33915: gap of 100 bp  
33916  
34646: contig of 732 bp in length  
34647  
34746: gap of 100 bp  
34747  
35475: contig of 729 bp in length  
35476  
35575: gap of 100 bp  
35576  
36283: contig of 708 bp in length  
36284  
36383: gap of 100 bp  
36384  
37116: contig of 733 bp in length  
37117  
37215: gap of 100 bp  
37216  
37935: contig of 719 bp in length  
37936  
38035: gap of 100 bp  
38036  
38777: contig of 742 bp in length  
38778  
38877: gap of 100 bp  
38878  
39600: contig of 723 bp in length  
39601  
39700: gap of 100 bp  
39701  
40414: contig of 714 bp in length  
40415  
40514: gap of 100 bp  
40516  
41248: contig of 734 bp in length  
41249  
41349: gap of 100 bp  
41349  
42089: contig of 741 bp in length  
42090  
42189: gap of 100 bp  
42189  
42932: contig of 743 bp in length  
42933  
43032: gap of 100 bp  
43033  
43765: contig of 733 bp in length  
43766  
43865: gap of 100 bp  
43866  
44581: contig of 716 bp in length  
44582  
44681: gap of 100 bp

```

* 44682 45412: contig of 721 bp in length
* 45413 45512: gap of 100 bp
* 45513 46239: contig of 727 bp in length
* 46240 46339: gap of 100 bp
* 46340 47063: contig of 724 bp in length
* 47064 47163: gap of 100 bp
* 47164 47884: contig of 720 bp in length
* 47884 47983: gap of 100 bp
* 47984 48718: contig of 735 bp in length
* 48719 48819: gap of 100 bp
* 48819 49535: contig of 717 bp in length
* 49536 49635: gap of 100 bp
* 49636 50359: contig of 724 bp in length
* 50360 50460: gap of 100 bp
* 50460 51195: contig of 736 bp in length
* 51196 51295: gap of 100 bp
* 51296 52032: contig of 737 bp in length
* 52033 52132: gap of 100 bp
* 52133 52837: contig of 705 bp in length
* 52838 52937: gap of 100 bp
* 52938 53648: contig of 711 bp in length
* 53649 53748: gap of 100 bp
* 53749 54477: contig of 729 bp in length
* 54478 54577: gap of 100 bp
* 54578 55313: contig of 736 bp in length
* 55314 55413: gap of 100 bp
* 55414 56129: contig of 716 bp in length
* 56130 56229: gap of 100 bp
* 56230 56945: contig of 716 bp in length
* 56946 57045: gap of 100 bp

```

```

Query Match 72.2% Score 13; DB 2; Length 75974;
Best Local Similarity 92.3%; Pred. No. 4,6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 6 CCGGAGANNNNNN 18
DB 12313 CCGGAGANNNNNN 12325

```

```

RESULT 170
AC023453
LOCUS Homo sapiens clone RP11-734K12, LOW-PASS SEQUENCE SAMPLING.
AC023453
AC023453.2 GI:9164172
VERSION HTG: HTGS PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

```

```

REFERENCE
AUTHORS Birren, B., Linton, L., Nuebaum, C., Lander, E., Abraham, H., Allen, N.,
TITLE 1 (bases 1 to 76113)
JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 2 (bases 1 to 76113)
Unpublished

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1 Birren, B., Linton, L., Nuebaum, C. and Lander, E.
2 (bases 1 to 76113)
Birren, B., Linton, L., Nuebaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,
Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,
Dearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,
Fenster, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,
Howland, J., Iliev, I., Johnson, R., Jones, C., Kam, L., Karatas, A.,
Klein, J., Landers, T., Laroque, K., Lehoczy, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McEwan, P., McGurk, A., McKernan, K., McNetters, R., Meltrin, J.,
Meneus, L., Mihova, T., Miranda, C., Mlenka, V., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M.,
Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

```

# TITLE JOURNAL COMMENT

Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,  
Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,  
Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and  
Zody, M.

Direct Submission  
Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6970673.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

----- Project Information -----  
Center project name: L6552  
Center clone name: 734\_K\_12

\* NOTE: This record contains 79 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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1 867: contig of 867 bp in length
868 967: gap of 100 bp
968 1914: contig of 947 bp in length
1915 2014: gap of 100 bp
2015 2863: contig of 849 bp in length
2864 2963: gap of 100 bp
2964 3820: contig of 857 bp in length
3821 3920: gap of 100 bp
3921 4780: contig of 860 bp in length
4781 4880: gap of 100 bp
4881 5781: contig of 901 bp in length
5782 5881: gap of 100 bp
5882 6775: contig of 884 bp in length
6776 6875: gap of 100 bp
6876 7736: contig of 861 bp in length
7737 7836: gap of 100 bp
7837 8724: contig of 888 bp in length
8725 8824: gap of 100 bp
8825 9701: contig of 877 bp in length
9702 9801: gap of 100 bp
9802 10667: contig of 866 bp in length
10668 10767: gap of 100 bp
10768 11614: contig of 847 bp in length
11615 11714: gap of 100 bp
11715 12575: contig of 861 bp in length
12576 12675: gap of 100 bp
12676 13577: contig of 902 bp in length
13578 13677: gap of 100 bp
13678 14570: contig of 893 bp in length
14571 14670: gap of 100 bp
14671 15519: contig of 849 bp in length
15520 15619: gap of 100 bp
15620 16480: contig of 861 bp in length
16481 16580: gap of 100 bp
16581 17431: contig of 851 bp in length
17432 17531: gap of 100 bp
17533 18410: contig of 879 bp in length
18411 18510: gap of 100 bp
18511 19381: contig of 871 bp in length
19382 19481: gap of 100 bp
19482 20311: contig of 830 bp in length
20312 20411: gap of 100 bp

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```

* 20412 21240: contig of 829 bp in length
* 21341 21340: gap of 100 bp
* 22203 22302: contig of 862 bp in length
* 22303 22302: gap of 100 bp
* 23177 23176: contig of 874 bp in length
* 23277 23276: gap of 100 bp
* 24128 24127: contig of 851 bp in length
* 24228 24227: gap of 100 bp
* 25091 25090: contig of 863 bp in length
* 25191 25190: gap of 100 bp
* 26067 26066: contig of 876 bp in length
* 26167 26166: gap of 100 bp
* 27043 27042: contig of 876 bp in length
* 27143 27142: gap of 100 bp
* 27990 27989: contig of 847 bp in length
* 28090 28089: gap of 100 bp
* 28966 28965: contig of 876 bp in length
* 29066 29065: gap of 100 bp
* 29937 29936: contig of 871 bp in length
* 30037 30036: gap of 100 bp
* 30887 30884: contig of 848 bp in length
* 30985 30984: gap of 100 bp
* 31838 31837: contig of 853 bp in length
* 31938 31937: gap of 100 bp
* 32778 32777: contig of 840 bp in length
* 32878 32877: gap of 100 bp
* 33771 33770: contig of 893 bp in length
* 33871 33870: gap of 100 bp
* 34712 34711: contig of 841 bp in length
* 34812 34811: gap of 100 bp
* 35672 35671: contig of 860 bp in length
* 35772 35771: gap of 100 bp
* 36628 36627: contig of 856 bp in length
* 36728 36727: gap of 100 bp
* 37575 37574: contig of 847 bp in length
* 37675 37674: gap of 100 bp
* 38568 38567: contig of 893 bp in length
* 38668 38667: gap of 100 bp
* 39552 39551: contig of 884 bp in length
* 39652 39651: gap of 100 bp
* 40512 40511: contig of 860 bp in length
* 40612 40611: gap of 100 bp
* 41451 41450: contig of 839 bp in length
* 41551 41550: gap of 100 bp
* 42412 42411: contig of 861 bp in length
* 42512 42511: gap of 100 bp
* 43396 43395: contig of 884 bp in length
* 43496 43495: gap of 100 bp
* 44335 44334: contig of 839 bp in length
* 44435 44434: gap of 100 bp
* 45286 45285: contig of 851 bp in length
* 45386 45385: gap of 100 bp
* 46222 46221: contig of 836 bp in length
* 46322 46321: gap of 100 bp
* 47154 47154: contig of 833 bp in length
* 47254 47254: gap of 100 bp
* 47755 47754: gap of 100 bp
* 48089 48088: contig of 834 bp in length
* 48189 48188: gap of 100 bp
* 49073 49072: contig of 884 bp in length
* 49173 49172: gap of 100 bp
* 50029 50028: contig of 856 bp in length
* 50129 50128: gap of 100 bp
* 50992 50991: contig of 863 bp in length
* 51092 51091: gap of 100 bp
* 51943 51942: contig of 851 bp in length
* 52043 52042: gap of 100 bp
* 52927 52927: contig of 885 bp in length
* 53028 53027: gap of 100 bp
* 53917 53916: contig of 885 bp in length
* 54017 54016: gap of 100 bp
* 54865 54864: contig of 848 bp in length
* 54965 54964: gap of 100 bp
* 55825: contig of 861 bp in length

```

```

* 55826 55925: gap of 100 bp
* 55926 55925: contig of 868 bp in length
* 56794 56893: gap of 100 bp
* 56894 56893: contig of 864 bp in length
* 57758 57857: gap of 100 bp
* 57858 57857: contig of 867 bp in length
* 58725 58824: gap of 100 bp
* 58825 58824: contig of 879 bp in length
* 59704 59803: gap of 100 bp
* 59804 59804: contig of 837 bp in length
* 60641 60740: gap of 100 bp
* 60741 61624: contig of 884 bp in length
* 61625 61725: gap of 100 bp
* 61725 62603: contig of 879 bp in length
* 62604 62703: gap of 100 bp
* 62704 63574: contig of 871 bp in length
* 63575 63675: gap of 100 bp
* 63675 64546: contig of 872 bp in length
* 64547 64646: gap of 100 bp
* 64647 65519: contig of 873 bp in length
* 65520 65619: gap of 100 bp
* 65620 66487: contig of 868 bp in length
* 66488 66587: gap of 100 bp

Query Match      72.2%  Score 13;  DB 2;  Length 76113;
Best Local Similarity 92.3%  Pred. No. 4.6e+02;
Matches 12;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      6  CCTGCAGNNNNNN 18
Db      54858 CCTGCAGNNNNNN 54870

RESULT 171
AC021526      76856 bp  DNA  linear  HTG 13-JUL-2000
LOCUS      Homo sapiens clone RP11-351F2, LOW-PASS SEQUENCE SAMPLING.
DEFINITION
AC021526
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 76856)
AUTHORS      Birren,B., Lincon,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens chromosome, clone RP11-351F2
JOURNAL
REFERENCE
2 (bases 1 to 76856)
AUTHORS      Birren,B., Lincon,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckert,R., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepeil,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
D'Arbellano,K., Dewar,K., Domingo,M., Doyle,M., Fenebor,J.,
Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,U., Karasik,A., Klein,J.,
Landers,T., Lehoczek,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Mcdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisanu,C., Pollara,V., Raymond,C., Riley,R., Rochman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vasilev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705574.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIGR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: 15513  
Center clone name: 351\_F\_2

\* NOTE: This record contains 79 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
873: contig of 872 bp in length  
973: gap of 100 bp  
1854: contig of 882 bp in length  
1855: gap of 100 bp  
1955: contig of 836 bp in length  
2791: gap of 100 bp  
2891: contig of 872 bp in length  
3763: gap of 100 bp  
3863: contig of 873 bp in length  
4736: gap of 100 bp  
4835: contig of 853 bp in length  
5688: contig of 874 bp in length  
5789: gap of 100 bp  
6663: contig of 874 bp in length  
6763: gap of 100 bp  
7590: contig of 828 bp in length  
7591: gap of 100 bp  
7690: contig of 855 bp in length  
8545: gap of 100 bp  
8646: contig of 901 bp in length  
9547: gap of 100 bp  
9647: contig of 882 bp in length  
10529: gap of 100 bp  
10629: contig of 887 bp in length  
11516: gap of 100 bp  
11616: contig of 886 bp in length  
12502: gap of 100 bp  
12601: contig of 902 bp in length  
13503: gap of 100 bp  
13604: contig of 863 bp in length  
14466: gap of 100 bp  
14567: contig of 864 bp in length  
15431: gap of 100 bp  
15530: contig of 866 bp in length  
16397: gap of 100 bp  
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17472: contig of 862 bp in length  
18334: gap of 100 bp  
18435: contig of 873 bp in length  
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19407: contig of 890 bp in length  
20397: gap of 100 bp  
20998: contig of 819 bp in length  
21216: gap of 100 bp  
21317: contig of 857 bp in length  
22174: gap of 100 bp  
22273: contig of 904 bp in length  
23177: gap of 100 bp  
23277: contig of 896 bp in length  
24173: gap of 100 bp  
24274: contig of 888 bp in length  
25161: gap of 100 bp  
25262: contig of 890 bp in length

26152: gap of 100 bp  
26252: contig of 867 bp in length  
27119: gap of 100 bp  
27219: contig of 870 bp in length  
28089: gap of 100 bp  
28189: contig of 845 bp in length  
29034: gap of 100 bp  
29134: contig of 878 bp in length  
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30112: contig of 885 bp in length  
30997: gap of 100 bp  
31097: contig of 882 bp in length  
31979: gap of 100 bp  
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33095: contig of 899 bp in length  
33994: gap of 100 bp  
34094: contig of 882 bp in length  
34976: gap of 100 bp  
35076: contig of 899 bp in length  
35974: gap of 100 bp  
36075: contig of 893 bp in length  
36967: gap of 100 bp  
37068: contig of 870 bp in length  
37938: gap of 100 bp  
38038: contig of 854 bp in length  
38892: gap of 100 bp  
38992: contig of 885 bp in length  
39877: gap of 100 bp  
39976: contig of 885 bp in length  
40862: gap of 100 bp  
40962: contig of 869 bp in length  
41830: gap of 100 bp  
41930: contig of 853 bp in length  
42789: gap of 100 bp  
42889: contig of 882 bp in length  
43771: gap of 100 bp  
43871: contig of 882 bp in length  
44753: gap of 100 bp  
44853: contig of 841 bp in length  
45694: gap of 100 bp  
45794: contig of 867 bp in length  
46661: gap of 100 bp  
46761: contig of 882 bp in length  
47743: gap of 100 bp  
48627: contig of 884 bp in length  
48727: gap of 100 bp  
49557: contig of 830 bp in length  
49657: gap of 100 bp  
50518: contig of 861 bp in length  
50619: gap of 100 bp  
51463: contig of 845 bp in length  
51564: gap of 100 bp  
52443: contig of 880 bp in length  
52544: gap of 100 bp  
53421: contig of 877 bp in length  
53520: gap of 100 bp  
54113: contig of 893 bp in length  
54513: gap of 100 bp  
54514: contig of 893 bp in length  
55066: gap of 100 bp  
55507: contig of 878 bp in length  
56384: gap of 100 bp  
56484: contig of 891 bp in length  
57375: gap of 100 bp  
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58421: contig of 881 bp in length  
59302: gap of 100 bp  
59403: contig of 832 bp in length  
60234: gap of 100 bp  
60334: contig of 870 bp in length  
61204: gap of 100 bp  
61304: contig of 870 bp in length

\* 61305 62206: contig of 902 bp in length  
\* 62207 62306: contig of 100 bp in length  
\* 62307 63206: contig of 900 bp in length  
\* 63207 63306: gap of 100 bp  
\* 63307 64152: contig of 846 bp in length  
\* 64152 64252: gap of 100 bp  
\* 64252 65126: contig of 874 bp in length  
\* 65126 65227 65226: gap of 100 bp  
\* 65227 66109: contig of 883 bp in length  
\* 66109 66209: gap of 100 bp  
\* 66209 67083: contig of 874 bp in length  
\* 67083 67183: gap of 100 bp  
\* 67183 68039: contig of 856 bp in length  
\* 68039 68135: gap of 100 bp  
\* 68135 69001: contig of 862 bp in length  
\* 69001 69101: gap of 100 bp  
\* 69101 69002

Query Match 72.2%; Score 13; DB 2; Length 76856;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
||:|||||  
41824 CCTGAGNNNNNN 41836

RESULT 172  
AC015735  
LOCUS AC015735 84680 bp DNA linear HTG 13-JUL-2000  
DEFINITION Homo sapiens clone RP11-1D9, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC015735  
VERSION AC015735.2 GI:9108760  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 84680)  
Birren,B., Lincon,L., Nuebaum,C. and Lander,E.  
Homo sapiens chromosome, clone RP11-1D9  
Unpublished  
2 (bases 1 to 84680)  
Birren,B., Lincon,L., Nuebaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barina,N., Beckery,R., Boguslawski,L., Boukhalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donegan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatae,A., Klein,J., Lehotzky,J., Lieu,C., Locke,K., Macdonald,P., Margulis,N., McEwen,P., McGuck,A., McKernan,K., McLaughlin,J., Meldrum,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6446952.  
All repeats were identified using RepeatMasker:  
Sait, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L1435  
Center clone name: L\_D\_9  
\* NOTE: This record contains 86 individual

\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1  
\* 862: contig of 862 bp in length  
\* 863 962: gap of 100 bp  
\* 962 1864: contig of 902 bp in length  
\* 1864 1964: gap of 100 bp  
\* 1964 1965: contig of 883 bp in length  
\* 1965 2848: gap of 100 bp  
\* 2848 3824: contig of 877 bp in length  
\* 3824 3924: gap of 100 bp  
\* 3924 4807: contig of 883 bp in length  
\* 4807 4907: gap of 100 bp  
\* 4907 5781: contig of 874 bp in length  
\* 5781 5881: gap of 100 bp  
\* 5881 6769: contig of 888 bp in length  
\* 6769 6869: gap of 100 bp  
\* 6869 7741: contig of 872 bp in length  
\* 7741 7841: gap of 100 bp  
\* 7841 8717: contig of 876 bp in length  
\* 8717 8817: gap of 100 bp  
\* 8817 9687: contig of 870 bp in length  
\* 9687 9787: gap of 100 bp  
\* 9787 10674: contig of 887 bp in length  
\* 10674 10774: gap of 100 bp  
\* 10774 11628: contig of 854 bp in length  
\* 11628 11728: gap of 100 bp  
\* 11728 12605: contig of 877 bp in length  
\* 12605 12705: gap of 100 bp  
\* 12705 13603: contig of 898 bp in length  
\* 13603 13703: gap of 100 bp  
\* 13703 14623: contig of 920 bp in length  
\* 14623 14723: gap of 100 bp  
\* 14723 15615: contig of 892 bp in length  
\* 15615 15715: gap of 100 bp  
\* 15715 16613: contig of 898 bp in length  
\* 16613 16713: gap of 100 bp  
\* 16713 17592: contig of 879 bp in length  
\* 17592 17692: gap of 100 bp  
\* 17692 18593: contig of 901 bp in length  
\* 18593 18693: gap of 100 bp  
\* 18693 19575: contig of 882 bp in length  
\* 19575 19675: gap of 100 bp  
\* 19675 20562: contig of 887 bp in length  
\* 20562 20662: gap of 100 bp  
\* 20662 21529: contig of 867 bp in length  
\* 21529 21629: gap of 100 bp  
\* 21629 22538: contig of 909 bp in length  
\* 22538 22638: gap of 100 bp  
\* 22638 23494: contig of 856 bp in length  
\* 23494 23594: gap of 100 bp  
\* 23594 24475: contig of 881 bp in length  
\* 24475 24575: gap of 100 bp  
\* 24575 25454: contig of 879 bp in length  
\* 25454 25554: gap of 100 bp  
\* 25554 26449: contig of 895 bp in length  
\* 26449 27417: contig of 868 bp in length  
\* 27417 28399: contig of 882 bp in length  
\* 28399 28499: gap of 100 bp  
\* 28499 29382: contig of 883 bp in length  
\* 29382 29482: gap of 100 bp  
\* 29482 30389: contig of 907 bp in length  
\* 30389 30489: gap of 100 bp  
\* 30489 31354: contig of 865 bp in length

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* 31355 31454: gap of 100 bp
* 31455 32330: contig of 876 bp in length
* 32331 32430: gap of 100 bp
* 32431 33318: contig of 888 bp in length
* 33319 33418: gap of 100 bp
* 33419 34297: contig of 879 bp in length
* 34298 34397: gap of 100 bp
* 34398 35286: contig of 889 bp in length
* 35287 35386: gap of 100 bp
* 35387 36297: contig of 911 bp in length
* 36298 36397: gap of 100 bp
* 36398 37301: contig of 904 bp in length
* 37302 37401: gap of 100 bp
* 37402 38302: contig of 901 bp in length
* 38303 38402: gap of 100 bp
* 38403 39297: contig of 895 bp in length
* 39298 39397: gap of 100 bp
* 39398 40303: contig of 906 bp in length
* 40304 40403: gap of 100 bp
* 40404 41298: contig of 895 bp in length
* 41299 41398: gap of 100 bp
* 41399 42273: contig of 875 bp in length
* 42274 42373: gap of 100 bp
* 42374 43257: contig of 884 bp in length
* 43258 43357: gap of 100 bp
* 43358 44276: contig of 919 bp in length
* 44277 44376: gap of 100 bp
* 44377 45242: contig of 866 bp in length
* 45243 45342: gap of 100 bp
* 45343 46228: contig of 886 bp in length
* 46229 46328: gap of 100 bp
* 46329 47212: contig of 884 bp in length
* 47213 47312: gap of 100 bp
* 47313 48218: contig of 906 bp in length
* 48219 48318: gap of 100 bp
* 48319 49203: contig of 885 bp in length
* 49204 49303: gap of 100 bp
* 49304 50200: contig of 897 bp in length
* 50201 50301: gap of 100 bp
* 50302 51196: contig of 896 bp in length
* 51197 51296: gap of 100 bp
* 51297 51391: contig of 895 bp in length
* 51392 52291: gap of 100 bp
* 52292 53163: contig of 872 bp in length
* 53164 53263: gap of 100 bp
* 53264 54112: contig of 845 bp in length
* 54113 54212: gap of 100 bp
* 54213 55083: contig of 871 bp in length
* 55084 55183: gap of 100 bp
* 55184 56091: contig of 908 bp in length
* 56092 56191: gap of 100 bp
* 56192 57072: contig of 881 bp in length
* 57073 57172: gap of 100 bp
* 57173 58086: contig of 914 bp in length
* 58087 58186: gap of 100 bp
* 58187 59075: contig of 889 bp in length
* 59076 59175: gap of 100 bp
* 59176 60054: contig of 879 bp in length
* 60055 60154: gap of 100 bp
* 60155 61041: contig of 887 bp in length
* 61042 61141: gap of 100 bp
* 61142 62035: contig of 894 bp in length
* 62036 62135: gap of 100 bp
* 62136 63027: contig of 892 bp in length
* 63028 63127: gap of 100 bp
* 63128 64018: contig of 891 bp in length
* 64019 64118: gap of 100 bp
* 64119 65012: contig of 894 bp in length
* 65013 65112: gap of 100 bp
* 65113 65992: contig of 880 bp in length
* 65993 66092: gap of 100 bp
* 66093 66959: contig of 867 bp in length
* 66959 67059: gap of 100 bp

```

```

Query Match      72.2%  Score 13;  DB 2;  Length 84680;
Best Local Similarity 92.3%  Pred. No. 4,6e+02;
Matches 12;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;
QY      6 CCUGAGANNNNNN 18
Db       50194 CCTGAGANNNNNN 50206

```

## RESULT 173

AC140498

LOCUS

DEFINITION

SEQUENCE SAMPLING.

AC140498

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

```

* 67060 67914: contig of 855 bp in length
* 67915 68014: gap of 100 bp
* 68015 68906: contig of 892 bp in length
* 68907 69006: gap of 100 bp
* 69007 69899: contig of 893 bp in length
* 69900 69999: gap of 100 bp
* 70000 70926: contig of 927 bp in length
* 70927 71026: gap of 100 bp
* 71027 71913: contig of 887 bp in length

```

Center: Whitehead Institute/ MIT Center for Genome Research  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
 Project Information  
 Center project name: L29357  
 Center clone name: 3029\_C\_15

\* NOTE: This record contains 80 individual  
 \* sequencing reads that have not been assembled into

```
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 963: contig of 963 bp in length
* 964 1063: gap of 100 bp
* 1064 2039: contig of 976 bp in length
* 2040 2139: gap of 100 bp
* 2140 3099: contig of 960 bp in length
* 3100 3199: gap of 100 bp
* 3200 4183: contig of 984 bp in length
* 4184 4283: gap of 100 bp
* 4284 5281: contig of 998 bp in length
* 5282 5381: gap of 100 bp
* 5382 6395: contig of 1014 bp in length
* 6396 6495: gap of 100 bp
* 6496 7501: contig of 1006 bp in length
* 7502 7601: gap of 100 bp
* 7602 8626: contig of 1025 bp in length
* 8627 8726: gap of 100 bp
* 8727 9727: contig of 1001 bp in length
* 9728 9827: gap of 100 bp
* 9828 10826: contig of 999 bp in length
* 10827 10926: gap of 100 bp
* 10927 11899: contig of 973 bp in length
* 11900 11999: gap of 100 bp
* 12000 12952: contig of 953 bp in length
* 12953 13052: gap of 100 bp
* 13053 14016: contig of 964 bp in length
* 14017 15119: contig of 1003 bp in length
* 15120 15219: gap of 100 bp
* 15220 16221: contig of 1002 bp in length
* 16222 16321: gap of 100 bp
* 16322 17311: contig of 990 bp in length
* 17312 17411: gap of 100 bp
* 17412 18416: contig of 1005 bp in length
* 18417 18516: gap of 100 bp
* 18517 19481: contig of 965 bp in length
* 19482 19581: gap of 100 bp
* 19582 20591: contig of 1010 bp in length
* 20592 21689: contig of 998 bp in length
* 21690 21789: gap of 100 bp
* 21790 22812: contig of 1023 bp in length
* 22813 22912: gap of 100 bp
* 22913 23901: contig of 989 bp in length
* 23902 24001: gap of 100 bp
* 24002 24955: contig of 954 bp in length
* 24956 25055: gap of 100 bp
* 25056 26022: contig of 967 bp in length
* 26023 26122: gap of 100 bp
* 26123 27137: contig of 1015 bp in length
* 27138 27237: gap of 100 bp
* 27239 28268: contig of 1031 bp in length
* 28269 28368: gap of 100 bp
* 28369 29372: contig of 1004 bp in length
* 29373 29472: gap of 100 bp
* 29473 30467: contig of 995 bp in length
* 30468 30567: gap of 100 bp
* 30568 31562: contig of 995 bp in length
* 31563 31662: gap of 100 bp
* 31663 32652: contig of 990 bp in length
* 32653 32752: gap of 100 bp
* 32753 33767: contig of 1015 bp in length
* 33768 33867: gap of 100 bp
* 33868 34861: contig of 994 bp in length
* 34862 34961: gap of 100 bp
*
* 34962 35943: contig of 982 bp in length
* 35944 36043: gap of 100 bp
* 36044 37019: contig of 976 bp in length
* 37020 37119: gap of 100 bp
* 37120 38087: contig of 968 bp in length
* 38088 38187: gap of 100 bp
* 38188 39132: contig of 945 bp in length
* 39133 39232: gap of 100 bp
* 39233 40256: contig of 1024 bp in length
* 40257 40356: gap of 100 bp
* 40357 41379: contig of 1023 bp in length
* 41380 41479: gap of 100 bp
* 41480 42484: contig of 1005 bp in length
* 42485 42584: gap of 100 bp
* 42585 43605: contig of 1021 bp in length
* 43606 43705: gap of 100 bp
* 43706 44734: contig of 1029 bp in length
* 44735 44834: gap of 100 bp
* 44835 45838: contig of 1004 bp in length
* 45839 45938: gap of 100 bp
* 45939 46923: contig of 985 bp in length
* 46924 47023: gap of 100 bp
* 47024 48048: contig of 1025 bp in length
* 48049 48148: gap of 100 bp
* 48149 49137: contig of 985 bp in length
* 49138 49237: gap of 100 bp
* 49238 50219: contig of 982 bp in length
* 50220 50319: gap of 100 bp
* 50320 51311: contig of 992 bp in length
* 51312 51412: gap of 100 bp
* 51413 52414: contig of 1003 bp in length
* 52415 52514: gap of 100 bp
* 52515 53538: contig of 1024 bp in length
* 53539 53638: gap of 100 bp
* 53639 54644: contig of 1006 bp in length
* 54645 54744: gap of 100 bp
* 54745 55759: contig of 1015 bp in length
* 55760 55859: gap of 100 bp
* 55860 56852: contig of 993 bp in length
* 56853 56953: gap of 100 bp
* 56953 57930: contig of 978 bp in length
* 57931 58030: gap of 100 bp
* 58031 58964: contig of 934 bp in length
* 58965 59064: gap of 100 bp
* 59065 60083: contig of 1019 bp in length
* 60084 60183: gap of 100 bp
* 60184 61175: contig of 992 bp in length
* 61176 61275: gap of 100 bp
* 61276 62294: contig of 1019 bp in length
* 62295 62394: gap of 100 bp
* 62395 63406: contig of 1012 bp in length
* 63407 63506: gap of 100 bp
* 63507 64496: contig of 990 bp in length
* 64497 64596: gap of 100 bp
* 64597 65587: contig of 991 bp in length
* 65588 65687: gap of 100 bp
* 65688 66674: contig of 987 bp in length
* 66675 66774: gap of 100 bp
* 66775 67753: contig of 978 bp in length
* 67753 67852: gap of 100 bp
* 67853 68820: contig of 968 bp in length
* 68821 68920: gap of 100 bp
* 68921 69929: contig of 1009 bp in length
* 69930 70029: gap of 100 bp
* 70030 71048: contig of 1019 bp in length
* 71049 71148: gap of 100 bp
* 71149 72152: contig of 1004 bp in length
* 72153 72252: gap of 100 bp
* 72253 73261: contig of 1009 bp in length
* 73262 73361: gap of 100 bp
* 73362 74366: contig of 1005 bp in length
* 74367 74466: gap of 100 bp
* 74467 75459: contig of 993 bp in length
```



*	38436	39371:	contig of 936 bp in length
*	39372	39471:	gap of 100 bp
*	39472	40383:	contig of 912 bp in length
*	40384	40483:	gap of 100 bp
*	40484	41389:	contig of 906 bp in length
*	41390	41489:	gap of 100 bp
*	41490	42427:	contig of 938 bp in length
*	42428	42527:	gap of 100 bp
*	42528	43478:	contig of 951 bp in length
*	43479	43578:	gap of 100 bp
*	43579	44508:	contig of 930 bp in length
*	44609	45522:	contig of 914 bp in length
*	45523	45622:	gap of 100 bp
*	45623	45533:	contig of 911 bp in length
*	46534	46633:	gap of 100 bp
*	46634	47545:	contig of 912 bp in length
*	47546	47645:	gap of 100 bp
*	47646	48586:	contig of 941 bp in length
*	48587	48686:	gap of 100 bp
*	48687	49610:	contig of 924 bp in length
*	49611	49710:	gap of 100 bp
*	49711	50659:	contig of 949 bp in length
*	50660	50759:	gap of 100 bp
*	50760	51710:	contig of 951 bp in length
*	51711	51810:	gap of 100 bp
*	51811	52771:	contig of 961 bp in length
*	52772	52871:	gap of 100 bp
*	52872	53824:	contig of 953 bp in length
*	53825	53924:	gap of 100 bp
*	53925	54888:	contig of 964 bp in length
*	54889	54988:	gap of 100 bp
*	54989	55952:	contig of 964 bp in length
*	55953	56052:	gap of 100 bp
*	56053	56999:	contig of 947 bp in length
*	57000	57099:	gap of 100 bp
*	57100	58044:	contig of 945 bp in length
*	58045	58144:	gap of 100 bp
*	58145	59059:	contig of 915 bp in length
*	59060	59159:	gap of 100 bp
*	59160	60118:	contig of 959 bp in length
*	60119	60218:	gap of 100 bp
*	60219	61175:	contig of 957 bp in length
*	61176	61275:	gap of 100 bp
*	61276	62208:	contig of 933 bp in length
*	62209	62308:	gap of 100 bp
*	62309	63255:	contig of 947 bp in length
*	63256	63355:	gap of 100 bp
*	63356	64316:	contig of 961 bp in length
*	64317	64416:	gap of 100 bp
*	64417	65350:	contig of 934 bp in length
*	65351	66367:	contig of 917 bp in length
*	66368	66467:	gap of 100 bp
*	66468	67394:	contig of 927 bp in length
*	67395	67494:	gap of 100 bp
*	67495	68425:	contig of 931 bp in length
*	68426	68525:	gap of 100 bp
*	68526	69468:	contig of 943 bp in length
*	69469	69568:	gap of 100 bp
*	69569	70528:	contig of 960 bp in length
*	70529	70628:	gap of 100 bp
*	70629	71576:	contig of 948 bp in length
*	71577	71676:	gap of 100 bp
*	71677	72630:	contig of 954 bp in length
*	72631	72730:	gap of 100 bp
*	72731	73669:	contig of 939 bp in length
*	73670	73769:	gap of 100 bp

Query Match 72.2% Score 13; DB 2; Length 90108;  
 Best Local Similarity 92.3%; Pred. No. 4,6e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Qy      6 CCTGGAGNNNNNN 18
Db      7252 CCTGGAGNNNNNN 7264

RESULT 175
AX695818/c
LOCUS   AX695818
DEFINITION Sequence 1445 from Patent WO03008583.
ACCESSION AX695818
VERSION   AX695818.1 GI:29418972
KEYWORDS
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
  1 Morita,D.W. and Engelhard,E.K.
    Novel compositions and methods for cancer
    Patent: WO 03008583-A 1445 30-JUN-2003;
    Sagres Discovery (US)
    Location/Qualifiers
      1..92726
        /organism="Mus musculus"
        /mol_type="unassigned DNA"
        /db_xref="taxon:10090"

ORIGIN
Query Match 72.2% Score 13; DB 6; Length 92726;
Best Local Similarity 92.3%; Pred. No. 4,6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCTGGAGNNNNNN 18
Db      155 CCTGGAGNNNNNN 143

RESULT 176
AC013392
LOCUS   AC013392
DEFINITION Homo sapiens chromosome 2 clone RP11-429N24 map 2, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC013392.3 GI:9123920
VERSION   AC013392
KEYWORDS  HTG; HTGS_PHASE0.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 95591)
          2 (bases 1 to 95591)
          Homo sapiens chromosome 2, clone RP11-429N24
          Unpublished
          2 (bases 1 to 95591)
          Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
          Baldwin,J., Barna,N., Beckert,J., Boguslavsky,L., Boucknight,B.,
          Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
          Cooke,P., Dearielano,K., Dewar,K., Domono,M., Donelan,L., Doyle,M.,
          Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
          Galagan,J., Gardyna,S., Grant,G., Hages,B., Heathford,A., Horton,L.,
          Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
          Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
          McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
          Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
          Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
          Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
          Testfaye,S., Tittrell,A., Vasilev,H., Vo,A., Wheeler,J., Wu,X.,
          Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
          Direct Submission
          Submitted (09-NOV-1999) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
          On Jul 13, 2000 this sequence version replaced gi:6425709.
          All repeats were identified using RepeatMasker.

```

Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence.submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L3805  
Center clone name: 429\_N\_24

\* NOTE: This record contains 111 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
827: contig of 827 bp in length  
828  
927: gap of 100 bp  
928  
1726: contig of 799 bp in length  
1727  
1826: gap of 100 bp  
1827  
2635: contig of 809 bp in length  
2636  
2735: gap of 100 bp  
2736  
3547: contig of 812 bp in length  
3548  
3647: gap of 100 bp  
3648  
4424: contig of 777 bp in length  
4425  
4524: gap of 100 bp  
4525  
5303: contig of 779 bp in length  
5304  
5404  
6171: contig of 768 bp in length  
6172  
6271: gap of 100 bp  
6272  
7071: contig of 800 bp in length  
7072  
7171: gap of 100 bp  
7172  
7979: contig of 808 bp in length  
7980  
8079: gap of 100 bp  
8080  
8881: contig of 802 bp in length  
8882  
8981: gap of 100 bp  
8982  
9732: contig of 751 bp in length  
9733  
9832: gap of 100 bp  
9833  
10559: contig of 727 bp in length  
10560  
10659: gap of 100 bp  
10660  
11463: contig of 804 bp in length  
11464  
11563: gap of 100 bp  
11564  
12340: contig of 777 bp in length  
12341  
12440: gap of 100 bp  
12441  
13237: contig of 797 bp in length  
13238  
13337: gap of 100 bp  
13339  
14134: contig of 797 bp in length  
14135  
14234: gap of 100 bp  
14235  
15002: contig of 768 bp in length  
15003  
15102: gap of 100 bp  
15103  
15872: contig of 770 bp in length  
15873  
15972: gap of 100 bp  
15974  
16731: contig of 759 bp in length  
16732  
16831: gap of 100 bp  
16832  
17605: contig of 774 bp in length  
17606  
17705: gap of 100 bp  
17706  
18499: contig of 794 bp in length  
18499  
18599: gap of 100 bp  
18600  
19401: contig of 802 bp in length  
19402  
19501: gap of 100 bp  
19502  
20325: contig of 824 bp in length  
20326  
20425: gap of 100 bp  
20426  
21189: contig of 764 bp in length  
21190  
21289: gap of 100 bp  
21290  
22048: contig of 759 bp in length  
22049  
22148: gap of 100 bp  
22149  
22907: contig of 759 bp in length

22908  
23007: gap of 100 bp  
23008  
23775: contig of 768 bp in length  
23776  
23875: gap of 100 bp  
23876  
24694: contig of 809 bp in length  
24695  
24784: gap of 100 bp  
24785  
25560: contig of 776 bp in length  
25561  
25660: gap of 100 bp  
25661  
26446: contig of 786 bp in length  
26447  
26546: gap of 100 bp  
26547  
27322: contig of 776 bp in length  
27323  
27422: gap of 100 bp  
27423  
28179: contig of 757 bp in length  
28180  
28279: gap of 100 bp  
28280  
29044: contig of 765 bp in length  
29045  
29144: gap of 100 bp  
29145  
29942: contig of 798 bp in length  
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30042: gap of 100 bp  
30043  
30811: contig of 769 bp in length  
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30911: gap of 100 bp  
30912  
31663: contig of 752 bp in length  
31664  
31763: gap of 100 bp  
31764  
32540: contig of 777 bp in length  
32541  
32640: gap of 100 bp  
32641  
33471: contig of 831 bp in length  
33472  
33571: gap of 100 bp  
33572  
34358: contig of 787 bp in length  
34359  
34458: gap of 100 bp  
34459  
35239: contig of 781 bp in length  
35240  
35339: gap of 100 bp  
35340  
36111: contig of 772 bp in length  
36112  
36211: gap of 100 bp  
36212  
36966: contig of 755 bp in length  
36967  
37066: gap of 100 bp  
37067  
37814: contig of 747 bp in length  
37815  
37913: gap of 100 bp  
37914  
38694: contig of 781 bp in length  
38695  
38794: gap of 100 bp  
38795  
39559: contig of 765 bp in length  
39560  
39659: gap of 100 bp  
39660  
40413: contig of 754 bp in length  
40414  
40513: gap of 100 bp  
40514  
41335: contig of 822 bp in length  
41336  
41435: gap of 100 bp  
41436  
42174: contig of 739 bp in length  
42175  
42274: gap of 100 bp  
42275  
43080: contig of 806 bp in length  
43081  
43180: gap of 100 bp  
43181  
43971: contig of 791 bp in length  
43972  
44071: gap of 100 bp  
44072  
44876: contig of 805 bp in length  
44877  
44976: gap of 100 bp  
44977  
45791: contig of 815 bp in length  
45792  
45891: gap of 100 bp  
45892  
46720: contig of 829 bp in length  
46721  
46820: gap of 100 bp  
46821  
47558: contig of 738 bp in length  
47559  
47658: gap of 100 bp  
47659  
48475: contig of 817 bp in length  
48476  
48575: gap of 100 bp  
48576  
49384: contig of 809 bp in length  
49385  
49484: gap of 100 bp  
49485  
50346: contig of 862 bp in length  
50347  
50446: gap of 100 bp  
50447  
51295: contig of 845 bp in length  
51296  
51395: gap of 100 bp  
51396  
52202: contig of 807 bp in length  
52203  
52302: gap of 100 bp  
52303  
53120: contig of 818 bp in length  
53121  
53220: gap of 100 bp  
53221  
54050: contig of 830 bp in length  
54051  
54150: gap of 100 bp  
54151  
54967: contig of 817 bp in length  
54968  
55067: gap of 100 bp



```

* 55068 55868: contig of 801 bp in length
* 55869 55968: gap of 100 bp
* 55969 56805: contig of 837 bp in length
* 56806 56905: gap of 100 bp
* 56906 57747: contig of 842 bp in length
* 57748 57847: gap of 100 bp
* 57848 58650: contig of 803 bp in length
* 58651 58750: gap of 100 bp
* 58751 59553: contig of 803 bp in length
* 59554 59654: gap of 100 bp
* 59654 60387: contig of 733 bp in length
* 60387 61311: contig of 825 bp in length
* 61312 61411: gap of 100 bp
* 61412 62225: contig of 814 bp in length
* 62226 62325: gap of 100 bp
* 62326 63128: contig of 803 bp in length
* 63129 63228: gap of 100 bp
* 63229 64055: contig of 827 bp in length
* 64056 64155: gap of 100 bp

Query Match 72.2% Score 13; DB 2; Length 99591;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 6 CCGGAGNNNNNN 18
Db 35233 CCGGAGNNNNNN 35245

RESULT 177
AC142060
LOCUS
DEFINITION
Rattus norvegicus clone CH230-21H3, *** SEQUENCING IN PROGRESS ***
AC142060
AC142060.1 GI:29135531
HTG: HTGS_PHASE1.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 99630)

```

## COMMENT

```

REFERENCE
AUTHORS
Muzny, D., Marz, M., Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D.,
Anyalebechi, V., Ayogbi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gabregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guvarava, W.,
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Hollins, B., Howell, S., Huliyil, S., Hume, J., Idlebird, J., Jackson, A.,
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Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenz, L., Louie, L., Louie, H., Lozano, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A.,
Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,

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Morrison, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okwom, G.,
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Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polinder, A.,
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Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y.,
Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A.,
Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S.,
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Slason, I., Sitter, C.D., Smajic, D., Sneed, A., Sodergren, E.,
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Stavely, A., Tabors, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Trejos, Z., Usmani, K., Valae, R., Vera, V., Villasana, D.,
Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,
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Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R.,
Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 99630)
REFERENCE
AUTHORS
Worley, K.C.
TITLE
Submitted (21-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
JOURNAL
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GM02
Center clone name: CH230-21H3
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 69017 bases at least Q40
Consensus quality: 78942 bases at least Q30
Consensus quality: 85937 bases at least Q20
Estimated insert size: 76134; sum-of-contigs estimation
Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1062: contig of 1062 bp in length
1063 1162: gap of unknown length
1163 2260: contig of 1098 bp in length
2261 2360: gap of unknown length
2361 3395: contig of 1635 bp in length
3396 4095: gap of unknown length
4096 5304: contig of 1209 bp in length
5305 5404: gap of unknown length
5405 7022: contig of 1618 bp in length
7023 7122: gap of unknown length
7123 8323: contig of 1201 bp in length
8324 8424: gap of unknown length
8425 9745: gap of unknown length
9746 11107: contig of 1362 bp in length
11108 11207: gap of unknown length
11208 12312: contig of 1105 bp in length
12313 12412: gap of unknown length

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* 12413 13886: contig of 1474 bp in length
* 13887 13986: gap of unknown length
* 13887 15293: contig of 1307 bp in length
* 15294 15393: gap of unknown length
* 15394 16612: contig of 1219 bp in length
* 16613 16712: gap of unknown length
* 16713 18365: contig of 1653 bp in length
* 18366 18465: gap of unknown length
* 18466 19918: contig of 1453 bp in length
* 19919 20018: gap of unknown length
* 20019 21283: contig of 1265 bp in length
* 21284 23678: contig of 2295 bp in length
* 23679 23778: gap of unknown length
* 23779 25548: contig of 1770 bp in length
* 25549 25648: gap of unknown length
* 25649 26795: contig of 1047 bp in length
* 26796 28123: contig of 1328 bp in length
* 28124 28223: gap of unknown length
* 28224 29467: contig of 1144 bp in length
* 29468 31043: contig of 1576 bp in length
* 31044 31144: gap of unknown length
* 31144 32427: contig of 1284 bp in length
* 32428 34121: contig of 1594 bp in length
* 34122 34222: gap of unknown length
* 34222 35698: contig of 1477 bp in length
* 35699 35798: gap of unknown length
* 35799 37428: contig of 1630 bp in length
* 37429 39749: contig of 2221 bp in length
* 39750 39850: gap of unknown length
* 39850 41703: contig of 1854 bp in length
* 41704 41803: gap of unknown length
* 41804 43197: contig of 1394 bp in length
* 43198 43297: gap of unknown length
* 43298 44826: contig of 1529 bp in length
* 44827 44926: gap of unknown length
* 44927 46300: contig of 1374 bp in length
* 46301 46400: gap of unknown length
* 46401 48200: contig of 1800 bp in length
* 48201 50287: contig of 1987 bp in length
* 48301 50387: gap of unknown length
* 50388 51928: contig of 1541 bp in length
* 51929 52028: gap of unknown length
* 52029 53874: contig of 1846 bp in length
* 53875 53974: gap of unknown length
* 53975 56143: contig of 2169 bp in length
* 56144 56243: gap of unknown length
* 56244 58751: contig of 2408 bp in length
* 58752 60931: gap of unknown length
* 60932 61031: contig of 2180 bp in length
* 61032 62581: contig of 1550 bp in length
* 62582 62681: gap of unknown length
* 62682 64652: contig of 1971 bp in length
* 64653 64752: gap of unknown length
* 64753 67429: contig of 2677 bp in length
* 67430 67529: gap of unknown length
* 67530 69366: contig of 1837 bp in length
* 69367 69466: gap of unknown length
* 69467 71870: contig of 2404 bp in length
* 71871 73979: gap of unknown length
* 73980 74079: contig of 2009 bp in length
* 74080 76061: gap of unknown length
* 76062 76161: contig of 1982 bp in length
* 76162 79441: contig of 3280 bp in length
* 79442 79541: gap of unknown length
* 79542 83058: contig of 3517 bp in length

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FEATURES
  source
    1..99630
      /organism="Rattus norvegicus"
      /mol_type="genomic DNA"
      /db_xref="taxon:10116"

Query Match
  Best Local Similarity 72.2%; Score 13; DB 2; Length 99630;
  Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTGAGAGNNNNNN 18
Db 73973 CCTGAGAGNNNNNN 73985

RESULT 178
AC091367.0/c
WPCOMMENT
  Sequence split into 6 fragments
  Fragment Name Begin End
  AC091367_1 1 110000
  AC091367_2 100001 210000
  AC091367_3 200001 310000
  AC091367_4 300001 410000
  AC091367_5 400001 510000
  AC091367_6 500001 519219
  AC091367 519219 bp DNA linear HTG 26-SEP-2002
  DEFINITION
    Rattus norvegicus clone CH230-unknown, *** SEQUENCING IN PROGRESS
  *** 77 unordered pieces.
  ACCESSION
    AC091367 GI:23322497
  VERSION
    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
  KEYWORDS
    Rattus norvegicus (Norway rat)
  SOURCE
    Rattus norvegicus
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
    Rattus.
  1 (bases 1 to 519219)
  REFERENCE
    AUTHORS
      Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
      Alsbrooks, S.L., Amarantunge, H.C., Are, J.R., Ayele, M., Banks, T.,
      Barbarella, J., Benton, J., Bimberg, K., Blankenburg, K., Bonnin, D.,
      Boucek, J., Bowie, S., Bileva, M., Brown, E., Brown, M., Bryant, N.P.,
      Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
      Carron, T.R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
      Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C.,
      Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
      Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
      Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
      Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
      Eymann, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
      Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
      Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
      Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
      Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
      Hernandez, O., Hodgson, A., Hogue, M., Hollway, C., Hollins, B.,
      Homsi, F., Howard, S., Huber, V., Huliy, S., Hume, J., Jackson, L.E.,
      Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
      Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
      Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
      Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Loulesed, H.,
      Lozadó, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
      Maheshwari, M., Mapa, P., Martin, R., Mattindale, A., Martinez, E.,
      Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M.,
      Miner, G., Miner, Z., Mitchell, T., Mohabhat, K., Morgan, M., Morris, S.,
      Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,

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Nguyen, N., Nickerson, E., Nwokwkw, S., Ogun, M., Okunolu, G., Oregunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rivera, M., Rojas, A., Rojokoban, I., Rolfe, M., Ruiz, S., Savary, G., Scherzer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Soederren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swalek, A., Taber, P., Tameris, A., Tameris, K., Tang, H., Tatum, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Uman, K., Vazquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Unpublished  
Direct Submission  
2 (bases 1 to 519219)  
Worley, K.C.  
Submitted (18-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT  
Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Sep 26, 2002 this sequence version replaced gi:13661933.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: TUEX  
Center clone name: CH230-unknown  
----- Summary Statistics  
Assembly program: Phrap, version 0.990329  
Consensus quality: 167367 bases at least Q40  
Consensus quality: 176727 bases at least Q30  
Consensus quality: 187406 bases at least Q20  
Estimated insert size: 261798; sum-of-contigs estimation  
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_drfic\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_drfic_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 77 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 10492: contig of 10492 bp in length  
\* 10493 10592: gap of unknown length  
\* 10593 22069: contig of 11477 bp in length  
\* 22070 22169: gap of unknown length  
\* 22170 25007: contig of 2838 bp in length  
\* 25008 25107: gap of unknown length  
\* 25108 27865: contig of 2758 bp in length  
\* 27866 27965: gap of unknown length  
\* 27966 253152: contig of 225187 bp in length  
\* 253153 253252: gap of unknown length  
\* 253253 256213: contig of 2961 bp in length

256214 256313: gap of unknown length  
\* 256314 322664: contig of 66351 bp in length  
\* 322665 332764: gap of unknown length  
\* 332765 335240: contig of 12476 bp in length  
\* 335241 335340: gap of unknown length  
\* 335341 348395: contig of 13055 bp in length  
\* 348396 348495: gap of unknown length  
\* 348496 359045: contig of 10551 bp in length  
\* 359047 359146: gap of unknown length  
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\* 370031 370130: gap of unknown length  
\* 370131 381017: contig of 10887 bp in length  
\* 381018 381117: gap of unknown length  
\* 381118 391885: contig of 10766 bp in length  
\* 391886 391985: gap of unknown length  
\* 391986 407863: contig of 15878 bp in length  
\* 407864 407963: gap of unknown length  
\* 407964 419853: contig of 11890 bp in length  
\* 419854 419953: gap of unknown length  
\* 419954 423130: contig of 3177 bp in length  
\* 423131 423230: gap of unknown length  
\* 423231 427402: contig of 4172 bp in length  
\* 427403 427502: gap of unknown length  
\* 427503 428519: contig of 1017 bp in length  
\* 428520 428619: gap of unknown length  
\* 428620 429743: contig of 1124 bp in length  
\* 429744 429843: gap of unknown length  
\* 429844 431152: contig of 1309 bp in length  
\* 431153 431252: gap of unknown length  
\* 431253 432285: contig of 1032 bp in length  
\* 432286 432385: gap of unknown length  
\* 432386 433460: contig of 1076 bp in length  
\* 433461 433560: gap of unknown length  
\* 433561 434982: contig of 1422 bp in length  
\* 434983 435082: gap of unknown length  
\* 435083 436447: contig of 1365 bp in length  
\* 436448 436547: gap of unknown length  
\* 436548 437572: contig of 1025 bp in length  
\* 437573 437672: gap of unknown length  
\* 437673 438994: contig of 1322 bp in length  
\* 438995 439094: gap of unknown length  
\* 439095 440323: contig of 1229 bp in length  
\* 440324 440423: gap of unknown length  
\* 440424 441494: contig of 1071 bp in length  
\* 441495 441594: gap of unknown length  
\* 441595 443035: contig of 1441 bp in length  
\* 443036 443135: gap of unknown length  
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\* 444200 444299: gap of unknown length  
\* 444300 445615: contig of 1316 bp in length  
\* 445616 445715: gap of unknown length  
\* 445716 447329: contig of 1614 bp in length  
\* 447330 447429: gap of unknown length  
\* 447430 448522: contig of 1093 bp in length  
\* 448523 448622: gap of unknown length  
\* 448623 449996: contig of 1374 bp in length  
\* 449997 450096: gap of unknown length  
\* 450097 451111: contig of 1015 bp in length  
\* 451112 451211: gap of unknown length  
\* 451212 452216: contig of 1005 bp in length  
\* 452217 452316: gap of unknown length  
\* 452317 453405: contig of 1089 bp in length  
\* 453406 453505: gap of unknown length  
\* 453506 454758: contig of 1253 bp in length  
\* 454759 454859: gap of unknown length  
\* 454860 456425: contig of 1567 bp in length  
\* 456426 456525: gap of unknown length  
\* 456526 457806: contig of 1281 bp in length  
\* 457807 457906: gap of unknown length  
\* 457907 459589: contig of 1683 bp in length  
\* 459590 459689: gap of unknown length  
\* 459690 460963: contig of 1274 bp in length  
\* 460964 461063: gap of unknown length

\* 461064 462922: contig of 1859 bp in length  
\* 462923 463022: gap of unknown length  
\* 463023 464760: contig of 1738 bp in length  
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\* 464861 466416: contig of 1556 bp in length  
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Query Match 72.2%; Score 13; DB 2; Length 110000;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTGGAGNNNNNN 18  
Db 10599 CCTGGAGNNNNNN 10587

RESULT 179  
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WPCOMMENT  
Sequence split into 6 fragments LOCUS AC107099 Accession AC107099  
Fragment Name Begin End  
AC107099\_0 1 110000  
AC107099\_1 100001 210000  
AC107099\_2 200001 310000  
AC107099\_3 300001 410000  
AC107099\_4 400001 510000  
AC107099\_5 500001 541716  
Continuation (3 of 6) of AC107099 from base 200001 (AC107099 Rattus norvegicus clone CH2)

Query Match 72.2%; Score 13; DB 2; Length 110000;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
Db 26513 CCTGGAGNNNNNN 26525

RESULT 180  
AC130665\_1/c  
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Fragment Name Begin End  
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AC130665\_1 100001 210000  
AC130665\_2 200001 310000  
AC130665\_3 300001 389215  
Continuation (2 of 4) of AC130665 from base 100001 (AC130665 Mus musculus clone RP23-369)

Query Match 72.2%; Score 13; DB 2; Length 110000;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
Db 72266 CCTGGAGNNNNNN 72254

RESULT 181  
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WPCOMMENT  
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Fragment Name Begin End  
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AC145312\_1 100001 210000  
AC145312\_2 200001 310000  
AC145312\_3 300001 408009  
LOCUS AC145312 408009 bp DNA linear HTG 23-JUN-2003  
DEFINITION Homo sapiens chromosome 16 clone RP11-1398M15, WORKING DRAFT  
ACCESSION AC145312  
VERSION AC145312.1 GI:32141371  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.

SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
TITLE  
Sequencing of Human Chromosome 16  
JOURNAL  
Unpublished  
AUTHORS  
DOE Joint Genome Institute.  
TITLE  
DOE Joint Genome Institute.  
JOURNAL  
Submitted (23-JUN-2003) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>

Project Information  
Center Project Name: 2756769  
Center Clone name: RPCI-11\_1398M15

Summary Statistics  
Consensus quality: 367259 bases at least Q40  
Consensus quality: 376423 bases at least Q30  
Consensus quality: 383403 bases at least Q20  
Estimated insert size: 175000; agarose-fp estimation  
Estimated insert size: 399709; sum-of-coverage estimation  
Quality coverage: 12.41 in Q20 bases; agarose-fp estimation  
Quality coverage: 5.43 in Q20 bases; sum-of-coverage estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 84 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
1197 1196: contig of 1196 bp in length  
1297 1296: gap of unknown length  
2413 2412: contig of 1116 bp in length  
2513 2512: gap of unknown length  
4011 4010: contig of 1498 bp in length  
4111 4110: gap of unknown length  
5217 5217: contig of 1107 bp in length  
5318 5317: gap of unknown length  
6752 6752: contig of 1435 bp in length  
6852 6852: gap of unknown length  
6853 6853: contig of 1305 bp in length  
8158 8157: gap of unknown length  
8258 8257: gap of unknown length  
9437 9436: contig of 1179 bp in length  
9537 9536: gap of unknown length  
10665 10665: contig of 1129 bp in length  
10766 10765: gap of unknown length  
12133 12133: contig of 1368 bp in length  
12233 12233: gap of unknown length  
12234 12234: contig of 1101 bp in length  
13335 13334: gap of unknown length  
13435 13434: gap of unknown length  
14783 14783: contig of 1349 bp in length  
14883 14883: gap of unknown length  
16159 16159: contig of 1276 bp in length  
16160 16259: gap of unknown length  
16260 17298: contig of 1039 bp in length  
17299 17398: gap of unknown length  
17399 18565: contig of 1167 bp in length  
18566 18665: gap of unknown length  
18666 19866: contig of 1201 bp in length  
19867 19966: gap of unknown length  
19967 21433: contig of 1467 bp in length  
21434 21533: gap of unknown length  
21534 23000: contig of 1467 bp in length  
23001 23100: gap of unknown length  
23101 24648: contig of 1548 bp in length

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* 24649 24748: gap of unknown length
* 24749 26165: contig of 1417 bp in length
* 26166 26265: gap of unknown length
* 26266 27599: contig of 1334 bp in length
* 27600 27699: gap of unknown length
* 27700 29089: contig of 1390 bp in length
* 29090 29189: gap of unknown length
* 29190 30621: contig of 1432 bp in length
* 30622 30721: gap of unknown length
* 30722 32172: contig of 1451 bp in length
* 32173 32272: gap of unknown length
* 32273 33761: contig of 1489 bp in length
* 33762 33861: gap of unknown length
* 33862 35038: contig of 1177 bp in length
* 35039 35138: gap of unknown length
* 35139 36681: contig of 1543 bp in length
* 36682 36781: gap of unknown length
* 36782 38327: contig of 1546 bp in length
* 38328 38427: gap of unknown length
* 38428 39450: contig of 1023 bp in length
* 39451 39550: gap of unknown length
* 39551 40681: contig of 1131 bp in length
* 40682 40781: gap of unknown length
* 40782 42221: contig of 1440 bp in length
* 42222 42321: gap of unknown length
* 42322 43385: contig of 1064 bp in length
* 43386 43485: gap of unknown length
* 43486 45081: contig of 1596 bp in length
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* 45182 46279: contig of 1098 bp in length
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* 46380 47437: contig of 1058 bp in length
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* 47538 48993: contig of 1456 bp in length
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* 49094 50562: contig of 1469 bp in length
* 50563 50662: gap of unknown length
* 50663 52415: contig of 1753 bp in length
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* 52516 54065: contig of 1550 bp in length
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* 54166 55666: contig of 1501 bp in length
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* 62009 62108: gap of unknown length
* 62109 64347: contig of 2239 bp in length
* 64348 64447: gap of unknown length
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* 66254 68873: contig of 2620 bp in length
* 68874 68973: gap of unknown length
* 68975 71129: contig of 2156 bp in length
* 71130 71229: gap of unknown length
* 71230 73183: contig of 1954 bp in length
* 73184 73283: gap of unknown length
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* 75993 78233: contig of 2241 bp in length
* 78234 78333: gap of unknown length
* 78334 80553: contig of 2220 bp in length
* 80554 80653: gap of unknown length
* 80655 82812: contig of 2159 bp in length
* 82813 82912: gap of unknown length
* 82914 84728: contig of 1816 bp in length
* 84729 84828: gap of unknown length
* 84829 87233: contig of 2405 bp in length
* 87234 87334: gap of unknown length
* 87335 90139: contig of 2806 bp in length
* 90140 90239: gap of unknown length

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* 90240 92563: contig of 2324 bp in length
* 92564 92663: gap of unknown length
* 92664 95367: contig of 2704 bp in length
* 95368 95467: gap of unknown length
* 95468 98282: contig of 2815 bp in length
* 98283 98382: gap of unknown length
* 98383 100819: contig of 2437 bp in length
* 100820 100919: gap of unknown length
* 100920 103443: contig of 2524 bp in length
* 103444 103543: gap of unknown length
* 103544 106164: contig of 2621 bp in length
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* 106265 109600: contig of 3336 bp in length
* 109601 109700: gap of unknown length
* 109701 112652: contig of 2952 bp in length
* 112653 112752: gap of unknown length
* 112753 115031: contig of 2279 bp in length
* 115032 115131: gap of unknown length
* 115132 118017: contig of 2886 bp in length
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* 118118 120779: contig of 2662 bp in length
* 120780 120879: gap of unknown length
* 120880 124557: contig of 3678 bp in length
* 124558 124657: gap of unknown length
* 124659 129049: contig of 4392 bp in length
* 129050 129149: gap of unknown length
* 129150 133797: contig of 4648 bp in length
* 133798 133897: gap of unknown length
* 133898 139769: contig of 5872 bp in length
* 139770 139869: gap of unknown length
* 139870 145264: contig of 5395 bp in length
* 145265 145364: gap of unknown length
* 145365 151079: contig of 5715 bp in length
* 151080 151179: gap of unknown length
* 151180 156310: contig of 5131 bp in length
* 156311 156410: gap of unknown length
* 156411 162615: contig of 6205 bp in length
* 162715 162716: gap of unknown length
* 162716 163903: contig of 1188 bp in length
* 163904 173562: contig of 9559 bp in length

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Query Match 72.2% Score 13; DB 2; Length 110000;  
Beet Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 6 CCUGAGNNNNNN 18  
Db 19973 CCTGAGNNNNNN 19961

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AC055726_1 100001 210000
AC055726_2 200001 310000
AC055726_3 300001 410000
AC055726_4 400001 456720
LOCUS AC055726 456720 bp DNA linear HTG 27-JAN-2002
DEFINITION Homo sapiens chromosome 3 clone Rpl1-9aJ5, WORKING DRAFT SEQUENCE.
101 unordered pieces.
ACCESSION AC055726 GI:18377140
VERSION AC055726.13
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 456720)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

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Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayale, M., Banks, T.,  
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 Weinstein, G. and Gibbs, R.

Unpublished  
 Direct Submission  
 2 (bases 1 to 456720)  
 Worley, K.C.

Direct Submission  
 Submitted (18-APR-2000) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jan 27, 2002 this sequence version replaced gi:11128115.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information  
 Center project name: HAVU  
 Center clone name: RP11-98J5  
 Sequencing vector: M13, L08821  
 Chemistry: Dye-terminator Big Dye 73% of reads  
 Assembly program: Phrap, version 0.990325First call to  
 findPhrapList

Consensus quality: 369571 bases at least Q40  
 Consensus quality: 395345 bases at least Q30  
 Consensus quality: 411294 bases at least Q20  
 Estimated insert size: 393000; sum-of-contigs estimation  
 Quality coverage: 0x in Q20 bases; agarose-tp estimation  
 Quality coverage: 4.4x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
 \* NOTE: This sequence may represent more than one clone.  
 \* NOTE: This is a 'working draft' sequence. It currently

\* consists of 101 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1  
 794  
 894  
 1672  
 1772  
 1773  
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 3756  
 3855  
 5009  
 5109  
 6181  
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Query Match	72.2%	Score 13:	DB 2:	Length 116585;
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AC013324.3	GI:9123914			
HTG: HTGS_PHS0.				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
REFERENCE				
AUTHORS				

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*	17422	17551:	gap of 100 bp	in length
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*	22156	23005:	contig of 850 bp	in length
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*	34505	35504:	gap of 100 bp	in length
*	35505	36568:	contig of 864 bp	in length
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	*	37454	38310: contig of 857 bp in length
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	*	40318	41326: contig of 909 bp in length
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	*	44144	44243: gap of 100 bp
	*	44244	45131: contig of 888 bp in length
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	*	48202	49041: contig of 840 bp in length
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	*	65123	65983: contig of 861 bp in length
	*	65984	66083: gap of 100 bp
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	*	67023	67908: contig of 886 bp in length
	*	67909	68008: gap of 100 bp
	*	68009	68879: contig of 871 bp in length
	*	68880	68979: gap of 100 bp

Query Match

Best Local Similarity

Matches

72.2%  
92.3%  
12

Score 13; DB 2; Length 118540;  
Pred. No. 4.5e+02;  
Conservative

1; Mismatches 0; Gaps 0;

6 CCGAGAGNNNNN 18  
|||||

```

DB      117737  COTGAGNNNNNN 117725

RESULT 185
AL355675/c
LOCUS      AL355675
DEFINITION Homo sapiens chromosome 1 clone RP5-1132F1, 21 unordered pieces.
ACCESSION  AL355675
VERSION    AL355675.3 GI:9863739
KEYWORDS   HTG; HTGS _PHASE1; HTGS _CANCELLED.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS   Plumb, B.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
          CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
          Requests: clonerequest@sanger.ac.uk
          On Aug 21, 2000 this sequence version replaced gi:9213627.

COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: d1132F1
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 122442 bases at least Q40
Consensus quality: 126008 bases at least Q30
Consensus quality: 128093 bases at least Q20
Insert size: 130600; sum-of-contigs
Insert size: 151036; 12.1% error; agarose-fp
Quality coverage: 3.42x in Q20 bases; sum-of-contigs
Quality coverage: 3.13x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 4087: contig of 4087 bp in length
*
* 4088
* 4187: gap of 100 bp
* 4188
* 18184: contig of 13997 bp in length
*
* 18185
* 18284: gap of 100 bp
*
* 18285
* 20786: contig of 2502 bp in length
*
* 20787
* 20886: gap of 100 bp
*
* 20887
* 32597: contig of 1171 bp in length
*
* 32598
* 32698
* 38951: contig of 6254 bp in length
*
* 38952
* 39051: gap of 100 bp
*
* 39052
* 42761: contig of 3710 bp in length
*
* 42762
* 42861: gap of 100 bp
*
* 42862
* 50655: contig of 7794 bp in length
*
* 50656
* 50755: gap of 100 bp
*
* 50756
* 60116: contig of 9361 bp in length
*
* 60117
* 60216: gap of 100 bp
*
* 60217
* 62824: contig of 2608 bp in length
*
* 62825
* 62924: gap of 100 bp
*
* 62925
* 68919: contig of 5995 bp in length
*
* 68920
* 69019: gap of 100 bp
*
* 69020
* 86112: contig of 17093 bp in length
*
* 86113
* 86212: gap of 100 bp
*
* 86213
* 90244: contig of 4032 bp in length
*
* 90245
* 90344: gap of 100 bp
*
* 90345
* 93814: contig of 3470 bp in length

```

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* 93915 93914: gap of 100 bp
* 93915 98595: contig of 4681 bp in length
* 98595 98595: gap of 100 bp
* 98595 101339: contig of 2744 bp in length
* 101440 101539: gap of 100 bp
* 101540 108271: contig of 6732 bp in length
* 108272 108371: gap of 100 bp
* 108372 117614: contig of 9243 bp in length
* 117615 117714: gap of 100 bp
* 117715 120384: contig of 2670 bp in length
* 120385 120484: gap of 100 bp
* 120485 122837: contig of 2353 bp in length
* 122838 122937: gap of 100 bp
* 122938 130451: contig of 7514 bp in length
* 130452 130552: gap of 100 bp
* 130552 132600: contig of 2049 bp in length.
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120485..122837
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122938..130451
/note="assembly fragment:01222"
130552..132600
/note="assembly fragment:00803
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ORIGIN
Query Match 72.2%; Score 13; DB 2; Length 132600;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18
Db 122944 CCTGAGAGNNNNNN 122932

RESULT 186
AC102359 133669 bp DNA linear HTG 30-JUL-2002
DEFINITION Mus musculus clone RP23-22C8, LOW-PASS SEQUENCE SAMPLING.
AC102359
VERSION AC102359.2 GI:22004563
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 133669)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-22C8
Unpublished
2 (bases 1 to 133669)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Bana, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Hearford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., Laroque, K.,
Lamzares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Maclean, C., Macdonald, P., Major, U., Margulis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPeeters, R., Meldrum, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunhphang, P., Pierre, N., Pollara, V.,
Raymond, C., Retter, K., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 133669)
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Bana, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
Camarata, J., Chang, J., Chazaro, B., Chopel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, U., Matthews, C.,
McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunhphang, P., Pierre, N., Raymond, C., Retter, K., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zemdek, L., Zimmer, A. and Zody, M.
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TITLE  
JOURNAL  
COMMENT

Direct Submission  
Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 30, 2002 this sequence version replaced gi:17061445.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information

Center project name: L18567

Center clone name: 22\_C\_8

NOTE: This record contains 162 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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810 1539: contig of 730 bp in length  
1540 1639: gap of 100 bp  
1640 2356: contig of 717 bp in length  
2357 2456: gap of 100 bp  
2457 3162: contig of 706 bp in length  
3163 3262: gap of 100 bp  
3263 3988: contig of 726 bp in length  
3989 4088: gap of 100 bp  
4089 4827: contig of 739 bp in length  
4828 4927: gap of 100 bp  
4928 5665: contig of 738 bp in length  
5666 5765: gap of 100 bp  
5766 6496: contig of 731 bp in length  
6497 6596: gap of 100 bp  
6597 7321: contig of 725 bp in length  
7322 7421: gap of 100 bp  
7423 8153: contig of 732 bp in length  
8154 8253: gap of 100 bp  
8254 8976: contig of 723 bp in length  
8977 9076: gap of 100 bp  
9077 9796: contig of 720 bp in length  
9797 9896: gap of 100 bp  
9897 10613: contig of 717 bp in length  
10614 10713: gap of 100 bp  
10714 11417: contig of 704 bp in length  
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12247 12347: gap of 100 bp  
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17206 17305: gap of 100 bp  
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18031 18130: gap of 100 bp  
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18949 19666: contig of 718 bp in length  
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20578 21304: contig of 727 bp in length  
21305 21404: gap of 100 bp  
21405 22138: contig of 734 bp in length  
22139 22238: gap of 100 bp  
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27912 28011: gap of 100 bp  
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37867 38584: contig of 718 bp in length  
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38685 39423: contig of 738 bp in length  
39423 39523: gap of 100 bp  
39523 40258: contig of 736 bp in length  
40259 40358: gap of 100 bp  
40359 41090: contig of 732 bp in length  
41091 41190: gap of 100 bp  
41191 41916: contig of 726 bp in length  
41917 42016: gap of 100 bp  
42017 42740: contig of 724 bp in length  
42741 42840: gap of 100 bp  
42841 43565: contig of 725 bp in length  
43566 43665: gap of 100 bp  
43666 44385: contig of 720 bp in length  
44386 44485: gap of 100 bp  
44486 45217: contig of 732 bp in length  
45218 45317: gap of 100 bp  
45318 46035: contig of 718 bp in length  
46036 46135: gap of 100 bp  
46136 46851: contig of 716 bp in length  
46852 46951: gap of 100 bp  
46952 47682: contig of 731 bp in length

Query Match 72.2%; Score 13; DB 2; Length 133669;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



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\* 60052 60131: gap of unknown length  
\* 60132 61474: contig of 1343 bp in length  
\* 61474 61554: gap of unknown length  
\* 61555 64374: contig of 2820 bp in length  
\* 64375 64454: gap of unknown length  
\* 64455 67054: contig of 2600 bp in length  
\* 67055 67134: gap of unknown length  
\* 67135 70924: contig of 3790 bp in length  
\* 70925 71005 74744: contig of 3740 bp in length  
\* 74745 74824: gap of unknown length  
\* 74825 78675: contig of 3851 bp in length  
\* 78676 78756: gap of unknown length  
\* 78757 83637: contig of 4881 bp in length  
\* 83637 83717: gap of unknown length  
\* 83717 88989: contig of 5273 bp in length  
\* 88990 89059: gap of unknown length  
\* 89070 94572: contig of 5503 bp in length  
\* 94573 94652: gap of unknown length  
\* 94653 100243: contig of 5591 bp in length  
\* 100244 100323: gap of unknown length  
\* 100324 108401: contig of 8078 bp in length  
\* 108402 108481: gap of unknown length  
\* 108482 109098: contig of 617 bp in length  
\* 109099 109178: gap of unknown length  
\* 109179 109902: contig of 724 bp in length  
\* 109903 109982: gap of unknown length  
\* 109983 110645: contig of 664 bp in length  
\* 110647 110726: gap of unknown length  
\* 110727 111394: contig of 668 bp in length  
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\* 112200 112279: gap of unknown length  
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\* 112965 113044: gap of unknown length  
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\* 113676 114219: contig of 544 bp in length  
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\* 114912 114991: gap of unknown length  
\* 114992 115619: contig of 628 bp in length  
\* 115620 115699: gap of unknown length  
\* 115700 116092: contig of 393 bp in length  
\* 116093 116172: gap of unknown length  
\* 116173 116874: contig of 702 bp in length  
\* 116875 116954: gap of unknown length  
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\* 119127 119206: gap of unknown length  
\* 119207 119873: contig of 667 bp in length  
\* 119874 119953: gap of unknown length  
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\* 120622 121315: contig of 694 bp in length  
\* 121316 121395: gap of unknown length

Query Match 72.2% Score 13; DB 2; Length 136756;  
Best Local Similarity 92.3% Pred. No. 4.Se+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTGGAGNNNNNN 18  
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Db 30172 CCTGGAGNNNNNN 30184

RESULT 188

RN374E16/c  
LOCUS RN374E16 140714 bp DNA linear HTG 13-JUN-2002  
DEFINITION Rattus norvegicus clone RPCI-31-374E16 strain Brown Norway, WORKING  
RAFFT SEQUENCE, 118 unordered pieces.  
ACCESSION AL603726  
VERSION AL603726.2 GI:17154526  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1  
AUTHORS Sudbrak, R., Borzym, K., Mueller, I., Klages, S., Kosiura, A.,  
Walter, L., Guenther, E., Hurt, P., Lehnach, H., Himmelbauer, H. and  
Reinhardt, R.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 140714)  
AUTHORS  
TITLE MOLDENR.  
JOURNAL Direct Submission  
TITLES Submitted (10-AUG-2001) MPIMG, Abt. Lehnach, Max Planck Institut  
Fuer Molekulare Genetik, Innestrasse 73, Berlin, 14195 Germany  
COMMENT On Nov 29, 2001 this sequence version replaced gi:15149584.  
contig 01 1. 1251  
contig 02 1352 .3264  
contig 03 3365 .4425  
contig 04 4526 .5017  
contig 05 5118 .6184  
contig 06 6285 .6954  
contig 07 7055 .9462  
contig 08 9563 .10280  
contig 09 10381 .10681  
contig 10 10782 .12517  
contig 11 12618 .13628  
contig 12 13729 .14193  
contig 13 14294 .14692  
contig 14 14793 .15257  
contig 15 15358 .15741  
contig 16 15842 .16024  
contig 17 16125 .16370  
contig 18 16471 .16826  
contig 19 16927 .19591  
contig 20 19692 .20966  
contig 21 21067 .23531  
contig 22 23632 .23905  
contig 23 24006 .25114  
contig 24 25215 .25895  
contig 25 25996 .26775  
contig 26 26876 .27274  
contig 27 27375 .27751  
contig 28 27852 .28141  
contig 29 28242 .29828  
contig 30 29929 .32999  
contig 31 33100 .35425  
contig 32 35526 .36380  
contig 33 36481 .40393  
contig 34 40494 .40865  
contig 35 40966 .42721  
contig 36 42822 .43355  
contig 37 43456 .44345  
contig 38 44446 .44703  
contig 39 44804 .45142  
contig 40 45243 .46298  
contig 41 46399 .46890  
contig 42 46991 .49728  
contig 43 49829 .50587  
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contig 45 51435 .51907  
contig 46 52008 .53006  
contig 47 53107 .53670  
contig 48 53771 .54204  
contig 49 54305 .54782  
contig 50 54883 .55445

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Contig 52 .56397. .57181  
Contig 53 .57282. .57761  
Contig 54 .57862. .58482  
Contig 55 .58583. .59568  
Contig 56 .59669. .60357  
Contig 57 .60458. .61299  
Contig 58 .61400. .62399  
Contig 59 .62500. .63595  
Contig 60 .63696. .64135  
Contig 61 .64236. .65192  
Contig 62 .65293. .66006  
Contig 63 .66107. .67251  
Contig 64 .67352. .68356  
Contig 65 .68357. .69246  
Contig 66 .69347. .70512  
Contig 67 .70613. .71482  
Contig 68 .71583. .72741  
Contig 69 .72842. .73605  
Contig 70 .73706. .77780  
Contig 71 .77881. .77954  
Contig 72 .78055. .78878  
Contig 73 .78979. .80987  
Contig 74 .81088. .82590  
Contig 75 .82691. .83093  
Contig 76 .83194. .84378  
Contig 77 .84479. .85650  
Contig 78 .85751. .87194  
Contig 79 .87295. .87636  
Contig 80 .87737. .89531  
Contig 81 .89632. .90993  
Contig 82 .91094. .92594  
Contig 83 .92695. .93533  
Contig 84 .93634. .94070  
Contig 85 .94171. .95672  
Contig 86 .95773. .97862  
Contig 87 .97963. .99909  
Contig 88 .100010. .102482  
Contig 89 .102583. .104861  
Contig 90 .104962. .106935  
Contig 91 .107036. .110372  
Contig 92 .110473. .112722  
Contig 93 .112823. .114594  
Contig 94 .114695. .117342  
Contig 95 .117443. .117924  
Contig 96 .118025. .120662  
Contig 97 .120723. .122147  
Contig 98 .122248. .122967  
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Contig 101 .127734. .128371  
Contig 102 .128472. .128949  
Contig 103 .129050. .130133  
Contig 104 .130234. .130781  
Contig 105 .130882. .131775  
Contig 106 .131876. .132025  
Contig 107 .132126. .132518  
Contig 108 .132619. .133046  
Contig 109 .133147. .133581  
Contig 110 .133682. .134212  
Contig 111 .134313. .134745  
Contig 112 .134846. .135156  
Contig 113 .135457. .136177  
Contig 114 .136278. .136781  
Contig 115 .136882. .137320  
Contig 116 .137421. .139379  
Contig 117 .139480. .139590  
Contig 118 .139691. .140714.  
AC141918

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 118 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1251: contig of 1251 bp in length  
1252 1351: gap of 100 bp  
1352 3264: contig of 1913 bp in length  
3265 3364: gap of 100 bp  
3365 4425: contig of 1061 bp in length  
4426 4525: gap of 100 bp  
4526 5017: contig of 492 bp in length  
5018 5117: gap of 100 bp  
5118 6184: contig of 1067 bp in length  
6185 6284: gap of 100 bp  
6285 6954: contig of 670 bp in length  
6955 7054: gap of 100 bp  
7055 9463: contig of 2408 bp in length  
9463 9563: gap of 100 bp  
9563 10280: contig of 718 bp in length  
10281 10380: gap of 100 bp  
10381 10681: contig of 301 bp in length  
10682 10781: gap of 100 bp  
10782 12517: contig of 1736 bp in length  
12518 12617: gap of 100 bp  
12618 13628: contig of 1011 bp in length  
13629 13728: gap of 100 bp  
13729 14193: contig of 465 bp in length  
14194 14293: gap of 100 bp  
14294 14692: contig of 399 bp in length  
14693 14792: gap of 100 bp  
14793 15257: contig of 465 bp in length  
15258 15357: gap of 100 bp  
15358 15741: contig of 384 bp in length  
15742 15841: gap of 100 bp  
15842 16024: contig of 183 bp in length  
16025 16124: gap of 100 bp  
16125 16370: contig of 246 bp in length  
16371 16470: gap of 100 bp  
16471 16826: contig of 356 bp in length  
16827 16926: gap of 100 bp  
16927 16991: contig of 2665 bp in length  
16992 19691: gap of 100 bp  
19692 20966: contig of 1275 bp in length  
20967 21066: gap of 100 bp  
21067 22531: contig of 2465 bp in length  
22532 23631: gap of 100 bp  
23631 23905: contig of 274 bp in length  
23906 24006: gap of 100 bp  
24006 25114: contig of 1109 bp in length  
25115 25695: contig of 681 bp in length  
25696 25995: gap of 100 bp  
25996 26775: contig of 780 bp in length  
26776 27274: contig of 399 bp in length  
27275 27374: gap of 100 bp

Query Match 72.2% Score 13; DB 2; Length 140714;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
Db 45249 CCGTGGAGNNNNNN 45237

RESULT 189  
AC141918 143907 bp DNA linear HTG 21-MAR-2003  
LOCUS Rattus norvegicus clone CH230-341123, WORKING DRAFT SEQUENCE, 20  
DEFINITION unsorted pieces.  
ACCESSION AC141918  
VERSION AC141918.2 GI:29135393  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE  
ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.REFERENCE  
AUTHORS

1 (bases 1 to 143907)

Munzy,D,Marie., Metzger,M, Lee., Abramzon,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alebrooks,S., Amin,A., Anguiano,D.,  
Avalanche,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barneshead,M., Behamed,F.,  
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Hollins,B., Howells,S., Hulky,S., Hume,J., Idlebird,D., Jackson,A.,  
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,  
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Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,  
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,  
Lorenzowa,L., Louisedge,H., Lozada,R.J., Lu,X., Ma,J.,  
Maheshwari,M., Mahindartne,M., Mahmud,M., Malloy,K., Mangum,A.,  
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Mawhinley,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A.,  
Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,  
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Newton,N., Nguyen,N., Norris,S., Nwaokelimeh,O., Okonou,G.,  
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Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Polidexter,A.,  
Popovic,D., Primus,E., Pu,L.-L., Puzo,M., Quito,J., Rachlin,E.,  
Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,  
Reuter,M., Richards,S., Riggs,F., Rivers,C., Rodkey,T., Rojas,A.,  
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,  
Scott,G., Shatman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,  
Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,  
Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,  
Sytek,A., Taber,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,  
Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,  
Waldron,L., Walker,B., Wang,J., Wang,O., Wang,S., Warren,J.,  
Warren,R., Wei,X., White,F., Williams,G., Wilson,R., Wleciyk,R.,  
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,  
Yan,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,  
Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,  
Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.

TITLE  
JOURNAL

Unpublished

2 (bases 1 to 143907)

REFERENCE  
AUTHORS

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Direct Submission Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USAREFERENCE  
AUTHORS

3 (bases 1 to 143907)

TITLE  
JOURNAL

Worley,K.C.

Direct Submission Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

## COMMENT

On Mar 21, 2003 this sequence version replaced gi:29126272.

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

Project Information

Center project name: KEIG  
Center clone name: CH230-341123

Summary Statistics

Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 137103 bases at least Q40  
Consensus quality: 138905 bases at least Q30  
Consensus quality: 140423 bases at least Q20  
Estimated insert size: 138648; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbankdraft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbankdraft_data.html)).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 20 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

1 1071: contig of 1071 bp in length  
\* 1072 1171: gap of unknown length  
\* 1172 2612: contig of 1441 bp in length  
\* 2613 2712: gap of unknown length  
\* 2713 3962: contig of 1250 bp in length  
\* 3963 4062: gap of unknown length  
\* 4063 5820: contig of 1758 bp in length  
\* 5821 5920: gap of unknown length  
\* 5921 7092: contig of 1172 bp in length  
\* 7093 7192: gap of unknown length  
\* 7193 10187: contig of 2995 bp in length  
\* 10188 10287: gap of unknown length  
\* 10289 12373: contig of 2086 bp in length  
\* 12374 12473: gap of unknown length  
\* 12474 15633: contig of 3159 bp in length  
\* 15634 15732: gap of unknown length  
\* 15733 18655: contig of 2923 bp in length  
\* 18656 18755: gap of unknown length  
\* 18756 22166: contig of 3411 bp in length  
\* 22167 22265: gap of unknown length  
\* 22266 28829: contig of 6563 bp in length  
\* 28830 33929: gap of unknown length  
\* 33930 34020: contig of 4991 bp in length  
\* 34021 40458: gap of unknown length  
\* 40459 40558: gap of unknown length  
\* 40559 48823: contig of 8265 bp in length  
\* 48824 48923: gap of unknown length  
\* 48924 60713: contig of 11790 bp in length  
\* 60714 60813: gap of unknown length  
\* 60814 72715: contig of 11992 bp in length  
\* 72716 72815: gap of unknown length  
\* 72816 83723: contig of 10908 bp in length  
\* 83724 83823: gap of unknown length  
\* 83824 100067: contig of 16244 bp in length  
\* 100068 100167: gap of unknown length  
\* 100168 117398: contig of 17231 bp in length  
\* 117399 117498: gap of unknown length  
\* 117499 143907: contig of 26409 bp in length.

## FEATURES

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/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-341123"

## ORIGIN

Query Match 72.2%; Score 13; DB 2; Length 143907;  
Best local Similarity 92.3%; Pred. No. 4.5e+02;





\* 144550 144749: gap of 100 bp  
\* 144750 144832: contig of 83 bp in length.  
Location/Qualifiers

FEATURES  
Source  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="16"  
/map="16"  
/clone="RP11-2409"  
/clone\_id="RP11-11 Human Male BAC"  
1. 44757  
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misc\_feature  
clone\_end:SP6  
vector\_side:left"  
4858. 5978  
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72700. 76358  
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76459. 88576  
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88677. 100732  
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100833. 119590  
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119691. 144649  
/note="assembly\_fragment"  
144750. 144832  
/note="assembly\_fragment"

Query Match 72.2%; Score 13; DB 2; Length 144832;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGGAGNNNNN 18  
||:|||||||  
DB 63765 CCTGGAGNNNNN 63777

## RESULT 191

AC141949

LOCUS

DEFINITION

AC141949 145009 bp DNA linear HTG 24-MAR-2003  
Rattus norvegicus clone CH230-435L6, WORKING DRAFT SEQUENCE, 62  
unordered pieces.

ACCESSION

VERSION

KEYWORDS

SOURCE

AC141949.2 GI:29165546  
HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

## REFERENCE

AUTHORS

1 (bases 1 to 145009)  
Muzny,D.,Marle, Metzker,M.,Lee, Abramson,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Albrooks,S., Amin,A., Angiano,D.,  
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Bacc,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,  
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,  
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,  
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,  
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,  
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,  
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,  
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Dvali,B., Eaves,K.,  
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Faller,T., Fan,G.,  
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,  
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,  
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,M., Guvarva,W.,  
Gunnarsson,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,  
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,  
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogue,M.,  
Hollins,B., Howells,S., Huliy,S., Hume,J., Idler,D., Jackson,A.,  
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Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,  
Kowic,S., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,  
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,  
Lorenshuwa,L., Lounsbury,H., Lozano,R.J., Lu,X., Ma,J.,  
Maheshwari,M., Mahindaratne,M., Mahmood,M., Malloy,K., Mangum,A.,  
Mangum,B., Mapa,P., Martin,K., Martin,R., Martinez,E.,  
Mawhinney,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A.,  
Miner,G., Munja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,  
Morriss,S., Mundaas,M., Murphy,M., Nait,L., Nankervis,C., Neal,D.,  
Newton,N., Nguyen,N., Norris,S., Nwokilehen,O., Okwona,G.,  
Olapunsaagoo,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,  
Perez,A., Perez,L., Pfankoch,C., Plopper,F., Ponder,J.,  
Popovic,D., Primus,E., Pu,L.-L., Puzo,M., Quiroz,J., Rachlin,E.,  
Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,  
Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojes,A.,  
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Saverly,G., Scherer,S.,  
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Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villanana,D.,  
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Warren,R., Wei,X., White,F., Williams,G., Wilson,R., Wleciyk,R.,  
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,  
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,  
Zhao,S., Dunn,D., von Niederhausern,A., Weise,R., Smith,D.R.,  
Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

## TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (21-MAR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 145009)  
Worley,K.C.  
Direct Submission

## JOURNAL

## COMMENT

Submitted (24-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Mar 24, 2003 this sequence version replaced gi:29135377.

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

Center project name: XEJT

Center clone name: CH230-43516

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 122876 bases at least Q40

Consensus quality: 127474 bases at least Q30

Consensus quality: 131284 bases at least Q20

Estimated insert size: 121256; sum-of-contigs estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length

(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

NOTE: This is a 'working draft' sequence. It currently

consists of 62 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

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1      1048: contig of 1048 bp in length
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*      2439      3447: contig of 1009 bp in length
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*      3548      4558: contig of 1011 bp in length
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*      5852      7136: gap of unknown length
*      7137      7236: contig of 1285 bp in length
*      7237      8594: gap of unknown length
*      8595      8694: contig of 1358 bp in length
*      8695      9790: gap of unknown length
*      9790      9889: contig of 1095 bp in length
*      9890      11042: gap of unknown length
*      11043      11142: contig of 1153 bp in length
*      11143      12520: gap of unknown length
*      12521      12620: contig of 1378 bp in length
*      12621      13862: gap of unknown length
*      13863      13962: contig of 1242 bp in length
*      13963      15192: gap of unknown length
*      15193      15292: contig of 1230 bp in length
*      15293      16210: gap of unknown length
*      16211      16710: contig of 1318 bp in length
*      16711      18179: gap of unknown length
*      18180      18279: contig of 1469 bp in length
*      18280      19439: gap of unknown length
*      19440      19539: contig of 1160 bp in length
*      19540      21054: gap of unknown length
*      21055      21154: contig of 1515 bp in length
*      21155      22263: gap of unknown length
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*      22364      23594: gap of unknown length
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*      23695      25739: gap of unknown length
*      25740      25839: contig of 2045 bp in length
*      25840      27682: gap of unknown length
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*      27783      29322: gap of unknown length
*      29322: contig of 1540 bp in length

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*      29323      29423: gap of unknown length
*      29423      30548: contig of 1126 bp in length
*      30549      30648: gap of unknown length
*      30649      31905: contig of 1257 bp in length
*      31906      32005: gap of unknown length
*      32006      33205: contig of 1199 bp in length
*      33205      33305: gap of unknown length
*      33305      34778: contig of 1474 bp in length
*      34779      34878: gap of unknown length
*      34879      35927: contig of 1049 bp in length
*      35928      36027: gap of unknown length
*      36028      37320: contig of 1293 bp in length
*      37321      37420: gap of unknown length
*      37421      38889: contig of 1469 bp in length
*      38890      38989: gap of unknown length
*      38990      40261: contig of 1272 bp in length
*      40262      40361: gap of unknown length
*      40362      42122: contig of 1761 bp in length
*      42123      42222: gap of unknown length
*      42223      43389: contig of 1167 bp in length
*      43390      43490: gap of unknown length
*      43490      44562: contig of 1073 bp in length
*      44563      44662: gap of unknown length
*      44663      46375: contig of 1713 bp in length
*      46376      46475: gap of unknown length
*      46476      48324: contig of 1849 bp in length
*      48325      48424: gap of unknown length
*      48425      49883: contig of 1459 bp in length
*      49884      49983: gap of unknown length
*      49984      51910: contig of 1827 bp in length
*      51911      51910: gap of unknown length
*      51911      53704: contig of 1794 bp in length
*      53705      53804: gap of unknown length
*      53805      55258: contig of 1454 bp in length
*      55259      55358: gap of unknown length
*      55359      56920: contig of 1562 bp in length
*      56921      57020: gap of unknown length
*      57021      59109: contig of 2089 bp in length
*      59110      59209: gap of unknown length
*      59210      61669: contig of 2460 bp in length
*      61670      61769: gap of unknown length
*      61770      64277: contig of 2508 bp in length
*      64278      64377: gap of unknown length
*      64378      66761: contig of 2383 bp in length
*      66762      66860: gap of unknown length
*      66861      69204: contig of 2344 bp in length
*      69205      69304: gap of unknown length
*      69305      72908: contig of 3604 bp in length
*      72909      73008: gap of unknown length
*      73009      75798: contig of 2790 bp in length
*      75799      75898: gap of unknown length
*      75899      79161: contig of 3263 bp in length
*      79162      79261: gap of unknown length
*      79262      81697: contig of 2436 bp in length
*      81698      81797: gap of unknown length
*      81798      85199: contig of 3402 bp in length

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Query Match      72.2%      Score 13; DB 2; Length 145009;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      6      CCUGAGNNNNNN 18
DB      64271      CCTGAGNNNNNN 64283

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RESULT 192
AC143192      14555 bp      DNA      linear      HTG 09-APR-2003
LOCUS      Macaca mulatta clone CH250-263A1, *** SEQUENCING IN PROGRESS ***
DEFINITION      AC143192
ACCESSION      AC143192.1      GI:29567831
VERSION      HTG; HTGS_PHASE2; HTGS_PGI.
KEYWORDS

```

SOURCE  
ORGANISM  
Macaca mulatta (rhesus monkey)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca. 1 (bases 1 to 145555)  
Gaurios, M. and Miosavljivic, A.  
Pooled genomic indexing (PGI): mathematical analysis and experiment design  
(in) Guigo, R. and Gusfield, D. (Eds.);  
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI 2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28; Springer (2002)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 145555)  
Miosavljivic, A., Sodergren, E., Gaurios, M., Li, B., Jackson, A.R., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C., Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbato, J., Benton, J., Bimane, K., Blankenburg, K., Bonnin, D., Bouck, J., Burch, P., Briteva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dunn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Egan, A., Farhah, C., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrill, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louised, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Marondei, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzger, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokike, S., Ogun, M., Okwona, G., Otagunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shochat, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabot, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tellier, B., Thomas, N., Thomas, S., Usmami, K., Vaquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleciyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Kuchelapatti, R., Weinstein, G. and Gibbs, R.

TITLE  
JOURNAL  
Direct Submission  
Unpublished

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
3 (bases 1 to 145555)  
Worley, K.C.  
Direct Submission  
Submitted (05-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
4 (bases 1 to 145555)  
Worley, K.C.  
Direct Submission  
Submitted (09-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT  
Center: Baylor College of Medicine  
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: LAUI  
Center clone name: CH250-269A1  
----- Summary Statistics  
Chemistry: Dye-terminator Big Dye; inf% of reads  
Consensus quality: 5823 bases at least Q40  
Consensus quality: 6614 bases at least Q30  
Consensus quality: 7584 bases at least Q20  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: The contigs are based on the application  
\* of the PGI method using the human genome (NCBI build 31)  
\* as the comparative genome.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
1 145555: contig of 145555 bp in length.  
Location/Qualifiers  
1. 145555  
/organism="Macaca mulatta"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9544"  
/clone="CH250-269A1"  
1. 145555  
/note="assembly\_name:CH250-269A1.1A  
CONFIDENCE: 0.83"

FEATURES  
source  
misc\_feature  
1. 145555

ORIGIN  
Query Match 72.2%; Score 13; DB 2; Length 145555;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
Db 103728 CCTGAGANNNNN 103740

RESULT 193  
AC010803  
LOCUS  
AC010803 Homo sapiens clone RP11-2024, LOW-PASS SEQUENCE SAMPLING.  
DEFINITION  
AC010803 AC010803.3 GI:9120116  
VERSION  
AC010803.3  
KEYWORDS  
HTG; HTGS PHASE0.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 146487)  
Britten, B., Linton, L., Nuebaum, C. and Lander, E.  
Homo sapiens, clone RP11-2024  
Unpublished  
2 (bases 1 to 146487)  
Britten, B., Linton, L., Nuebaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Bouhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArlelano, K., Dewar, K., Domingo, R., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funk, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hages, B., Hearford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, U., Karatas, A., Klein, J., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

TITLE  
JOURNAL  
COMMENT

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tresanay, S., Turrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
Submitted (23-SEP-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced g1.6730898.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L2687

Center clone name: 2\_O\_24

NOTE: This record contains 148 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 866: contig of 866 bp in length  
\* 867 966: gap of 100 bp  
\* 967 1831: contig of 865 bp in length  
\* 1832 1931: gap of 100 bp  
\* 1932 2814: contig of 883 bp in length  
\* 2815 2914: gap of 100 bp  
\* 2915 3793: contig of 879 bp in length  
\* 3794 3893: gap of 100 bp  
\* 3894 4777: contig of 884 bp in length  
\* 4778 4877: gap of 100 bp  
\* 4878 5733: contig of 856 bp in length  
\* 5734 5833: gap of 100 bp  
\* 5834 6709: contig of 876 bp in length  
\* 6710 6809: gap of 100 bp  
\* 6810 7681: contig of 872 bp in length  
\* 7682 7781: gap of 100 bp  
\* 7782 8662: contig of 881 bp in length  
\* 8663 8762: gap of 100 bp  
\* 8763 9643: contig of 881 bp in length  
\* 9644 9743: gap of 100 bp  
\* 9744 10613: contig of 870 bp in length  
\* 10614 10713: gap of 100 bp  
\* 10713 11570: contig of 857 bp in length  
\* 11571 11670: gap of 100 bp  
\* 11671 12555: contig of 885 bp in length  
\* 12556 12655: gap of 100 bp  
\* 12656 13508: contig of 853 bp in length  
\* 13509 13608: gap of 100 bp  
\* 13609 14490: contig of 882 bp in length  
\* 14491 14590: gap of 100 bp  
\* 14591 15479: contig of 889 bp in length  
\* 15480 15579: gap of 100 bp  
\* 15580 16444: contig of 865 bp in length  
\* 16445 17426: contig of 882 bp in length  
\* 17427 17526: gap of 100 bp  
\* 17527 18389: contig of 873 bp in length  
\* 18400 18499: gap of 100 bp  
\* 18500 19392: contig of 893 bp in length  
\* 19393 19492: gap of 100 bp  
\* 19493 20385: contig of 893 bp in length  
\* 20386 20485: gap of 100 bp

20486 21361: contig of 876 bp in length  
\* 21362 21461: gap of 100 bp  
\* 21462 22337: contig of 876 bp in length  
\* 22338 22437: gap of 100 bp  
\* 22438 23319: contig of 882 bp in length  
\* 23320 23419: gap of 100 bp  
\* 23420 24296: contig of 877 bp in length  
\* 24297 24396: gap of 100 bp  
\* 24397 25255: contig of 859 bp in length  
\* 25256 25355: gap of 100 bp  
\* 25356 26264: contig of 909 bp in length  
\* 26265 26364: gap of 100 bp  
\* 26365 27236: contig of 872 bp in length  
\* 27237 27337: gap of 100 bp  
\* 27337 28201: contig of 865 bp in length  
\* 28202 28301: gap of 100 bp  
\* 28302 29192: contig of 891 bp in length  
\* 29193 29292: gap of 100 bp  
\* 29293 30161: contig of 869 bp in length  
\* 30162 30261: gap of 100 bp  
\* 30262 31139: contig of 878 bp in length  
\* 31140 31239: gap of 100 bp  
\* 31240 32113: contig of 874 bp in length  
\* 32114 32213: gap of 100 bp  
\* 32214 33083: contig of 870 bp in length  
\* 33084 33183: gap of 100 bp  
\* 33184 34060: contig of 877 bp in length  
\* 34061 34160: gap of 100 bp  
\* 34161 35048: contig of 888 bp in length  
\* 35049 35148: gap of 100 bp  
\* 35149 36024: contig of 876 bp in length  
\* 36025 36124: gap of 100 bp  
\* 36125 36979: contig of 855 bp in length  
\* 36980 37079: gap of 100 bp  
\* 37080 37941: contig of 862 bp in length  
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\* 38042 38937: contig of 896 bp in length  
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\* 40017 40899: contig of 883 bp in length  
\* 40900 40999: gap of 100 bp  
\* 41000 41913: contig of 914 bp in length  
\* 41914 42013: gap of 100 bp  
\* 42014 42801: contig of 888 bp in length  
\* 42902 43001: gap of 100 bp  
\* 43002 43868: contig of 867 bp in length  
\* 43869 43968: gap of 100 bp  
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\* 49787 50658: contig of 872 bp in length  
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\* 50759 51634: contig of 876 bp in length  
\* 51635 51734: gap of 100 bp  
\* 51735 52630: contig of 896 bp in length  
\* 52631 52730: gap of 100 bp  
\* 52731 53619: contig of 889 bp in length  
\* 53620 53719: gap of 100 bp  
\* 53720 54578: contig of 859 bp in length  
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* 56548 56647: gap of 100 bp
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* 67415 68393: contig of 879 bp in length
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* 69445 70299: contig of 855 bp in length
* 70300 70399: gap of 100 bp
* 70400 71285: contig of 886 bp in length

```

```

Query Match 72.2% Score 13; DB 2; Length 146487;
Best Local Similarity 92.3% Pred. NO. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 6 CCUGAGNNNNNN 18
Db 102508 CCTGAGNNNNNN 102520

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RESULT 194
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Rattus norvegicus clone CH230-524N23. *** SEQUENCING IN PROGRESS
*** 56 unordered pieces.
ACCESSION AC141155
VERSION AC141155.2 GI:28975843
KEYWORDS HTG; HTGS PHASE1.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 147352)
Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alibrooks, S., Amin, A., Angiano, D.,
Ayaladebchi, V., Ayogei, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Barnamed, F.,
Biswal, K., Blair, D., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Devila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Frazer, C. M., Gabisel, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gedregeogis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunnarsson, P., Haaland, W., Hamli, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL

```

```

COMMENT

```

```

Hollins, B., Howells, S., Hulik, S., Hume, J., Idtkebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshewa, L., Louisedge, H., Lozada, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindratne, M., Mahmud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A.,
Morris, G., Munja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
Morrison, S., Mundaasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Nwokenlueh, O., Okunolu, G.,
Olanunnaogun, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Ponder, A.,
Petrovic, D., Primus, E., Pu, L., L., Puzo, M., Quiroz, J., Rachlin, E.,
Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y.,
Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A.,
Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S.,
Scott, G., Shatman, S., Shen, H., Sherry, J., Shvartbeyn, A.,
Slason, I., Sitter, C. D., Smaje, D., Sneed, A., Sodergren, E.,
Song, X. Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A.,
Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseña, D.,
Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J.,
Warren, R., Wei, X., White, P., Williams, G., Willson, R., Wiczak, R.,
Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R.,
Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 147352)
Worley, K. C.
Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 147352)
Worley, K. C.
Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Mar 17, 2003 this sequence version replaced gi:28894510.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KERN
Center clone name: CH230-524N23
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 134150 bases at least Q40
Consensus quality: 140679 bases at least Q30
Consensus quality: 145481 bases at least Q20
Estimated insert size: 131271; sum-of-contigs estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbankdraft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 56 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1000: contig of 1000 bp in length

```

1001	1100: gap of unknown length
1101	2284: contig of 1184 bp in length
2285	2384: gap of unknown length
2385	3633: contig of 1249 bp in length
3634	3733: gap of unknown length
3734	5288: contig of 1555 bp in length
5289	5388: gap of unknown length
5389	6430: contig of 1042 bp in length
6431	6530: gap of unknown length
7889	7988: gap of unknown length
9372	9371: contig of 1383 bp in length
9472	10504: gap of unknown length
10505	10604: gap of unknown length
10605	11618: contig of 1014 bp in length
11619	11718: gap of unknown length
11719	13123: contig of 1405 bp in length
13124	13223: gap of unknown length
13224	14475: contig of 1252 bp in length
14476	14575: gap of unknown length
14576	16149: contig of 1574 bp in length
16150	16249: gap of unknown length
16250	17392: contig of 1143 bp in length
17393	17492: gap of unknown length
17493	18914: contig of 1422 bp in length
18915	19014: gap of unknown length
19015	20108: contig of 1094 bp in length
20109	20208: gap of unknown length
20209	21542: contig of 1334 bp in length
21543	21642: gap of unknown length
21643	23405: contig of 1763 bp in length
23406	23505: gap of unknown length
23506	25572: contig of 2067 bp in length
25573	25672: gap of unknown length
25673	27764: contig of 2092 bp in length
27765	27864: gap of unknown length
27865	29323: contig of 1459 bp in length
29324	29423: gap of unknown length
29424	31542: contig of 2119 bp in length
31543	31642: gap of unknown length
31643	33812: contig of 2170 bp in length
33813	33912: gap of unknown length
33913	36361: contig of 2449 bp in length
36362	36461: gap of unknown length
36462	38607: contig of 2146 bp in length
38608	38707: gap of unknown length
41044	41043: contig of 2336 bp in length
41044	41143: gap of unknown length
41144	42381: contig of 1238 bp in length
42382	42481: gap of unknown length
42482	44281: contig of 2020 bp in length
44502	44601: gap of unknown length
44602	46994: contig of 2393 bp in length
46995	47094: gap of unknown length
47095	48335: contig of 1441 bp in length
48336	48635: gap of unknown length
48636	50214: contig of 1579 bp in length
50215	50314: gap of unknown length
50315	52826: contig of 2512 bp in length
52827	52926: gap of unknown length
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55472	55571: gap of unknown length
55572	57702: contig of 2131 bp in length
57703	57802: gap of unknown length
57803	60817: contig of 3015 bp in length
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63950	64049: gap of unknown length
64050	66578: contig of 2529 bp in length
66579	66678: gap of unknown length
66679	68904: contig of 2226 bp in length
68905	69004: gap of unknown length

69005	71188: contig of 2184 bp in length
71189	71288: gap of unknown length
71289	73507: contig of 2219 bp in length
73508	73607: gap of unknown length
73608	76943: contig of 3336 bp in length
76944	77043: gap of unknown length
77044	80072: contig of 3029 bp in length
80073	80172: gap of unknown length
80173	82865: contig of 2593 bp in length
82766	82865: gap of unknown length
82866	85497: contig of 2632 bp in length
85498	85597: gap of unknown length
85598	89600: contig of 4003 bp in length
89601	89701: gap of unknown length
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92960	93059: gap of unknown length
93060	97133: contig of 4074 bp in length
97134	97233: gap of unknown length
97234	100495: contig of 3262 bp in length
100496	100595: gap of unknown length
100596	104694: contig of 4099 bp in length
104695	104794: gap of unknown length
104795	108059: contig of 3265 bp in length

Query Match	72.2%;	Score 13;	DB 2;	Length 147352;
Best Local Similarity	92.3%;	Pred. No. 4.5e+02;		
Matches 12;	Conservative	1;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy	6	CCUGAGNNNNNN 18
Db	9365	CCTGAGNNNNNN 9377

RESULT 195	
LOCUS AC080177/c	
DEFINITION Homo sapiens chromosome 14, clone RP11-45F22 map 14, WORKING DRAFT	
ACCESSION AC080177.2	GI:11276227
VERSION AC080177.2	GI:11276227
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT	
SOURCE Homo sapiens (human)	
ORGANISM Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
1 (bases 1 to 147571)	
Homo sapiens chromosome 14, clone RP11-45F22	
Unpublished	
2 (bases 1 to 147571)	
Birtten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barrera, N., Baetsen, V., Beda, F., Boguslavsky, L., Bouhagaller, B., Brown, A., Burkett, G., Campoliano, A., Castle, A., Choquel, Y., Colangelo, M., Collins, S., Collimore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hago, B., Heatford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kam, L., Karacas, A., Lakoque, K., Lamasz, R., Landers, T., Lebeckzy, U., Levine, R., Liu, C., Liu, G., Macdonald, P., Marquis, N., McArthur, M., McEwan, P., McKernan, K., McSheeters, R., Meldrum, J., Menus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tittrell, A., Travers, M., Trigglio, J., Vassiliev, H., Veli, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.	
Direct Submission	
Submitted (28-SEP-2000) Whitehead Institute/MIT Center for Genome Research	

REFERENCE  
AUTHORS  
3 (bases 1 to 147571)  
Birtten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Barina, N., Baerlein, V., Beda, F., Boguslavsky, L.,  
Borkhater, B., Brown, A., Burdett, G., Campolano, A., Castle, A.,  
Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
DeRellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,  
FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,  
Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,  
Iliev, I., Johnson, R., Jones, C., Kam, L., Karacas, A., Lacroque, K.,  
Lamasares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G.,  
Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K.,  
McChester, R., Meldrim, J., Menus, L., Mhova, T., Mlenga, V.,  
Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,  
O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K.,  
Pierre, N., Pisanu, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,  
Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,  
Sougnas, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J.,  
Titrill, A., Travers, M., Trigilio, J., Vasilev, H., Viel, R., Vo, A.,  
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, D.,  
Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 22, 2000 this sequence version replaced gi:10334897.  
All repeats were identified using RepeatMasker:  
Smt, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WITBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L1152  
Center clone name: 45 F 22  
----- Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 121934 bases at least Q40  
Consensus quality: 133474 bases at least Q30  
Consensus quality: 139354 bases at least Q20  
Insert size: 173000; agarose-fp  
Insert size: 142971; sum-of-contigs  
Quality coverage: 2.5 in Q20 bases; agarose-fp  
Quality coverage: 3.0 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 47 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preseeded.  
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\* 1 230: contig of 230 bp in length  
\* 231 330: gap of 100 bp  
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\* 1103 2250: gap of 100 bp  
\* 2151 3132: contig of 882 bp in length  
\* 2251 3132: gap of 100 bp  
\* 3133 4327: contig of 1095 bp in length  
\* 3232 4427: gap of 100 bp  
\* 4328 5247: contig of 820 bp in length  
\* 4428 5347: gap of 100 bp  
\* 5248 6772: contig of 1425 bp in length  
\* 5348 6872: gap of 100 bp  
\* 6773 7730: contig of 858 bp in length  
\* 6873 7830: gap of 100 bp  
\* 7731 8960: contig of 1130 bp in length  
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\* 8961 9060: gap of 100 bp  
\* 9061 20307: contig of 11247 bp in length  
\* 20308 20408: gap of 100 bp  
\* 20408 21752: contig of 1344 bp in length  
\* 21752 21852: gap of 100 bp  
\* 21852 23280: contig of 1428 bp in length  
\* 23280 23380: gap of 100 bp  
\* 23380 24917: contig of 1537 bp in length  
\* 24917 25016: gap of 100 bp  
\* 25016 26637: contig of 1621 bp in length  
\* 26637 26737: gap of 100 bp  
\* 26737 28879: contig of 2142 bp in length  
\* 28879 28979: gap of 100 bp  
\* 28980 30532: contig of 1553 bp in length  
\* 30533 30632: gap of 100 bp  
\* 30633 31915: contig of 1283 bp in length  
\* 31916 32015: gap of 100 bp  
\* 32015 33952: contig of 1937 bp in length  
\* 33953 34052: gap of 100 bp  
\* 34053 36246: contig of 2194 bp in length  
\* 36247 36346: gap of 100 bp  
\* 36347 38033: contig of 1688 bp in length  
\* 38035 38134: gap of 100 bp  
\* 38135 39957: contig of 1823 bp in length  
\* 39958 40057: gap of 100 bp  
\* 40058 41308: contig of 1251 bp in length  
\* 41309 41409: gap of 100 bp  
\* 41409 43477: contig of 2069 bp in length  
\* 43478 43577: gap of 100 bp  
\* 43578 46524: contig of 2947 bp in length  
\* 46525 46624: gap of 100 bp  
\* 46625 50197: contig of 3573 bp in length  
\* 50198 50297: gap of 100 bp  
\* 50298 53324: contig of 2927 bp in length  
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\* 53325 55187: contig of 1863 bp in length  
\* 55188 55287: gap of 100 bp  
\* 55288 57329: contig of 2042 bp in length  
\* 57330 57429: gap of 100 bp  
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\* 59924 62602: contig of 2679 bp in length  
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\* 92199 95858: contig of 3660 bp in length  
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\* 104254 109134: contig of 4881 bp in length  
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\* 124566 134844: gap of 100 bp  
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* 134945 146657: contig of 11713 bp in length
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            1. 230
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Query Match 72.2%; Score 13; DB 2; Length 147571;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCGAGNNNNNN 18
Db 115367 CCTGAGNNNNNN 115355

RESULT 196
AC141654/c 149652 bp DNA linear HTG 24-MAR-2003
LOCUS Rattus norvegicus clone CH230-516H6, WORKING DRAFT SEQUENCE, 19
DEFINITION unorderd piece.
AC141654
AC141654.3 GI:29165560
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Rattus norvegicus (Norway rat).
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 149652)
Muzny,D,Marle,M, Metzker,M, Lee, A, Abramson, S, Adams, C, Alder, J,
Allen, C, Allen, H, Alsbrooks, S, Amin, A, Anguiano, D,
Anyalebechi, V, Aoyagi, A, Ayodeji, M, Baca, E, Baden, H,
Baldwin, D, Bandaranaike, D, Barber, M, Barnstead, M, Benham, F,
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Bryant, N, Buhay, C, Burch, P, Burrell, K, Calderon, E,
Cardenas, V, Carter, K, Cavazos, I, Caesar, H, Center, A,
Chacko, J, Chavez, D, Chen, G, Chen, R, Chen, Y, Chen, Z, Chu, J,
Cleveland, C, Cockrell, R, Cox, C, Coyle, M, Cree, A, D'Souza, L,
Davila, M, Davis, C, Davy-Carroll, L, De Anda, C, Dederich, D,
Delgado, O, Denson, S, Deramo, C, Ding, Y, Dinh, H, Diya, K,
Draper, H, Dugan-Rocha, S, Dunn, A, Durbin, K, Duval, B, Eaves, K,
Egan, A, Escotto, M, Eugene, C, Evans, C, A, Falls, T, Fan, G,
Fernandez, S, Finley, M, Flagg, N, Forbes, L, Foster, M, Foster, P,
Frazer, C, W, Gabisi, A, Ganta, R, Garcia, A, Garner, T, Garza, M,
Gebregiorgis, E, Geer, K, Gill, R, Grady, M, Guertel, W, Guevara, W,
Gunaratne, P, Haaland, W, Hamill, C, Hamilton, C, Hamilton, K,
Harvey, Y, Havlak, P, Hawes, A, Henderson, N, Hernandez, J,
Hernandez, R, Hines, S, Hladun, S, L, Hodgson, A, Hogue, M,
Hollins, B, Howells, S, Hulyk, S, Hume, J, Idlebird, D, Jackson, A,
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Maximney, S, McLeod, M, McNeill, T, Meenen, E, Milosavljevic, A,
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Newton, N, Nguyen, N, Norris, S, Nwaokeme, O, Okunolu, G,
Olanpunsagoo, A, Pal, S, Parks, K, Pasternak, S, Paul, H,
Perez, A, Perez, L, Pfannkuch, C, Plopper, F, Poindexter, A,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: KSHB
Center clone name: CH230-516H6
----- Summary Statistics -----
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 140432 bases at least Q40
Consensus quality: 143346 bases at least Q40
Consensus quality: 145310 bases at least Q30
Estimated insert size: 145510; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
----- NOTE: Estimated insert size may differ from sequence length -----
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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11705 14522: contig of 2818 bp in length
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17344 21026: contig of 3683 bp in length

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* 21027 21126: gap of unknown length
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* 113624 113723: gap of unknown length
* 113723 113724: gap of unknown length
* 113724 149652: contig of 35929 bp in length.
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/clone="CH230-516H6"

FEATURES
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1. 149652

ORIGIN
Query Match 72.2%; Score 13; DB 2; Length 149652;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 CCUGAGANNNNNN 18
||:|||||||
39168 CCTGAGANNNNNN 39156

RESULT 197
AC091792/c
LOCUS
DEFINITION
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Felis catus clone RP86-145H12, WORKING DRAFT SEQUENCE, 5 ordered
pieces.
AC091792
VERSION
AC091792.2 GI:21104895
KEYWORDS
HTG; HTGS PHASE2; HTGS_DRAFT.
SOURCE
Felis catus (cat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
1 (bases 1 to 150967)
Benjamin, B., Blakeley, R. W., Bouffard, G. G., Breen, K., Brinkley, C.,
Ahnter, N., Antonellis, A., Ayala, K., Beckstrom-Sternberg, S. M.,
Brooks, S., Dietrich, N. L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J. R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q. L., Maduro, V. B.,
Margulies, E. H., Masiello, C., Maekari, B., Mastrian, S. D.,
McCloskey, J. C., McDowell, J., Paquirigan, C., Pearson, R.,
Portnoy, M. E., Prasad, A., Schueler, M. G., Stantrop, S., Thomas, J. W.,
Thomas, P. J., Touchman, J. W., Taugen, C., Vogt, J. L., Walker, M. A.,
Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.,
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 150967)
Green, E. D.
REFERENCE
Direct Submission
Submitted (07-JUN-2001) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 150967)
Green, E. D.
REFERENCE
Direct Submission
Submitted (23-MAY-2002) NIH Intramural Sequencing Center, 8717

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COMMENT
Groveomont Circle, Gaithersburg, MD 20877, USA
On May 23, 2002 this sequence version replaced gi:14327785.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nih.gov
----- Project Information
Center project name: ctd
Center clone name: 145H12

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149914 bases at least Q40
Consensus quality: 150239 bases at least Q30
Consensus quality: 150421 bases at least Q20
Insert size: 130000; agarose-fp
Insert size: 150567; sum-of-contigs
Quality coverage: 13.36x in Q20 bases; agarose-fp
Quality coverage: 11.53x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
1 25568: contig of 25568 bp in length
* 25569 25668: gap of unknown length
* 25669 36116: contig of 10448 bp in length
* 36117 36216: gap of unknown length
* 36217 104093: contig of 67877 bp in length
* 104094 104193: gap of unknown length
* 104194 142495: contig of 38302 bp in length
* 142496 142595: gap of unknown length
* 142596 150967: contig of 8372 bp in length.
Location/Qualifiers
1. 150967
/organism="Felis catus"
/mol_type="genomic DNA"
/db_xref="taxon:9685"
/clone="RP86-145H12"
/clone_lib="RP86"
1. 34207
/notes="clone overlaps with GenBank Accession Number
AC098816 clone RP86-615J23 (center project name coy)"
1. 25568
/notes="assembly_fragment"
vector_end: spe
clone_end: spe
misc_feature
25669..36116
/notes="assembly_fragment"
36217..104093
/notes="assembly_fragment"
104194..142495
/notes="assembly_fragment"

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misc_feature      .112235. .150967
                  /note="clone overlaps with GenBank Accession Number
                  AC105458 clone RP86-283114 (center project name coz)"
misc_feature      142596. .150967
                  /note="assembly_fragment
                  clone_end:T7
                  vector_side:right"
ORIGIN
Query Match      72.2%; Score 13; DB 2; Length 150967;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy               6 CCUGAGGNNNNNN 18
Db              104200 CCTGGAGNNNNNN 104188

RESULT 198
AC150970/c
LOCUS
DEFINITION
  AC150970 152179 bp DNA linear HTG 04-SEP-2004
  Bos taurus clone CH240-312P22, WORKING DRAFT SEQUENCE, 16 unordered
  pieces.
ACCESSION
  AC150970
VERSION
  AC150970.2 GI:51491793
KEYWORDS
  HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE
  Bos taurus (cow)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
  Bovinae; Bos.
  1 (bases 1 to 152179)
  Muzny,D., Metzker,M., Adams,C., Agbai II,O., Allen,C.,
  Albrook,S., Archer,P., Arrondo,H., Bandaranaike,D., Bangura,L.,
  Beltran,R., Beraducci,A., Biswal,K., Blyth,P.,
  Bonham,H., Buhay,C., Burch,P., Cadore,I., Canada,A., Cardenas,V.,
  Carter,K., Cavazos,I., Chacko,J., Chahrouh,M., Chavez,D., Chen,A.,
  Chen,G., Chen,R., Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R.,
  Coyle,M., Cree,A., Curry,S., Dai,W., Davila,M.L., Davis,C.,
  Davy-Carroll,L., De Anda,C., Delgado,O., Denon,S., Detamo,C.,
  Ding,Y., Dinh,H., Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A.,
  Durbin,K., Dziuda,D., Egan,A., Escotte,M., Espinosa,V., Eugene,C.,
  Pa,M., Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
  Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T.,
  Gaskin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D.,
  Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeberlen,K.,
  Hall,B., Hamid,H., Hamilton,K., Harber,B., Harris,R., Haylak,P.,
  Hines,A., Hitchens,M., Hodgson,A., Hognes,M., Hollins,B.,
  Howell,L.T., Hulik,S., Hume,J., Imo,K., Jackson,A., Jackson,L.,
  Jacob,L., Jiang,H., Johnson,B., Johnson,R., Kalafus,K., Kelly,S.,
  Keys,T., Khan,Z., King,L., Kovar,C., Kowis,A., Kowis,C., Lara,F.,
  Leal,S., Lee,K., Lee,S., Legall,F.I., Lemon,S., Lewis,L., Li,B.,
  Li,Y., Li,Z., Linell,M., Liu,W., Liu,Y.-S., Liu,Y., Lyanage,D.,
  London,P., Lopez,J., Lorensunewa,L., Lozado,R., Luk,T., Madu,R.,
  Maheshwari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E.,
  McCelland,H., McPherson,J., Mercadao,C., Milosavljevic,A.,
  Minja,E., Morgan,M., Morris,S., Muradasa,M., Murray,D.,
  Nazareth,L., Ngo,D., Nguyen,N., Norwig-Bastaguh,E., Nott,A.,
  Nwackeleme,O., Obregon,M., Ochi-Okorie,C., Odeh,E., Okunnu,G.,
  Okunnu,K., Parker,D., Pasternak,S., Patel,B., Patel,V., Paul,H.,
  Perez,A., Perez,L., Petrosino,D., Pham,T., Primus,B., Pu,L.-D.,
  Puazo,M., Qin,X., Quinn,A., Quiroz,J., Rabata,D., Rachlin,E.,
  Reigh,R., Ren,Y., Reuter,M., Richards,S., Rives,C., Rodriguez,F.,
  Rojals,A., Ruiz,S.J., Sana,M., Sanders,W., Santibanez,J., Santos,R.,
  Savery,G., Scherer,S., Shen,H., Shen,Y., Sisson,I., Speed,A.,
  Sodergren,E., Song,X.-Z., Sorrelle,R., Svatek,A., Taylor,E.,
  Taylor,T., Thomas,N., Thorm,R., Thormon,R., Trejos,Z., Uemami,K.,
  Valero,C., Verdusco,D., Villaseca,D., Virk,D., Volkov,A.,
  Walron,L., Walker,B., Wang,Q., Wang,S., Warren,J., Wei,X.,
  Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R., Wu,J.,
  Yakub,S., Yan,K., Yau,Y., Yu,F., Zhang,J., Zhang,L., Zhang,Z.,
  Zhou,J., Weinstein,G. and Gibbs,R.

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TITLE
JOURNAL
REFERENCE
  2 (bases 1 to 152179)
AUTHORS
  Morley,K.C.
TITLE
  Direct Submission
JOURNAL
  Submitted (17-AUG-2004) Human Genome Sequencing Center, Department
  of Molecular and Human Genetics, Baylor College of Medicine, One
  Baylor Plaza, Houston, TX 77030, USA
  3 (bases 1 to 152179)
AUTHORS
  Morley,K.C.
TITLE
  Direct Submission
JOURNAL
  Submitted (04-SEP-2004) Human Genome Sequencing Center, Department
  of Molecular and Human Genetics, Baylor College of Medicine, One
  Baylor Plaza, Houston, TX 77030, USA
  On Aug 22, 2004 this sequence version replaced gi:51315474.
  ----- Genome Center
  Center: Baylor College of Medicine
  Center code: BCM
  Web site: http://www.hgsc.bcm.tmc.edu/
  Contact: hgsc-help.tmc.edu
  Project Information
  Center project name: FBGY
  Center clone name: CH240-312P22
  ----- Summary Statistics
  Sequencing vector: Plasmid
  Chemistry: Dye-terminator Big Dye: 100% of reads
  Assembly program: Phrap; version 0.990329
  Consensus quality: 152191 bases at least Q40
  Consensus quality: 155092 bases at least Q30
  Consensus quality: 158513 bases at least Q20
  Estimated insert size: 162494, sum-of-contigs estimation
  Estimated insert size: 165056, agarose-fp estimation
  Quality coverage: 3x in Q20 bases; agarose-fp estimation
  Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
  -----
  * NOTE: Estimated insert size may differ from sequence length
  * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
  * NOTE: This is a 'working draft' sequence. It currently
  * consists of 16 contigs. The true order of the pieces
  * is not known and their order in this sequence record is
  * arbitrary. Gaps between the contigs are represented as
  * runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved.
  1
  3933: contig of 3933 bp in length
  3934
  4033: gap of unknown length
  4034
  6212: contig of 2179 bp in length
  6213
  6312: gap of unknown length
  6313
  10782: contig of 4470 bp in length
  10783
  10882: gap of unknown length
  10883
  34456: contig of 23574 bp in length
  34457
  34556: gap of unknown length
  34557
  43491: contig of 8935 bp in length
  43492
  43591: gap of unknown length
  43592
  54663: contig of 11072 bp in length
  54664
  54763: gap of unknown length
  54764
  57816: contig of 3053 bp in length
  57817
  57916: gap of unknown length
  57917
  65126: contig of 7210 bp in length
  65127
  65226: gap of unknown length
  65227
  76143: contig of 10917 bp in length
  76144
  76243: gap of unknown length
  76244
  78896: contig of 2653 bp in length
  78897
  78996: gap of unknown length
  78997
  91136: contig of 12140 bp in length
  91137
  91236: gap of unknown length
  91237
  94157: contig of 2921 bp in length
  94158
  94257: gap of unknown length
  94258
  112511: contig of 18254 bp in length
  112512
  112611: gap of unknown length
  112612
  116634: contig of 4023 bp in length
  116635
  116734: gap of unknown length

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* 116735 132245: contig of 15511 bp in length
* 132246 132345: gap of unknown length
* 132346 152179: contig of 19834 bp in length.
      Location/Qualifiers
        source          1. 152179
                        /organism="Bos taurus"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9913"
                        /clone="CH240-312P2"

ORIGIN
Query Match      72.2% Score 13; DB 2; length 152179;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCUGAGAGNNNNNN 18
      |||:|||||
Db      6319 CCTGGAGNNNNNN 6307

RESULT 199
LOCUS      AC016082      152679 bp DNA linear HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-24B21, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC016082
VERSION     AC016082.2 GI:9129716
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 152679)
AUTHORS     Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE       Homo sapiens, clone RP11-24B21
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 152679)
AUTHORS     Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
            Baldwin, J., Barna, N., Becker, R., Boguski, L., Bouckgeater, B.,
            Brown, A., Casale, A., Cangelosi, M., Collins, S., Collymore, A.,
            Cooke, P., Dearrellano, K., Dewar, K., Domingo, M., Donelan, L., Doyle, M.,
            Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
            Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
            Howland, J. C., Johnson, R., Jones, C., Kann, L., Karas, A., Klein, J.,
            Lehouck, J., Liu, C., Locke, K., MacDonald, P., Margulis, N.,
            McMan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
            Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
            Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
            Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
            Teeffey, S., Tittell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
            Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
            Direct Submission
            Submitted (20-NOV-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            On Jul 13, 2000 this sequence version replaced gi:6456232.
            All repeats were identified using RepeatMasker:
            Smit, A.P.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIPR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            ----- Project Information
            Center project name: L4422
            Center clone name: 24_B_21
            -----
            * NOTE: This record contains 167 individual
            * contigs. Reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.

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* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 754: contig of 754 bp in length
755 854: gap of 100 bp
855 1623: contig of 769 bp in length
1624 1723: gap of 100 bp
1724 2489: contig of 766 bp in length
2490 2589: gap of 100 bp
2590 3332: contig of 743 bp in length
3333 3432: gap of 100 bp
3433 4180: contig of 748 bp in length
4181 4280: gap of 100 bp
4281 5054: contig of 774 bp in length
5055 5154: gap of 100 bp
5155 5951: contig of 797 bp in length
5952 6051: gap of 100 bp
6052 6831: contig of 780 bp in length
6832 6931: gap of 100 bp
6932 7712: contig of 781 bp in length
7713 7812: gap of 100 bp
7813 8599: contig of 787 bp in length
8600 8699: gap of 100 bp
8700 9380: contig of 681 bp in length
9381 9480: gap of 100 bp
9481 10256: contig of 776 bp in length
10257 10356: gap of 100 bp
10357 11133: contig of 777 bp in length
11134 11233: gap of 100 bp
11234 12024: contig of 791 bp in length
12025 12124: gap of 100 bp
12125 12915: contig of 791 bp in length
12916 13015: gap of 100 bp
13016 13779: contig of 764 bp in length
13780 13879: gap of 100 bp
13880 14639: contig of 760 bp in length
14640 14739: gap of 100 bp
14740 15520: contig of 781 bp in length
15521 15620: gap of 100 bp
15621 16395: contig of 775 bp in length
16396 16495: gap of 100 bp
16496 17257: contig of 762 bp in length
17258 17357: gap of 100 bp
17358 18121: contig of 764 bp in length
18122 18221: gap of 100 bp
18222 19003: contig of 782 bp in length
19004 19103: gap of 100 bp
19104 19888: contig of 785 bp in length
19889 19988: gap of 100 bp
19989 20749: contig of 761 bp in length
20750 20849: gap of 100 bp
20850 21623: contig of 774 bp in length
21624 21723: gap of 100 bp
21724 22515: contig of 793 bp in length
22516 22616: gap of 100 bp
22617 23398: contig of 782 bp in length
23399 23498: gap of 100 bp
23499 24280: contig of 782 bp in length
24281 24380: gap of 100 bp
24381 25163: contig of 783 bp in length
25164 25263: gap of 100 bp
25264 26052: contig of 789 bp in length
26053 26152: gap of 100 bp
26153 26924: contig of 772 bp in length
26925 27024: gap of 100 bp
27025 27812: contig of 788 bp in length
27813 27912: gap of 100 bp
27913 28710: contig of 798 bp in length
28711 28810: gap of 100 bp
28811 29579: contig of 769 bp in length
29580 29679: gap of 100 bp
29680 30459: contig of 780 bp in length

```

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* 30460 30559: gap of 100 bp
* 30560 31344: contig of 785 bp in length
* 31345 31444: gap of 100 bp
* 31445 32236: contig of 792 bp in length
* 32237 32336: gap of 100 bp
* 32337 33086: contig of 750 bp in length
* 33087 33186: gap of 100 bp
* 33187 33981: contig of 795 bp in length
* 33982 34081: gap of 100 bp
* 34082 34857: contig of 776 bp in length
* 34858 34957: gap of 100 bp
* 34958 35739: contig of 782 bp in length
* 35740 35839: gap of 100 bp
* 35840 36617: contig of 778 bp in length
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* 36718 37494: contig of 777 bp in length
* 37495 37594: gap of 100 bp
* 37595 38331: contig of 737 bp in length
* 38332 38431: gap of 100 bp
* 38432 39189: contig of 758 bp in length
* 39190 39289: gap of 100 bp
* 39290 40053: contig of 764 bp in length
* 40054 40153: gap of 100 bp
* 40154 40939: contig of 786 bp in length
* 40940 41039: gap of 100 bp
* 41040 41813: contig of 774 bp in length
* 41814 41913: gap of 100 bp
* 41914 42698: contig of 785 bp in length
* 42699 42798: gap of 100 bp
* 42799 43669: contig of 771 bp in length
* 43670 44455: contig of 786 bp in length
* 44456 44556: gap of 100 bp
* 44557 45340: contig of 785 bp in length
* 45341 45440: gap of 100 bp
* 45441 46232: contig of 792 bp in length
* 46233 46332: gap of 100 bp
* 46333 47100: contig of 768 bp in length
* 47101 47200: gap of 100 bp
* 47201 47948: contig of 748 bp in length
* 47949 48048: gap of 100 bp
* 48049 48810: contig of 762 bp in length
* 48811 48910: gap of 100 bp
* 48911 49672: contig of 762 bp in length
* 49673 49772: gap of 100 bp
* 49773 50558: contig of 786 bp in length
* 50559 50659: gap of 100 bp
* 50660 51425: contig of 766 bp in length
* 51426 51524: gap of 100 bp
* 51525 52300: contig of 776 bp in length
* 52301 52400: gap of 100 bp
* 52401 53170: contig of 770 bp in length
* 53171 53270: gap of 100 bp
* 53271 54055: contig of 785 bp in length
* 54056 54155: gap of 100 bp
* 54156 54937: contig of 782 bp in length
* 54938 55037: gap of 100 bp
* 55038 55802: contig of 765 bp in length
* 55803 55902: gap of 100 bp
* 55903 56664: contig of 762 bp in length
* 56665 56764: gap of 100 bp
* 56765 57537: contig of 773 bp in length
* 57538 57637: gap of 100 bp
* 57638 58396: contig of 759 bp in length
* 58397 58496: gap of 100 bp
* 58497 59279: contig of 783 bp in length
* 59280 59379: gap of 100 bp
* 59380 60177: contig of 798 bp in length
* 60178 60277: gap of 100 bp
* 60278 61065: contig of 788 bp in length
* 61066 61165: gap of 100 bp
* 61166 61948: contig of 783 bp in length
* 61949 62048: gap of 100 bp

```

```

Query Match      72.2%  Score 13; DB 2; Length 152679;
Best Local Similarity 92.3%  Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCUGAGANNNNNN 18
Db      79853 CCTGAGANNNNNN 79865

RESULT 200
AC150792
LOCUS      153541 bp      DNA      linear      HTG 14-SRP-2004
DEFINITION Bos taurus clone CH240-397115, WORKING DRAFT SEQUENCE, 3 ordered
            pieces.
ACCESSION  AC150792.3  GI:52000546
VERSION     AC150792
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1 (bases 1 to 153541)
AUTHORS     Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,
            Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,
            Beraducci,A., Biswal,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,
            Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I.,
            Chacko,J., Chahrouh,M., Chavez,D., Chen,A., Chen,G., Chen,R.,
            Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Crean,R.,
            Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De
            Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H.,
            Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Durbin,K.,
            Dziuda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M.,
            Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
            Fowler,G., Fu,Q., Fun,E., Garcia,A., Garcia,R., Garner,T.,
            Gaskin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D.,
            Gonzalez-Garay,M., Guevara,W., Holder,M., Haland,W., Haeberlen,K.,
            Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Havlak,P.,
            Hawes,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J.,
            Hines,S., Hitchens,M., Hodgson,A., Hogue,M., Hollins,B.,
            Howell,L.T., Huylk,S., Hume,J., Iino,K., Jackson,A., Jackson,L.,
            Jacob,D., Jiang,H., Johnson,B., Johnson,R., Kalatus,K., Kelly,S.,
            Keys,T., Khan,Z., King,L., Kovar,C., Kowals,A., Kowals,C., Lara,F.,
            Leal,S., Lee,K., Lee,S., Legall,F.I., Lemon,S., Lewis,L., Li,B.,
            Li,Y., Li,Z., Linnell,M., Liu,W., Liu,Y.-S., Liu,Y., Liyanage,D.,
            London,P., Lopez,J., Lorenshewa,L., Lozano,R., Luk,T., Madu,R.,
            Maheshwari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E.,
            McClelland,H., McPherson,J., Mercadeo,C., Metzger,M.,
            Milosavljevic,A., Minja,E., Morgan,M., Morris,S., Mundasa,M.,
            Murray,D., Nazareth,L., Ngo,D., Nguyen,N., Norwig-Eastach,E.,
            Nott,A., Nwaokemelehen,O., Obregon,M., Ochi-Okorie,C., Odeh,E.,
            Okunolu,G., Okunolu,K., Parker,D., Pasternak,S., Patel,B.,
            Patel,V., Paul,H., Perez,A., Perez,L., Petrosino,J., Pham,T.,
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            Zhang,Z., Zhou,J., Weinstein,G. and Gibbs,R.
            Direct Submission
TITLE       Unpublished
JOURNAL     2 (bases 1 to 153541)
REFERENCE   Worley,K.C.
AUTHORS     Direct Submission
TITLE       Direct Submission

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## JOURNAL

## REFERENCE

Submitted (10-AUG-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 153541)  
Worley, K.C.

## JOURNAL

## COMMENT

Submitted (14-SEP-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Sep 14, 2004 this sequence version replaced gi:51172638.

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help.tmc.edu

Project Information

Center project name: FBXK

Center clone name: CH240-397L15

Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 163292 bases at least Q40

Consensus quality: 163699 bases at least Q30

Estimated insert size: 164140 bases at least Q20

Quality coverage: 15x in Q20 bases; sum-of-contigs estimation

\*\*\*\*\*  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* The sequence data in this record represents an 'enhanced' version  
\* of a Phase 2 submission. The indicated order and orientation of  
\* each sequence has been established using one or more of the  
\* following: read-pair data from individual subclones, overlaps  
\* with neighboring clones, alignment with available reference  
\* sequence (e.g., human), and/or confirmation by PCR testing.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 81569: contig of 81569 bp in length  
\* 81570 81619: gap of 50 bp  
\* 81620 132377: contig of 50758 bp in length  
\* 132378 132577: gap of 200 bp  
\* 132578 153541: contig of 20964 bp in length.  
Location/Qualifiers  
1. 153541

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Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18

DB 132371 CCTGAGNNNNNN 132383

Search completed: April 25, 2005, 13:38:08  
Job time : 824.211 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:42 ; Search time 206.053 Seconds  
(without alignments)  
517.127 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18

Sequence: 1 GCGGUCGUGAGNNNNNN 18

Scoring table: OLIGO\_NUC

Searched: 4390206 seqs, 2959870667 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: N\_Geneseq\_16Dec04.\*

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13: geneeqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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7	14	77.8	503	13	ADQ5353
8	13	72.2	418	5	AAS76001
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29	12	66.7	16	8	ABX74358	ABX74358 Hepatitis
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C 236	12	66.7	25	2	AAQ65050	AAq65050 Antisense
C 237	12	66.7	25	2	AAQ65105	AAq65105 Antisense
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C 239	12	66.7	25	2	AAQ65042	AAq65042 Antisense



240	12	66.7	25	2	AA065069	Aag65069	Antisense	313	12	66.7	30	2	AA065097	Aag65097	Antisense
241	12	66.7	25	2	AA065080	Aag65080	Antisense	314	12	66.7	30	2	AA065085	Aag65085	Antisense
242	12	66.7	25	2	AA065059	Aag65059	Antisense	315	12	66.7	30	2	AAT64889	Aat64889	Hepatitis
243	12	66.7	25	2	AA065092	Aag65092	Antisense	316	12	66.7	30	6	ABN80437	ABN80437	Oligonuci
244	12	66.7	25	9	ACI87049	ACI87049	Human mic	317	12	66.7	32	6	AAK96674	AAK96674	Synthetic
245	12	66.7	26	2	AA065043	Aag65043	Antisense	318	12	66.7	39	2	AAV00354	AAV00354	Bacillus
246	12	66.7	26	2	AA065070	Aag65070	Antisense	319	12	66.7	39	5	AAF73272	AAF73272	Oligonuci
247	12	66.7	26	2	AA065093	Aag65093	Antisense	320	12	66.7	39	10	ADD41449	ADD41449	Hepatitis
248	12	66.7	26	2	AA065036	Aag65036	Antisense	321	12	66.7	42	2	AAT92127	AAT92127	Template
249	12	66.7	26	2	AA065151	Aag65151	Antisense	322	12	66.7	42	2	AAT92132	AAT92132	Product o
250	12	66.7	26	2	AA065051	Aag65051	Antisense	323	12	66.7	45	12	ADK70812	ADK70812	5' mRNA D
251	12	66.7	26	2	AA065060	Aag65060	Antisense	324	12	66.7	47	3	AAZ68250	AAZ68250	Human map
252	12	66.7	26	2	AA065081	Aag65081	Antisense	325	12	66.7	48	2	AAZ23541	AAZ23541	HCV DNA f
253	12	66.7	26	2	AA065106	Aag65106	Antisense	326	12	66.7	48	2	AAZ23542	AAZ23542	Human DNA
254	12	66.7	26	2	AA065120	Aag65120	Antisense	327	12	66.7	48	11	ADU54923	ADU54923	Human iRX
255	12	66.7	26	2	AA065030	Aag65030	Antisense	328	12	66.7	50	4	AAK92382	AAK92382	Oligonuci
256	12	66.7	26	2	AA065135	Aag65135	Antisense	329	12	66.7	51	4	AAL32522	AAL32522	Human SNP
257	12	66.7	26	2	AA070178	AaQ70178	Hepatitis	330	12	66.7	51	4	AAL32875	AAL32875	Human SNP
258	12	66.7	26	6	AAK96673	AaK96673	Synthetic	331	12	66.7	52	2	AAT92125	AAT92125	Template
259	12	66.7	27	2	AA065071	Aag65071	Antisense	332	12	66.7	52	2	AAT92128	AAT92128	Product o
260	12	66.7	27	2	AA065044	Aag65044	Antisense	333	12	66.7	57	6	ACN25672	ACN25672	KNV Amber
261	12	66.7	27	2	AA065052	Aag65052	Antisense	334	12	66.7	70	2	AAT11268	AAT11268	Hepatitis
262	12	66.7	27	2	AA065037	Aag65037	Antisense	335	12	66.7	86	12	ADJ53747	ADJ53747	HBV specti
263	12	66.7	27	2	AA065061	Aag65061	Antisense	336	12	66.7	97	12	ACH81857	ACH81857	Human gen
264	12	66.7	27	2	AA065082	Aag65082	Antisense	337	12	66.7	124	12	ACH80864	ACH80864	Human gen
265	12	66.7	27	2	AA065121	Aag65121	Antisense	338	12	66.7	127	6	ABX03545	ABX03545	Hepatitis
266	12	66.7	27	2	AA065152	Aag65152	Antisense	339	12	66.7	138	2	AAT11267	AAT11267	Hepatitis
267	12	66.7	27	2	AA065107	Aag65107	Antisense	340	12	66.7	138	12	ACH82339	ACH82339	Human gen
268	12	66.7	27	2	AA065026	Aag65026	Antisense	341	12	66.7	140	2	AAT11269	AAT11269	Hepatitis
269	12	66.7	27	2	AA065031	Aag65031	Antisense	342	12	66.7	155	3	AAZ57775	AAZ57775	Hepatitis
270	12	66.7	27	2	AA065136	Aag65136	Antisense	343	12	66.7	159	2	AA043069	AA043069	-255 to -
271	12	66.7	27	2	AA065094	Aag65094	Antisense	344	12	66.7	159	2	AA043071	AA043071	-255 to -
272	12	66.7	27	6	ABX03516	ABX03516	Hepatitis	345	12	66.7	177	2	AAQ79456	AAQ79456	HCV isoLa
273	12	66.7	27	6	AAD43828	Ad43828	Adapter o	346	12	66.7	177	2	AAQ68067	AAQ68067	HCV isoLa
274	12	66.7	28	2	AA065045	Aag65045	Antisense	347	12	66.7	177	2	AAQ79459	AAQ79459	HCV isoLa
275	12	66.7	28	2	AA065053	Aag65053	Antisense	348	12	66.7	177	2	AAQ68068	AAQ68068	HCV isoLa
276	12	66.7	28	2	AA065032	Aag65032	Antisense	349	12	66.7	177	2	AAQ79454	AAQ79454	HCV isoLa
277	12	66.7	28	2	AA065095	Aag65095	Antisense	350	12	66.7	177	2	AAQ68069	AAQ68069	HCV isoLa
278	12	66.7	28	2	AA065122	Aag65122	Antisense	351	12	66.7	177	2	AAQ79457	AAQ79457	HCV isoLa
279	12	66.7	28	2	AA065137	Aag65137	Antisense	352	12	66.7	177	2	AAQ68063	AAQ68063	HCV isoLa
280	12	66.7	28	2	AA065108	Aag65108	Antisense	353	12	66.7	177	2	AAQ79460	AAQ79460	HCV isoLa
281	12	66.7	28	2	AA065153	Aag65153	Antisense	354	12	66.7	177	2	AAQ79455	AAQ79455	HCV isoLa
282	12	66.7	28	2	AA065072	Aag65072	Antisense	355	12	66.7	177	2	AAQ68066	AAQ68066	HCV isoLa
283	12	66.7	28	2	AA065027	Aag65027	Antisense	356	12	66.7	177	2	AAQ79448	AAQ79448	HCV isoLa
284	12	66.7	28	2	AA065038	Aag65038	Antisense	357	12	66.7	177	2	AAQ79458	AAQ79458	HCV isoLa
285	12	66.7	28	2	AA065083	Aag65083	Antisense	358	12	66.7	178	2	AAQ68064	AAQ68064	HCV isoLa
286	12	66.7	28	6	AAK96672	AaK96672	Synthetic	359	12	66.7	180	2	AAQ31083	AAQ31083	HCV-1 gen
287	12	66.7	29	2	AA065109	Aag65109	Antisense	360	12	66.7	180	2	AAQ31082	AAQ31082	HCV-1 gen
288	12	66.7	29	2	AA065046	Aag65046	Antisense	361	12	66.7	184	2	AAQ43061	AAQ43061	-255 to -
289	12	66.7	29	2	AA065096	Aag65096	Antisense	362	12	66.7	184	2	AAQ43068	AAQ43068	-255 to -
290	12	66.7	29	2	AA065033	Aag65033	Antisense	363	12	66.7	184	2	AAQ43067	AAQ43067	-255 to -
291	12	66.7	29	2	AA065138	Aag65138	Antisense	364	12	66.7	187	2	AAQ43059	AAQ43059	-255 to -
292	12	66.7	29	2	AA065123	Aag65123	Antisense	365	12	66.7	190	12	ACH89341	ACH89341	Human gen
293	12	66.7	29	2	AA065073	Aag65073	Antisense	366	12	66.7	194	2	AAQ43073	AAQ43073	-255 to -
294	12	66.7	29	2	AA065054	Aag65054	Antisense	367	12	66.7	194	2	AAQ43074	AAQ43074	-255 to -
295	12	66.7	29	2	AA065154	Aag65154	Antisense	368	12	66.7	194	2	AAQ43072	AAQ43072	-255 to -
296	12	66.7	29	2	AA065063	Aag65063	Antisense	369	12	66.7	194	2	AAQ43070	AAQ43070	-255 to -
297	12	66.7	29	2	AA065028	Aag65028	Antisense	370	12	66.7	194	2	AAQ43075	AAQ43075	-255 to -
298	12	66.7	29	2	AA065084	Aag65084	Antisense	371	12	66.7	201	13	ADS40150	ADS40150	Human aut
299	12	66.7	29	2	AA065039	Aag65039	Antisense	372	12	66.7	202	2	AAQ14084	AAQ14084	HCV-I (1-
300	12	66.7	29	2	AA065075	Aag65075	HCV conse	373	12	66.7	202	2	AAQ14083	AAQ14083	HCV-T (1-
301	12	66.7	30	2	AA065047	Aag65047	Antisense	374	12	66.7	209	8	ADA93664	ADA93664	Competito
302	12	66.7	30	2	AA065124	Aag65124	Antisense	375	12	66.7	217	12	ACH83248	ACH83248	Human gen
303	12	66.7	30	2	AA065040	Aag65040	Antisense	376	12	66.7	221	3	AAK25474	AAK25474	Human sec
304	12	66.7	30	2	AA065155	Aag65155	Antisense	377	12	66.7	226	2	AAT24352	AAT24352	Human gen
305	12	66.7	30	2	AA065034	Aag65034	Antisense	378	12	66.7	226	12	ADO05658	ADO05658	HCV templ
306	12	66.7	30	2	AA065110	Aag65110	Antisense	379	12	66.7	230	12	ADO05662	ADO05662	PCR ampli
307	12	66.7	30	2	AA065139	Aag65139	Antisense	380	12	66.7	230	12	ADO05661	ADO05661	PCR ampli
308	12	66.7	30	2	AA065029	Aag65029	Antisense	381	12	66.7	230	12	ACH88756	ACH88756	Human gen
309	12	66.7	30	2	AA065064	Aag65064	Antisense	382	12	66.7	232	12	AAV70460	AAV70460	Partial s
310	12	66.7	30	2	AA065074	Aag65074	Antisense	383	12	66.7	232	6	ABL46070	ABL46070	Hepatitis
311	12	66.7	30	2	AA065055	Aag65055	Antisense	384	12	66.7	232	12	ADK82260	ADK82260	Hepatitis
312	12	66.7	30	2	AA065055	Aag65055	Antisense	385	12	66.7	232	12	ADK82260	ADK82260	Hepatitis

C 386	12	66.7	239	2	AAV70459	AAV70459 Partial s	459	12	66.7	297	4	ABA68279	ABA68279 Human fce
C 387	12	66.7	239	2	AAV70455	AAV70455 Partial s	460	12	66.7	297	4	AAI48494	AAI48494 Probe #17
C 388	12	66.7	239	6	ABL46065	ABL46065 Hepatitis	461	12	66.7	297	4	AAK42417	AAK42417 Human bon
C 389	12	66.7	239	6	ABL46069	ABL46069 Hepatitis	462	12	66.7	297	4	AAK16653	AAK16653 Human bra
C 390	12	66.7	239	12	ADK82255	ADK82255 Hepatitis	463	12	66.7	297	4	ABE42024	ABE42024 Human 1lv
C 391	12	66.7	239	12	ADK82259	ADK82259 Hepatitis	464	12	66.7	297	6	ABE16471	ABE16471 Human gen
C 392	12	66.7	240	2	AAV70461	AAV70461 Partial s	465	12	66.7	299	8	ABX55952	ABX55952 Bovine ES
C 393	12	66.7	240	2	AAV70461	AAV70461 Partial s	466	12	66.7	299	10	AAD55565	AAD55565 IG57272 H
C 394	12	66.7	240	6	ABL46066	ABL46066 Hepatitis	467	12	66.7	300	2	AAI21438	AAI21438 Human gen
C 395	12	66.7	240	6	ABL46071	ABL46071 Hepatitis	468	12	66.7	300	3	AAZ49261	AAZ49261 Human hyd
C 396	12	66.7	240	12	ADK82261	ADK82261 Hepatitis	469	12	66.7	305	2	AAZ97088	AAZ97088 HCV ampli
C 397	12	66.7	240	12	ADK82256	ADK82256 Hepatitis	470	12	66.7	305	6	ABN79969	ABN79969 Hepatitis
C 398	12	66.7	241	6	AAAD3290	AAAD3290 HCV targe	471	12	66.7	305	6	ABN79970	ABN79970 Hepatitis
C 399	12	66.7	242	2	AAQ37742	AAQ37742 HCV ampli	472	12	66.7	306	2	AAQ67079	AAQ67079 Hepatitis
C 400	12	66.7	242	2	AAV70454	AAV70454 Partial s	473	12	66.7	306	6	ABE53053	ABE53053 Hepatitis
C 401	12	66.7	244	2	AAV70449	AAV70449 HCV subty	474	12	66.7	308	3	AAA75294	AAA75294 Novel hep
C 402	12	66.7	244	2	AAV70452	AAV70452 HCV subty	475	12	66.7	308	12	ADN35973	ADN35973 HCV cDNA
C 403	12	66.7	244	6	ABL46052	ABL46052 Hepatitis	476	12	66.7	309	3	ACI11778	ACI11778 Human sec
C 404	12	66.7	244	6	ABL46059	ABL46059 Hepatitis	477	12	66.7	312	3	AAZ36198	AAZ36198 Adapted H
C 405	12	66.7	244	6	ABL46059	ABL46059 Hepatitis	478	12	66.7	314	3	AAZ36197	AAZ36197 Adapted H
C 406	12	66.7	244	6	ABL46064	ABL46064 Hepatitis	479	12	66.7	319	2	AAZ40689	AAZ40689 Human sec
C 407	12	66.7	244	12	ADK82254	ADK82254 Hepatitis	480	12	66.7	321	4	ABL13141	ABL13141 Drosophi1
C 408	12	66.7	244	12	ADK82351	ADK82351 Hepatitis	481	12	66.7	326	6	ABK70880	ABK70880 HCV genom
C 409	12	66.7	244	12	ADK82347	ADK82347 Hepatitis	482	12	66.7	326	12	ADP20410	ADP20410 Hepatitis
C 410	12	66.7	244	12	ADK82232	ADK82232 Hepatitis	483	12	66.7	327	3	AAZ36199	AAZ36199 Adapted H
C 411	12	66.7	244	12	ADK82350	ADK82350 Hepatitis	484	12	66.7	327	6	ABK70884	ABK70884 HCV genom
C 412	12	66.7	244	12	ADK82249	ADK82249 Hepatitis	485	12	66.7	328	2	AAZ77074	AAZ77074 Hepatitis
C 413	12	66.7	244	12	ADK82249	ADK82249 Hepatitis	486	12	66.7	328	6	ABL46275	ABL46275 Hepatitis
C 414	12	66.7	252	2	AAQ31071	AAQ31071 HCV-1 gen	487	12	66.7	328	6	ABL46273	ABL46273 Hepatitis
C 415	12	66.7	252	2	AAQ31069	AAQ31069 HCV-1 gen	488	12	66.7	328	8	AAZ53724	AAZ53724 Hepatitis
C 416	12	66.7	252	2	AAQ31070	AAQ31070 HCV-1 gen	489	12	66.7	328	8	AAZ49655	AAZ49655 Human int
C 417	12	66.7	252	2	AAQ31068	AAQ31068 HCV-1 gen	490	12	66.7	333	6	ABK70873	ABK70873 HCV genom
C 418	12	66.7	252	2	AAQ31081	AAQ31081 HCV-1 gen	491	12	66.7	333	2	AAQ98272	AAQ98272 Hepatitis
C 419	12	66.7	252	2	AAQ31067	AAQ31067 HCV-1 gen	492	12	66.7	337	2	AAZ76668	AAZ76668 HCV1.1 tr
C 420	12	66.7	252	2	AAQ31072	AAQ31072 HCV-1 gen	493	12	66.7	337	6	AAV53895	AAV53895 HCV1.1 RN
C 421	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	494	12	66.7	338	3	AAZ52863	AAZ52863 FEN-1 re1
C 422	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	495	12	66.7	339	3	AAZ52863	AAZ52863 Tagged se
C 423	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	496	12	66.7	341	2	AAZ52863	AAZ52863 Human sec
C 424	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	497	12	66.7	341	2	AAZ52863	AAZ52863 5' untran
C 425	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	498	12	66.7	341	2	AAZ52863	AAZ52863 Hepatitis
C 426	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	499	12	66.7	341	2	AAZ52863	AAZ52863 5' untran
C 427	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	500	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 428	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	501	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 429	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	502	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 430	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	503	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 431	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	504	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 432	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	505	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 433	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	506	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 434	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	507	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 435	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	508	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 436	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	509	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 437	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	510	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 438	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	511	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 439	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	512	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 440	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	513	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 441	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	514	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 442	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	515	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 443	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	516	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 444	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	517	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 445	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	518	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 446	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	519	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 447	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	520	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 448	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	521	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 449	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	522	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 450	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	523	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 451	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	524	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 452	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	525	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 453	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	526	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 454	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	527	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 455	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	528	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 456	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	529	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 457	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	530	12	66.7	341	2	AAZ52863	AAZ52863 Infection
C 458	12	66.7	256	2	AAQ32981	AAQ32981 HCV BI 5'	531	12	66.7	341	2	AAZ52863	AAZ52863 Infection

C 532	12	66.7	373	13	ADQ52891	Adq52891 Novel can	605	12	66.7	480	10	AD857360	Ad857360 Toxicity-
C 533	12	66.7	374	12	ADK11630	Adk11630 Breast ca	606	12	66.7	480	10	AD104970	Ad104970 Rat odora
C 534	12	66.7	375	12	ADQ04032	Adq04032 Hepatitis	607	12	66.7	480	2	AAQ32446	Aaq32446 HCV core-
C 535	12	66.7	378	10	ADK66080	Adk66080 Standardl	608	12	66.7	483	2	AAQ32445	Aaq32445 HCV core-
C 536	12	66.7	381	4	AAH71906	Aah71906 Human cer	609	12	66.7	483	2	AAQ32453	Aaq32453 HCV core-
C 537	12	66.7	383	6	AAK15309	Aak15309 Hepatitis	610	12	66.7	483	2	AAQ32447	Aaq32447 HCV core-
C 538	12	66.7	384	4	AA504594	AA504594 Gene expr	611	12	66.7	483	2	AAQ32444	Aaq32444 HCV core-
C 539	12	66.7	384	6	ABK15314	Abk15314 Hepatitis	612	12	66.7	484	4	AAK73138	Aak73138 Human imm
C 540	12	66.7	386	2	AAT29117	Aat29117 Hepatitis	613	12	66.7	484	4	AAK80321	Aak80321 Human imm
C 541	12	66.7	386	5	ABV11141	Abv11141 Human pro	614	12	66.7	485	6	AAK63937	Aak63937 CDNA enco
C 542	12	66.7	386	9	ADB116263	Adb116263 Cleavage	615	12	66.7	490	4	AA530914	AA530914 Human CDN
C 543	12	66.7	387	4	AAH69940	Aah69940 Human cer	616	12	66.7	492	6	ABL89981	AbL89981 Human pol
C 544	12	66.7	390	4	AA532240	Aa532240 Mouse uri	617	12	66.7	494	5	AA571629	Aa571629 DNA enco
C 545	12	66.7	391	5	AA566301	Aa566301 Novel hum	618	12	66.7	498	4	AA186991	AA186991 Human pol
C 546	12	66.7	391	6	ABQ72616	Abq72616 Human MD	619	12	66.7	500	13	AD534658	Ad534658 Hepatitis
C 547	12	66.7	393	6	ABA96260	Aba96260 Hepatitis	620	12	66.7	500	13	AD534660	Ad534660 Hepatitis
C 548	12	66.7	394	2	AAQ61266	Aaq61266 Human bra	621	12	66.7	500	13	AD534661	Ad534661 Hepatitis
C 549	12	66.7	394	5	ABV11103	Abv11103 Human pro	622	12	66.7	502	12	AD534659	Ad534659 Hepatitis
C 550	12	66.7	394	6	ABL83200	AbL83200 Human ova	623	12	66.7	502	12	ACH75615	Ach75615 Human gen
C 551	12	66.7	395	4	AA559135	AA559135 Human can	624	12	66.7	504	2	AAQ12239	AaQ12239 Clone 164
C 552	12	66.7	397	5	ABV01972	Abv01972 Human pro	625	12	66.7	506	12	ACH75056	Ach75056 Human gen
C 553	12	66.7	398	5	ABV01934	Abv01934 Human pro	626	12	66.7	508	4	AA117280	AA117280 Probe #72
C 554	12	66.7	401	3	AA665960	Aa665960 Human lun	627	12	66.7	508	4	ABA62087	AbA62087 Human foe
C 555	12	66.7	401	6	ABL49179	AbL49179 Human lun	628	12	66.7	508	4	AA142030	AA142030 Probe #10
C 556	12	66.7	401	6	ABO92365	AbO92365 Human lun	629	12	66.7	508	4	ABA29528	AbA29528 Probe #79
C 557	12	66.7	401	6	ABO92365	AbO92365 Human lun	630	12	66.7	508	4	AAK36307	Aak36307 Human bon
C 558	12	66.7	401	10	ADA28354	Ada28354 Human lun	631	12	66.7	508	4	AAK10404	Aak10404 Human bra
C 559	12	66.7	401	12	ADH36918	Adh36918 Human lun	632	12	66.7	508	4	AB535986	Ab535986 Human liv
C 560	12	66.7	403	5	AA565763	Aa565763 DNA enco	633	12	66.7	508	6	AB510382	Ab510382 Human gen
C 561	12	66.7	404	5	ABL82185	AbL82185 Human ova	634	12	66.7	510	4	AAK84409	AaK84409 Human imm
C 562	12	66.7	408	10	ADC32161	AdC32161 Human nov	635	12	66.7	510	4	AAK84410	AaK84410 Human imm
C 563	12	66.7	408	4	AAH70703	Aah70703 Human cer	636	12	66.7	510	12	ACH73904	Ach73904 Human gen
C 564	12	66.7	409	3	AACT4799	Aac74799 Human ORF	637	12	66.7	513	12	ACH67159	Ach67159 Human gen
C 565	12	66.7	410	5	ADL40350	AdL40350 Human ova	638	12	66.7	519	12	ADL81839	AdL81839 Human lun
C 566	12	66.7	411	5	ACH29499	Ach29499 Human adu	639	12	66.7	530	12	ADP72173	AdP72173 Renal tox
C 567	12	66.7	412	6	ABA96259	Aba96259 Hepatitis	640	12	66.7	532	12	ACH69548	Ach69548 Human gen
C 568	12	66.7	416	5	AA580250	AA580250 DNA enco	641	12	66.7	533	13	ADQ51434	AdQ51434 Novel can
C 569	12	66.7	418	6	ABX35423	Abx35423 Bovine ES	642	12	66.7	535	5	ABV39222	Abv39222 Human pro
C 570	12	66.7	420	12	ADQ80848	AdQ80848 Hepatitis	643	12	66.7	544	13	ADQ78538	AdQ78538 Novel can
C 571	12	66.7	422	8	ACC79264	Acc79264 Hepatitis	644	12	66.7	544	13	AAQ79776	AaQ79776 Hepatitis
C 572	12	66.7	428	5	AA591871	AA591871 DNA enco	645	12	66.7	556	2	AAK00458	AaK00458 Hepatitis
C 573	12	66.7	431	5	ABV32287	Abv32287 Human pro	646	12	66.7	556	2	AAK26743	AaK26743 Sequence
C 574	12	66.7	433	5	ABV07225	Abv07225 Human pro	647	12	66.7	556	2	ADF66079	AdF66079 Hepatitis
C 575	12	66.7	434	7	ADS72443	AdS72443 Human kid	648	12	66.7	556	4	AA332731	Aa332731 Human bec
C 576	12	66.7	440	5	ABV32249	Abv32249 Human pro	649	12	66.7	557	12	ACH73429	Ach73429 Human gen
C 577	12	66.7	440	5	ABV41180	Abv41180 Human pro	650	12	66.7	559	12	ACH68699	Ach68699 Human gen
C 578	12	66.7	440	5	ABV41218	Abv41218 Human pro	651	12	66.7	560	2	AAZ07662	AaZ07662 HCV J1 co
C 579	12	66.7	446	9	ACH41449	Ach41449 Human foe	652	12	66.7	562	4	AAH11923	AaH11923 Human CDN
C 580	12	66.7	447	8	AB236902	Ab236902 Human GEN	653	12	66.7	562	12	ACH68155	Ach68155 Human gen
C 581	12	66.7	452	2	AAV86924	AAv86924 EST clone	654	12	66.7	566	13	ADQ53929	AdQ53929 Novel can
C 582	12	66.7	457	5	ACH41467	Ach41467 Human foe	655	12	66.7	569	6	AB511486	Ab511486 Human gen
C 583	12	66.7	458	9	ABV37165	Abv37165 Human pro	656	12	66.7	569	12	ACH67981	Ach67981 Human gen
C 584	12	66.7	459	6	ABQ77833	AbQ77833 Human PTO	657	12	66.7	571	12	ACH69618	Ach69618 Human gen
C 585	12	66.7	460	13	ADQ57171	AdQ57171 Novel can	658	12	66.7	572	13	AD534704	Ad534704 sRNA-1 P
C 586	12	66.7	461	2	AAT27988	Aat27988 Hepatitis	659	12	66.7	578	13	ADQ49838	AdQ49838 Novel can
C 587	12	66.7	462	2	AAV09665	AAv09665 Human cat	660	12	66.7	584	4	ABA31365	AbA31365 Probe #98
C 588	12	66.7	463	3	AA806646	Aa806646 Human sec	661	12	66.7	584	6	AB512474	Ab512474 Human gen
C 589	12	66.7	469	9	ADA27108	Ada27108 Human nov	662	12	66.7	587	3	AAZ57395	AaZ57395 Hepatitis
C 590	12	66.7	469	12	AD866644	Ad866644 Novel hum	663	12	66.7	587	12	ADL87163	AdL87163 DNA up-re
C 591	12	66.7	470	9	ACD28233	Acd28233 Human BT2	664	12	66.7	590	13	ADQ55673	AdQ55673 Novel can
C 592	12	66.7	470	9	ACH28402	Ach28402 Human adu	665	12	66.7	591	6	ABO56531	AbO56531 Human col
C 593	12	66.7	475	4	AA113958	AA113958 Probe #38	666	12	66.7	600	11	ACH92766	Ach92766 Breast ca
C 594	12	66.7	475	4	ABA55681	AbA55681 Human foe	667	12	66.7	602	12	ADQ51140	AdQ51140 Novel can
C 595	12	66.7	475	4	AA135338	AA135338 Probe #40	668	12	66.7	610	5	ABV21206	Abv21206 Human pro
C 596	12	66.7	475	4	AAK29377	Aak29377 Human bon	669	12	66.7	610	5	ABV27027	Abv27027 Human pro
C 597	12	66.7	475	4	AAK03903	Aak03903 Human bra	670	12	66.7	610	5	ABV27059	Abv27059 Human pro
C 598	12	66.7	475	4	AB528997	Ab528997 Human liv	671	12	66.7	610	5	ABV1238	Abv1238 Human pro
C 599	12	66.7	475	6	AB503936	Ab503936 Human gen	672	12	66.7	617	5	AA575955	AA575955 DNA enco
C 600	12	66.7	475	10	ADF28115	Adf28115 Human neu	673	12	66.7	621	3	AA535286	Aa535286 Human ade
C 601	12	66.7	477	9	ACH34902	Ach34902 Human end	674	12	66.7	621	3	AA571408	Aa571408 Human low
C 602	12	66.7	478	12	ACH87352	Ach87352 Human gen	675	12	66.7	621	10	ABD297102	Abd297102 Human nuc
C 603	12	66.7	480	2	AAQ29877	AaQ29877 Pheromone	676	12	66.7	621	11	ABD20951	Abd20951 Human pul
C 604	12	66.7	480	6	ABK63172	AbK63172 Rat seque	677	12	66.7	625	4	ABA08653	AbA08653 Human Zn

C 678	12	66.7	631	4	AAS30882	Aas30882 Human cDN	C 751	12	66.7	842	6	ABK24021	Abk24021 B7-7-relate
C 679	12	66.7	631	12	ACH87610	Ach87610 Human gen	C 752	12	66.7	843	5	AA575956	AA575956 DNA encod
C 680	12	66.7	637	13	ADQ53698	Adq53698 Novel can	C 753	12	66.7	846	6	ABO89154	ABO89154 Human pro
C 681	12	66.7	646	10	ADE09608	Ad09608 Novel DNA	C 754	12	66.7	857	5	AA564511	AA564511 DNA encod
C 682	12	66.7	646	13	ADRO7612	Adro7612 Full leng	C 755	12	66.7	861	6	AB552108	AB552108 Human but
C 683	12	66.7	650	4	ABA09468	Ab09468 Human cat	C 756	12	66.7	866	4	AA194061	AA194061 Human neu
C 684	12	66.7	652	2	AAT27966	Aat27966 Hepatitis	C 757	12	66.7	888	4	AAH32577	AAH32577 Human sec
C 685	12	66.7	663	13	AAA75292	Aaa75292 Bacterial	C 758	12	66.7	904	13	ABD32563	ABD32563 Human can
C 686	12	66.7	665	3	AAH75292	Aah75292 Novel hep	C 759	12	66.7	916	5	AA568258	AA568258 DNA encod
C 687	12	66.7	665	12	ADN35969	Adn35969 HCV cDNA	C 760	12	66.7	923	8	AAT28348	Aat28348 Hepatitis
C 688	12	66.7	668	5	AAH26695	Aah26695 Human bre	C 761	12	66.7	950	8	ABX72221	Abx72222 Human NOV
C 689	12	66.7	669	5	AAH97948	Aah97948 Murine 7-	C 762	12	66.7	961	4	AA111631	AA111631 Probe #15
C 690	12	66.7	684	4	AAH72670	Aah72670 Human cer	C 763	12	66.7	961	4	ABAS3323	ABas3323 Human f0e
C 691	12	66.7	685	2	AAZ11719	Aaz11719 Hepatitis	C 764	12	66.7	961	4	AA132930	AA132930 Probe #16
C 692	12	66.7	685	10	ADA49755	Ada49755 HCV 5'UTR	C 765	12	66.7	961	4	AB422903	AB422903 Human bre
C 693	12	66.7	685	12	ADN03472	Adn03472 Hepatitis	C 766	12	66.7	961	4	ABA23100	ABA23100 Probe #15
C 694	12	66.7	686	2	AAQ44921	Aaq44921 Hepatitis	C 767	12	66.7	961	4	AAK27031	AAK27031 Human bon
C 695	12	66.7	688	10	ADE09592	Ade09592 Novel DNA	C 768	12	66.7	961	4	AAK01588	AAK01588 Human bra
C 696	12	66.7	700	3	AAH92795	Aah92795 Human inf	C 769	12	66.7	961	4	AB526617	AB526617 Human liv
C 697	12	66.7	703	3	AAZ57396	Aaz57396 Hepatitis	C 770	12	66.7	961	5	AA101558	AA101558 Probe #15
C 698	12	66.7	710	6	ABT09501	Abt09501 Phase-1 R	C 771	12	66.7	961	6	AB501611	AB501611 Human gen
C 699	12	66.7	710	10	ADG30929	Adg30929 Liver tox	C 772	12	66.7	963	4	AAAC89281	AAc89281 Human bra
C 700	12	66.7	710	12	ADG45517	Adg45517 Liver inf	C 773	12	66.7	977	12	ACH90998	ACH90998 Human gen
C 701	12	66.7	710	12	ADH22819	Adh22819 Partial D	C 774	12	66.7	994	10	ABR07354	ABr07354 Novel cod
C 702	12	66.7	713	3	AAA08097	Aaa08097 Hepatitis	C 775	12	66.7	1001	13	ADQ81128	ADq81128 Human phe
C 703	12	66.7	713	12	ADR20088	Adr20088 Human imm	C 776	12	66.7	1008	10	AD122503	AD122503 Rat liver
C 704	12	66.7	720	3	ABL52861	AbL52861 Hepatitis	C 777	12	66.7	1009	6	AB189555	AB189555 Human pol
C 705	12	66.7	721	6	ABK75107	Abk75107 Bacillus	C 778	12	66.7	1018	5	ABAI15978	ABai15978 Human ner
C 706	12	66.7	725	3	AAZ97434	Aaz97434 Human pro	C 779	12	66.7	1019	10	AD160268	AD160268 Secreted
C 707	12	66.7	725	10	ADK11634	Adk11634 Breast ca	C 780	12	66.7	1024	5	ABAB3180	ABab3180 HOSR-3 (c
C 708	12	66.7	732	5	AA564405	Aas64405 DNA encod	C 781	12	66.7	1024	6	AB576392	AB576392 cDNA encod
C 709	12	66.7	736	3	AAZ97433	Aaz97433 Human pro	C 782	12	66.7	1024	10	ABX74465	ABx74465 Human cDN
C 710	12	66.7	736	10	ADK11633	Adk11633 Breast ca	C 783	12	66.7	1024	10	ABZ83502	ABz83502 Tox/colog
C 711	12	66.7	752	4	AAH04810	Aah04810 Human cDN	C 784	12	66.7	1024	10	ABZ83331	ABz83331 Tox/colog
C 712	12	66.7	770	10	ADC26809	Adc26809 Human lip	C 785	12	66.7	1024	11	ADM10943	ADM10943 Human O64
C 713	12	66.7	780	3	AAZ57789	Aaz57789 Hepatitis	C 786	12	66.7	1024	11	ADM10944	ADM10944 Human O64
C 714	12	66.7	786	4	AAD05242	Aad05242 Human sec	C 787	12	66.7	1024	12	ADJ11274	ADJ11274 Human ova
C 715	12	66.7	786	6	AAD32528	Ad32528 Human B7-	C 788	12	66.7	1024	12	ADJ11273	ADJ11273 Human ova
C 716	12	66.7	789	3	AAZ46029	Aaz46029 Gene enco	C 789	12	66.7	1024	12	ADM43534	ADM43534 Human ova
C 717	12	66.7	793	4	AAH07485	Aah07485 Human cDN	C 790	12	66.7	1026	2	AAV73480	AAv73480 Human mye
C 718	12	66.7	793	4	AAH07485	Aah07485 Human cDN	C 791	12	66.7	1031	2	AAV73480	AAv73480 Human mye
C 719	12	66.7	794	10	ADE08933	Ade08933 Novel DNA	C 792	12	66.7	1031	2	AAV73480	AAv73480 Human mye
C 720	12	66.7	799	5	AA571896	Aas71896 DNA encod	C 793	12	66.7	1057	2	AAV84604	AAV84604 Human sec
C 721	12	66.7	803	2	AAO70437	Aao70437 Recombina	C 794	12	66.7	1057	4	ABAB3387	ABab3387 Human sec
C 722	12	66.7	803	2	AAO70438	Aao70438 Recombina	C 795	12	66.7	1057	4	ACH04888	ACH04888 Novel hum
C 723	12	66.7	803	2	AAO70439	Aao70439 Recombina	C 796	12	66.7	1057	5	ACD44658	ACd44658 Human cDN
C 724	12	66.7	803	2	AAQ70100	Aaq70100 Recombina	C 797	12	66.7	1057	5	AA583425	AA583425 DNA encod
C 725	12	66.7	806	4	ABA122065	AbA122065 Probe #11	C 798	12	66.7	1089	12	ADO29788	ADO29788 Human nov
C 726	12	66.7	806	4	ABA67141	AbA67141 Human f0e	C 799	12	66.7	1092	6	AB139804	AB139804 Human NS
C 727	12	66.7	806	4	AAI47357	Aai47357 Probe #16	C 800	12	66.7	1104	12	ADK71921	ADK71921 Human kin
C 728	12	66.7	806	4	ABA49226	AbA49226 Human bre	C 801	12	66.7	1105	2	AAT09952	AAt09952 H1gn-af1i
C 729	12	66.7	806	4	AAK14315	Aak14315 Human bon	C 802	12	66.7	1105	10	ADCT7760	ADc7760 Human 314
C 730	12	66.7	806	4	AAK15382	Aak15382 Human bra	C 803	12	66.7	1105	10	ACA56883	ACa56883 Human sig
C 731	12	66.7	806	4	ABS40915	AbS40915 Human liv	C 804	12	66.7	1105	12	AD156679	AD156679 Human pol
C 732	12	66.7	806	5	AAI07759	Aai07759 Probe #77	C 805	12	66.7	1120	12	ADO84424	ADO84424 Human tum
C 733	12	66.7	806	6	ABS15324	AbS15324 Human gen	C 806	12	66.7	1131	2	AAZ40843	AAz40843 Secreted
C 734	12	66.7	808	4	AAH07625	Aah07625 Human cDN	C 807	12	66.7	1131	11	ADM77865	ADM77865 Human cDN
C 735	12	66.7	817	13	AD534705	Ad534705 siRNA-2 P	C 808	12	66.7	1131	12	ADP19141	ADp19141 Human sec
C 736	12	66.7	819	6	AAH50556	Aah50556 Human B7-	C 809	12	66.7	1132	5	AAH64784	AAh64784 Human sec
C 737	12	66.7	819	6	ABK88228	Abk88228 DNA encod	C 810	12	66.7	1147	13	ACN39111	ACn39111 Tumour-as
C 738	12	66.7	819	6	AAI70887	Aai70887 Human co-	C 811	12	66.7	1157	10	ADC64640	ADC64640 Human tra
C 739	12	66.7	819	12	ADQ76312	Adq76312 Human B7-	C 812	12	66.7	1171	12	ADOC26862	ADOC26862 Hepatitis
C 740	12	66.7	821	6	ABL51013	AbL51013 Human EDA	C 813	12	66.7	1176	6	ABL51020	ABL51020 Human EDA
C 741	12	66.7	821	6	AAAD8355	Aad8355 Human B7-	C 814	12	66.7	1176	9	ACD07906	ACd07906 DNA encod
C 742	12	66.7	822	8	AAAD8355	Aad8355 Human B7-	C 815	12	66.7	1183	12	ADL14952	ADl14952 Human gla
C 743	12	66.7	822	8	AAAD8355	Aad8355 Human B7-	C 816	12	66.7	1185	5	AA580276	AA580276 DNA encod
C 744	12	66.7	822	9	ADA03076	Ada03076 Human hCG	C 817	12	66.7	1192	11	AD131274	AD131274 Human cDN
C 745	12	66.7	822	9	ADA66307	Ada66307 Human hCG	C 818	12	66.7	1193	5	AD145984	AD145984 Human ova
C 746	12	66.7	822	10	AD72814	Ad72814 Human hCG	C 819	12	66.7	1202	8	ABZ18474	ABz18474 Group IIT
C 747	12	66.7	822	11	AD127154	Ad127154 Human cod	C 820	12	66.7	1207	4	AAH99734	AAH99734 Human pro
C 748	12	66.7	824	11	AAH34088	Aah34088 Human col	C 821	12	66.7	1209	6	AAZ36968	AAZ36968 Human B7-
C 749	12	66.7	828	9	ADB82098	AdB82098 Human cDN	C 822	12	66.7	1210	4	AA163821	AA163821 Human pol
C 750	12	66.7	828	9	ADB82098	AdB82098 Human cDN	C 823	12	66.7	1210	4	AA163821	AA163821 Human pol

824	12	66.7	1210	12	ADM24372	Adm24372 Human PRO	897	12	66.7	1614	8	ABZ24646	ABZ24646 Novel hum
825	12	66.7	1212	3	AAA75127	Aa75127 CDNA enco	898	12	66.7	1632	10	ADD26578	Add26578 Human par
826	12	66.7	1223	6	AA227371	Aa227371 Human PD-	899	12	66.7	1635	5	AA158558	Aa158558 Human pol
827	12	66.7	1223	6	AA141871	Aa141871 Human PD-	900	12	66.7	1635	5	ADQ98775	Adq98775 DNA enco
828	12	66.7	1223	8	ABX13050	Abx13050 Human PD-	901	12	66.7	1635	9	ADBA48535	Adba48535 Novel hum
829	12	66.7	1223	8	ADA03075	Ada03075 Human hCG	902	12	66.7	1638	4	AA159268	Aa159268 Human pol
830	12	66.7	1223	9	ADA66359	Ada66359 Human hCG	903	12	66.7	1644	2	AAK60775	Aak60775 Soybean c
831	12	66.7	1223	10	ADB72813	Adb72813 Human hCG	904	12	66.7	1644	10	ADD19238	Add19238 Human CDN
832	12	66.7	1223	10	ABT14005	Abt14005 Human PD-	905	12	66.7	1650	5	AA591844	Aa591844 DNA enco
833	12	66.7	1223	11	ADL27153	Adl27153 Human CDN	906	12	66.7	1662	8	ABZ42687	Abz42687 Human mel
834	12	66.7	1237	3	AAFI6043	Aafi6043 Human pro	907	12	66.7	1665	6	ABK43363	Abk43363 DNA enco
835	12	66.7	1247	3	AAA64172	Aaa64172 DNA enco	908	12	66.7	1669	4	AAH17479	Aah17479 Human CDN
836	12	66.7	1248	6	ABZ11962	Abz11962 Human pol	909	12	66.7	1670	4	AA526675	Aa526675 Human gen
837	12	66.7	1248	12	ADMA4480	Adma4480 Novel hum	910	12	66.7	1670	8	ABX74024	Abx74024 Human nov
838	12	66.7	1251	6	ABK63916	Abk63916 CDNA enco	911	12	66.7	1678	3	AAF15718	Aaf15718 Human pro
839	12	66.7	1270	2	AAV60668	Aav60668 Fragment	912	12	66.7	1707	3	AAAC5834	Aaac5834 S. lavend
840	12	66.7	1272	11	ABD00501	Abd00501 Klebsiell	913	12	66.7	1711	10	ADAE10253	Adae10253 S. lavend
841	12	66.7	1285	3	AAAC59828	Aaac59828 Human sec	914	12	66.7	1717	10	ADD48175	Add48175 Human gen
842	12	66.7	1294	4	AA527163	Aa527163 CDNA enco	915	12	66.7	1714	6	ABL34972	Ab134972 Rat CDNA
843	12	66.7	1294	4	ABK43862	Abk43862 DNA enco	916	12	66.7	1733	12	ADH13735	Adh13735 Human ENZ
844	12	66.7	1294	10	ADB93341	Adb93341 Human CDN	917	12	66.7	1741	2	AAV73481	Aav73481 Human mye
845	12	66.7	1294	12	AD154249	Ad154249 CDNA enco	918	12	66.7	1747	5	ABV24646	Abv24646 Human pro
846	12	66.7	1295	5	ADL63657	Adl63657 Human ova	919	12	66.7	1752	4	AA513672	Aa513672 CDNA enco
847	12	66.7	1297	10	ADE28248	Ade28248 Human MDP	920	12	66.7	1752	6	ABO78589	Ab078589 Nucleotid
848	12	66.7	1314	3	AAAC98802	Aaac98802 Human pan	921	12	66.7	1752	6	AA138753	Aa138753 Rat lambd
849	12	66.7	1314	6	ABO54135	Ab054135 Human ova	922	12	66.7	1752	10	ADP76244	Adp76244 Rat Pec-1
850	12	66.7	1323	11	ACN89216	Acn89216 Breast ca	923	12	66.7	1765	2	AAQ79141	Aaq79141 Hepatitis
851	12	66.7	1326	2	AAV73478	Aav73478 Human mye	924	12	66.7	1765	2	AAQ79143	Aaq79143 Hepatitis
852	12	66.7	1340	2	AAZ42034	Aaz42034 Human end	925	12	66.7	1773	4	ABA95456	Ab95456 Therrus c
853	12	66.7	1344	3	AAA80619	Aaa80619 Human sec	926	12	66.7	1777	6	ABK99966	Abk99966 DNA enco
854	12	66.7	1344	10	ADA27043	Ada27043 Human nov	927	12	66.7	1798	12	ADH45315	Adh45315 Human enz
855	12	66.7	1344	12	ADD19201	Add19201 Human CDN	928	12	66.7	1801	12	ADM87048	Adm87048 Human pro
856	12	66.7	1344	12	ADB66573	Adb66573 Novel hum	929	12	66.7	1814	6	AAD36972	Aad36972 Human B7-
857	12	66.7	1356	6	ABK24018	Abk24018 DNA enco	930	12	66.7	1816	5	AA584220	Aa584220 DNA enco
858	12	66.7	1372	4	AAF59618	Aaf59618 Human cel	931	12	66.7	1819	4	AAH14818	Aah14818 Human CDN
859	12	66.7	1407	4	AA104515	Aa104515 Human rep	932	12	66.7	1824	13	ADR24373	Adr24373 Breast ca
860	12	66.7	1410	13	ADS58688	Ads58688 Bacterial	933	12	66.7	1824	12	ADN98871	Adn98871 Novel hum
861	12	66.7	1427	2	AAV20959	Aav20959 Human rec	934	12	66.7	1824	12	ADO00440	Ado00440 Novel hum
862	12	66.7	1467	6	ABV78216	Abv78216 Human MRP	935	12	66.7	1837	4	AA160238	Aa160238 Human pol
863	12	66.7	1467	6	ABZ35792	Abz35792 Human MRP	936	12	66.7	1842	2	AAZ77570	Aaz77570 Human ova
864	12	66.7	1467	6	ABX10035	Abx10035 Human MMP	937	12	66.7	1851	3	AAZ56729	Aaz56729 Human tra
865	12	66.7	1467	6	ABL91757	Ab191757 Human pol	938	12	66.7	1851	13	AD510426	Ad510426 Human the
866	12	66.7	1477	6	ABL61107	Ab161107 Decoycti	939	12	66.7	1854	12	ADO87127	Ado87127 Human tum
867	12	66.7	1493	5	AA576103	Aa576103 DNA enco	940	12	66.7	1856	8	ACC69466	Acc69466 Human mal
868	12	66.7	1494	3	AAAC46817	Aaac46817 Arabidops	941	12	66.7	1861	13	AD510078	Ad510078 Human the
869	12	66.7	1500	2	AAV20961	Aav20961 Human TFE	942	12	66.7	1863	2	AAQ15363	Aaq15363 Fragment
870	12	66.7	1511	9	AA161122	Aa161122 Human CID	943	12	66.7	1864	2	AAQ15362	Aaq15362 Fragment
871	12	66.7	1511	12	ADM98087	Adm98087 Human CID	944	12	66.7	1864	12	ADQ24314	Adq24314 Human sof
872	12	66.7	1536	3	AAA37847	Aaa37847 Human obe	945	12	66.7	1875	10	ADT60591	Adt60591 Secreted
873	12	66.7	1547	4	AAK91014	Aak91014 Human dig	946	12	66.7	1880	2	AAQ24466	Aaq24466 NAMB hepa
874	12	66.7	1547	5	AA532049	Aa532049 Human liv	947	12	66.7	1884	2	AAQ24467	Aaq24467 NAMB hepa
875	12	66.7	1547	4	ABN90404	Abn90404 Human liv	948	12	66.7	1890	4	ABL13343	Ab113343 Drosophi
876	12	66.7	1549	11	ADJ5317	Adj5317 Human liv	949	12	66.7	1899	3	AAAC99049	Aaac99049 Human pan
877	12	66.7	1549	6	ABO70339	Ab070339 Listeria	950	12	66.7	1897	4	AAH34645	Aah34645 Human col
878	12	66.7	1551	8	ABO91947	Ab091947 Human NF-	951	12	66.7	1897	4	ABL03791	Ab103791 Drosophi
879	12	66.7	1551	8	ABZ24644	Abz24644 Novel hum	952	12	66.7	1901	12	ADQ19936	Adq19936 Human sof
880	12	66.7	1551	8	ACC42290	Acc42290 Human MAP	953	12	66.7	1908	13	ADT42221	Adt42221 Bacterial
881	12	66.7	1554	2	AAQ32451	Aaq32451 HCV core-	954	12	66.7	1913	8	ACC69467	Acc69467 Human mal
882	12	66.7	1562	2	AAV60672	Aav60672 Fragment	955	12	66.7	1915	8	ABZ24647	Abz24647 Novel hum
883	12	66.7	1566	11	ADN38899	Adn38899 Cancer/an	956	12	66.7	1917	3	AAA37848	Aaa37848 Human obe
884	12	66.7	1574	6	ABL51009	Ab151009 Human BDA	957	12	66.7	1918	4	AAH74769	Aah74769 Nucleotid
885	12	66.7	1574	9	ACD07895	Ac07895 CDNA enco	958	12	66.7	1918	8	ABT17361	Abt17361 Human SLC
886	12	66.7	1577	10	ADD48173	Add48173 Rat gene	959	12	66.7	1925	8	AAU54485	Aau54485 Human CIP
887	12	66.7	1578	5	AA580253	Aa580253 DNA enco	960	12	66.7	1927	13	ADR21620	Adr21620 Human enz
888	12	66.7	1587	4	AA161054	Aa161054 Human pol	961	12	66.7	1962	11	ABT17363	Abt17363 Human SLC
889	12	66.7	1587	13	AD511418	Ad511418 Human the	962	12	66.7	1962	4	AA114105	Aa114105 Probe #40
890	12	66.7	1595	8	ABT17362	Abt17362 Human SLC	963	12	66.7	1969	4	ABA55830	Ab55830 Human f0e
891	12	66.7	1599	5	AA578921	Aa578921 DNA enco	964	12	66.7	1969	4	AA155486	Aa155486 Probe #41
892	12	66.7	1599	8	ABZ24645	Abz24645 Novel hum	965	12	66.7	1969	4	ABA45341	Ab45341 Human bre
893	12	66.7	1601	12	ADL15479	Adl15479 Human nep	966	12	66.7	1969	4	ABA25506	Ab25506 Probe #39
894	12	66.7	1608	10	AAQ71977	Aaq71977 Murine IL	967	12	66.7	1969	4	AAK29533	Aak29533 Human bon
895	12	66.7	1610	10	AD160463	Ad160463 Secreted	968	12	66.7	1969	4	AAK04048	Aak04048 Human bra
896	12	66.7	1610	10	AD160463	Ad160463 Secreted	969	12	66.7	1969	4	AAK04048	Aak04048 Human bra

```
C 970 12 66.7 1969 4 ABS29157
C 971 12 66.7 1969 5 AAT03958
C 972 12 66.7 1969 6 ABS04084
C 973 12 66.7 1970 4 AAF32686
C 974 12 66.7 1974 5 AAS80252
C 975 12 66.7 1983 13 ADR85425
C 976 12 66.7 1985 10 ADP26576
C 977 12 66.7 1989 12 ADH13748
C 978 12 66.7 1992 4 AAL46384
C 979 12 66.7 1998 10 ADE07178
C 980 12 66.7 1998 10 ADE07178
C 981 12 66.7 2004 6 ABO86145
C 982 12 66.7 2022 3 AAF21635
C 983 12 66.7 2025 13 ADQ85640
C 984 12 66.7 2025 13 ADQ86738
C 985 12 66.7 2033 2 AAQ64913
C 986 12 66.7 2033 2 AAQ86788
C 987 12 66.7 2043 5 ABV30333
C 988 12 66.7 2050 12 ADQ87055
C 989 12 66.7 2052 6 ABK43375
C 990 12 66.7 2058 8 AAD53168
C 991 12 66.7 2061 6 ABQ86144
C 992 12 66.7 2076 5 AAS74039
C 993 12 66.7 2076 5 AAS74039
C 994 12 66.7 2094 6 AAS74039
C 995 12 66.7 2098 10 ADB31325
C 996 12 66.7 2106 2 AAQ43905
C 997 12 66.7 2106 2 AAQ86773
C 998 12 66.7 2106 2 AAT18792
C 999 12 66.7 2110 10 ADB63624
C1000 12 66.7 2116 2 AAQ12242
```

## ALIGNMENTS

```
RESULT 1
ID AAT80248 standard; DNA; 18 BP.
AC AAT80248;
XX
DT 15-OCT-1997 (first entry)
XX
DE Oligo HCV94 used in luciferase assay.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
PN WO9639500-A2.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002427.
XX
PR 06-JUN-1995; 95US-00471968.
XX
PA (HOF) HOFFMANN LA ROCHE & CO AG F.
XX
PA (HYBR-) HYBRIDON INC.
XX
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX
DR WPI; 1997-043122/04.
XX
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
PS Claim 19; Page 31; 100pp; English.
```

```
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
SQ Sequence 18 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 6 Other;
Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGAGAGNNNNN 18
Db 1 GGGGUCGAGAGNNNNN 18
```

```
RESULT 2
ID ABS65832 standard; DNA; 18 BP.
AC ABS65832;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #38.
```

```
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
```

OS Synthetic.

PN US2002081577-A1.

PD 27-JUN-2002.

PF 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

PR 02-JUL-1996; 96US-0021104P.

PA (KILK/) KILKUSKIE R L.

PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.

PA (ROBE/) ROBERTS N A.

PA (WALT/) WALTHER D M.

XX

XX

XX

XX

XX

XX

XX

Claim 22; Page 10; 74pp; English.

The invention describes synthetic oligonucleotides complementary to a portion of the 5' untranslated region of hepatitis C virus (HCV), useful for diagnosing and treating hepatitis C virus infection, in antisense technology and gene

CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 CC  
 SQ Sequence 18 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 6 Other;  
 Query Match 100.0%; Score 18; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAGANNNNNN 18  
 1 GGGGUCCTCGAGANNNNNN 18  
 Db 1 GGGGUCCTCGAGANNNNNN 18

RESULT 3  
 AAT80277  
 ID AAT80277 standard; DNA; 24 BP.  
 XX  
 AC AAT80277;  
 XX  
 DT 15-OCT-1997 (first entry)  
 XX  
 DE Oligo HCVJ34, used in luciferase assay.  
 XX  
 KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KW inhibition; replication; expression; detection; chronic hepatitis;  
 KW acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..24  
 FT /\*tag= a  
 FT /note= "Phosphorothioate linkages"  
 XX  
 PN W09639500-A2.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96WO-EP002427.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 DR WPI; 1997-043122/04.  
 XX  
 PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepatocarcinoma.  
 PT  
 PS Claim 19; Page 33; 100pp; English.  
 XX  
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This oligo was used in a luciferase assay to determine

CC whether it binds successfully to its target  
 XX  
 SQ Sequence 24 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 12 Other;  
 Query Match 100.0%; Score 18; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAGANNNNNN 18  
 1 GGGGUCCTCGAGANNNNNN 18  
 Db 1 GGGGUCCTCGAGANNNNNN 18

RESULT 4  
 ABS65861  
 ID ABS65861 standard; DNA; 24 BP.  
 XX  
 AC ABS65861;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #67.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLFE/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 PT  
 PS Claim 22; Page 11; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 CC

SO Sequence 24 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 12 Other;  
Query Match 100.0%; Score 18; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCGAGGAGNNNNN 18  
1 |||||  
Db 1 GGGGUCGAGGAGNNNNN 18  
RESULT 5  
AAD43827  
ID AAD43827 standard; DNA; 29 BP.  
AC AAD43827;  
XX  
XX 14-NOV-2002 (first entry)  
XX  
XX Adapter oligo #5 used to illustrate the method of the invention.  
XX  
XX Single stranded polynucleotide tag; cleavage agent; gene expression; ds.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 9..10  
FT /\*tag= a  
FT /note= "Nicking site"  
FT misc\_feature 27..28  
FT /\*tag= b  
FT /note= "Nicking site"  
XX  
XX WO200259357-A2.  
XX  
XX 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002MO-DK000052.  
XX  
XX 24-JAN-2001; 2001DK-00000126.  
XX 12-FEB-2001; 2001US-0267704P.  
XX  
XX (GENO-) GENOMIC EXPRESSION APS.  
XX  
XX Pedersen ML;  
XX  
XX WPI; 2002-636542/68.  
XX  
XX Obtaining single stranded polynucleotide tags from a biological sample,  
XX for analyzing gene expression or diagnosing clinical conditions,  
XX comprises employing nicking endonucleases that cleave complementary  
XX strands.  
XX  
XX Disclosure, Page 284; 302pp; English.  
XX  
XX The invention relates to a method for obtaining a single stranded  
XX polynucleotide tag from a biological sample by cleaving one of the  
XX complementary strands of a double stranded polynucleotide with a cleavage  
XX agent capable of recognising a double stranded polynucleotide comprising  
XX complementary strands and cleaving only one of the strands of the  
XX polynucleotide in the process of generating a single stranded  
XX polynucleotide tag. The method is useful for separating, analysing,  
XX quantifying or obtaining single stranded polynucleotides comprising tags  
XX originating partly, and preferably wholly from a source of DNA and/or RNA  
XX in a sample comprising biological cells. The method is particularly for  
XX analysing gene expression (expression profiling or differential gene  
XX expression), or in diagnosing clinical conditions. The present sequence  
XX is an adapter oligonucleotide used to illustrate the method of the  
XX invention  
XX  
XX Sequence 29 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 18 Other;  
XX  
XX Query Match 83.3%; Score 15; DB 6; Length 29;

Best Local Similarity 86.7%; Pred. No. 79;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 4 GUCCUGAGGAGNNNNN 18  
|||:|||||  
Db 3 GTCCTGAGGAGNNNNN 17  
RESULT 6  
ABK50461  
ID ABK50461 standard; DNA; 2400 BP.  
XX  
XX ABK50461;  
XX  
XX 13-AUG-2002 (first entry)  
XX  
XX Human caspase 5, apoptosis-related cysteine protease modified DNA.  
XX  
XX Human; caspase 5; apoptosis-related cysteine protease; CASP5; gene; ds;  
XX haplotyping; haplotype pair; cancer; single nucleotide polymorphism;  
XX hereditary nonpolyposis colorectal cancer; gastrointestinal tumour;  
XX endometrial tumour; chromosome 11q22.2-q22.3.  
XX  
XX Homo sapiens.  
XX  
XX WO200226769-A2.  
XX  
XX 04-APR-2002.  
XX  
XX 01-OCT-2001; 2001MO-US030878.  
XX  
XX 29-SEP-2000; 2000US-0236568P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Choi JY, Klien SE, Russo DP;  
XX  
XX WPI; 2002-435191/46.  
XX  
XX Novel caspase 5 apoptosis-related cysteine protease, useful  
XX therapeutically and in screening for drugs targeting protease  
XX polypeptide.  
XX  
XX Example 2; Page 114-115; 115pp; English.  
XX  
XX The invention relates to single nucleotide polymorphisms in the gene  
XX encoding the human caspase 5, apoptosis-related cysteine protease (CASP5)  
XX polypeptide. A method for haplotyping the CASP5 gene in an individual  
XX comprises identifying the nucleotide at one or more polymorphic sites and  
XX determining whether one of the copies of the gene is defined by one of  
XX the CASP5 haplotypes given in the specification or whether both copies  
XX are defined by a haplotype pair. This method is useful in genotyping,  
XX whereby all possible haplotype pairs can be assigned to specific  
XX genotypes. An association between a trait and a haplotype or haplotype  
XX pair of the CASP5 gene can be identified by comparing the frequency of  
XX the haplotype or haplotype pair in a population exhibiting the trait with  
XX the frequency of the haplotype or haplotype pair in a reference  
XX population, where a higher haplotype frequency in the trait population  
XX indicates the trait is associated with the haplotype or haplotype pair.  
XX CASP5 and its corresponding DNA are used for studying the expression and  
XX function of CASP5, for use in screening for candidate drugs to treat  
XX diseases related to CASP5 activity, such as cancer (e.g. hereditary  
XX nonpolyposis colorectal cancer, gastrointestinal tumours and endometrial  
XX tumours). This sequence represents genomic DNA modified to facilitate  
XX electronic searching of the CASP5 haplotypes  
XX  
XX Sequence 2400 BP; 366 A; 209 C; 272 G; 333 T; 0 U; 1220 Other;  
XX  
XX Query Match 83.3%; Score 15; DB 6; Length 2400;  
XX Best Local Similarity 86.7%; Pred. No. 57;  
XX Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 4 GUCCUGAGGAGNNNNN 18



```

Db      1732  GTCCCTGGAGNNNNNN 1746
          |||:|||||

```

## RESULT 7

ADQ55353/c  
ID ADQ55353 standard; DNA; 503 BP.

AC ADQ55353 ;

DT 21-OCT-2004 (first entry)

Novel canine microarray-related DNA sequence SegID6655.

KM canine/microarray; drug screening; toxicity assay;  
KM environmental pollutant; cellular response; gene expression profile;  
KM toxic response; liver necrosis; fatty liver disease;  
KM protein adduct formation; hepatitis; dog; ds.

**OS** **Canis familiaris.**

PN WO2004063324-A2.

PD 29-JUL-2004

PF 05-MAY-2003; 2003WO-US013853.

PR 03-MAY-2002; 2002US-0377240P.

PA	(GENE-)	GENE LOGIC INC.
PA	(PFIZ )	PFIZER PROD INC.

PI Diggans JC, Porter M, Wei T;

DR WPI; 2004-561890/54.

PT New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism.

PS Claim 1; SEQ ID NO 6655; 41pp; English.

This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine nucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention is therefore useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a disease state. The sequences are useful as diagnostic agents or markers to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that modulate gene expression or activity. The database is useful for producing electronic Northern blots that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell. The methods are useful for determining the similarity of a toxic response to one or more individual compounds. The methods are useful for predicting at least one toxic response or the likelihood that a compound or test agent will induce various specific pathologies such as those of the liver (liver necrosis, fatty liver disease, protein adduct formation or hepatitis), those of the kidney, heart, brain or testes, or other pathologies associated with at least one of the toxins. The methods are also useful for predicting or elucidating the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the production of a canine microarray of the invention.

SQ Sequence 503 BP; 86 A; 142 C; 86 G; 125 T; 0 U; 64 Other;

Query Match	77.8%	Score 14;	DB 13;	Length 503;
Best Local Similarity	85.7%	Pred. No. 2.2e+02;		
Matches 12;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;

QY	4	GUCCUGGAGNNNN	17
		: : : : : :	
Db	126	GTCCTGGAGNNNN	113

## RESULT 8

ID AAS76001 standard; cDNA; 418 BP

AC AAS76001,

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #11805.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

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PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73  
DR P-BENB; ABG11914

Nov. 3 1907 at 601.

PT New isolated polynucleotide and encoded polypeptide, useful in diagnostics, forensics, gene mapping, identification of mutations PT responsible for genetic disorders or other traits and to assess biodiversity.

PS Claim 1; SEQ ID NO 11805; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [http://wipo.int/pub/publ/pct\\_sequences](http://wipo.int/pub/publ/pct_sequences)

SQ Sequence 418 BP; 45 A; 71 C; 91 G; 51 T; 0 U; 160 Other;

Query Match 72.2%; Score 13; DB 5; Length 418;

Best Local Similarity 92.3%; Pred. No. 7.9e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||||  
Db 140 CCTGGAGNNNNNN 152

## RESULT 9

AA197596/c  
ID AA197596 standard; cDNA; 784 BP.

XX AA197596;

AC 13-NOV-2001 (first entry)

XX Human neuroblastoma expressed polynucleotide SEQ ID NO 3671.

XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.

OS Homo sapiens.

PN WO200166719-A1.

PD 13-SEP-2001.

XX 02-MAR-2001; 2001WO-JP001629.

XX 07-MAR-2000; 2000JP-00159195.

XX (CHIB-) CHIBA PREFECTURE.

PA (HISM) HISAMITSU PHARM CO LTD.

PI Nakagawara A;

XX WPI; 2001-56584/63.

XX Nucleic acids originating in gene expressed in human neuroblastoma,  
PT useful as probe or primer in diagnosing prognosis of human neuroblastoma,  
PT malignancy and susceptibility indicator or tumour marker for anti-cancer  
PT agents.

XX Claim 1; Page 2664; 2979pp; Japanese.

CC The invention relates to novel genes (AA193926-AA197963) expressed in  
CC human neuroblastoma. The nucleic acids are applicable as a probe or  
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and  
CC susceptibility indicators or tumour markers for anti-cancer agents. The  
CC gene information for diagnosing prognosis is related to factors similar  
CC to that for N-myc and TrkA genes

XX Sequence 784 BP; 189 A; 223 C; 193 G; 153 T; 0 U; 26 Other;

XX Query Match 72.2%; Score 13; DB 4; Length 784;

XX Best Local Similarity 84.6%; Pred. No. 7.5e+02;

XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAGN 13  
|||:|||||  
Db 570 GGGGTCCTGAGN 558

## RESULT 10

ADQ22970/c  
ID ADQ22970 standard; DNA; 3286 BP.

XX ADQ22970;

XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 5790.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

KW ds.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/A1.

XX Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.

XX Example 2; SEQ ID NO 5790; 210pp; English.

CC The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytotatic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC DNA of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 3286 BP; 648 A; 1104 C; 881 G; 629 T; 0 U; 24 Other;

XX Query Match 72.2%; Score 13; DB 12; Length 3286;

XX Best Local Similarity 92.3%; Pred. No. 6.8e+02;

XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||||  
Db 278 CCTGGAGNNNNNN 266

## RESULT 11

ADQ22880/c  
ID ADQ22880 standard; DNA; 5132 BP.

XX ADQ22880;

XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 5700.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

XX ds.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Aziz N, Gineburg WM, Zlotnick A;  
 XX  
 DR WPI; 2004-441208/41.  
 XX  
 PT Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 XX  
 PS Example 2; SEQ ID NO 5700; 210bp; English.  
 XX  
 CC The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytostatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 CC acid sequences may be useful in diagnostic and screening applications.  
 CC The current sequence is that of a human soft tissue sarcoma-upregulated  
 CC DNA of the invention. The current sequence is not shown within the  
 CC specification per se but was submitted in CD format by the inventor.  
 XX  
 SQ Sequence 5132 BP; 1201 A; 1394 C; 1336 G; 1169 T; 0 U; 32 Other;  
 XX  
 OY Query Match 72.2%; Score 13; DB 12; Length 5132;  
 Best Local Similarity 92.3%; Pred. No. 6.5e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 CCUGGAGNNNNNN 18  
 Db 1012 CCTGGAGNNNNNN 1000  
 XX  
 RESULT 12  
 ADA02927/c  
 ID ADA02927 standard; DNA; 92726 BP.  
 XX  
 AC ADA02927;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Mouse Pk3r1 carcinoma associated gene, SEQ ID NO:1445.  
 XX  
 KM Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;  
 KM prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;  
 KM gene; ds.  
 XX  
 OS Mus sp.  
 XX  
 PN WO2003057146-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041414.  
 XX  
 PR 26-DEC-2001; 2001US-00035832.  
 XX  
 PA (SAGR-) SAGRES DISCOVERY.  
 XX  
 PI Morris DW;  
 XX  
 DR WPI; 2003-587066/55.  
 XX  
 PT New recombinant nucleic acid encoding carcinoma associated protein.  
 PT useful for preparing compositions for treating carcinomas.  
 XX  
 PS Claim 1; SEQ ID NO 1445; 245bp; English.  
 XX

CC The invention relates to recombinant carcinoma associated (CA) nucleic  
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to  
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The  
 CC invention also encompasses expression vectors and host cells comprising a  
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically  
 CC binds to the protein, and a biochip comprising CA nucleic acid or  
 CC fragments thereof. The sequences of the invention were identified using  
 CC oncogenic retroviruses, which insert into the genome of the host organism  
 CC at random. Many of these do not carry transduced host oncogenes or  
 CC pathogenic trans-acting viral genes, meaning that cancer incidence is a  
 CC direct consequence of the effects of proviral integration into host  
 CC protooncogenes. The CA nucleic acid sequences can be used to diagnose  
 CC carcinoma (especially breast cancer, prostate cancer, lymphoma or  
 CC leukaemia) or a propensity to carcinoma by determination of the sequence  
 CC of a CA gene, or by determination of CA gene expression in particular  
 CC tissues. CA nucleic acids, proteins and antibodies are also useful as  
 CC therapeutic agents and in screening and evaluating drug candidates. The  
 CC present sequence represents a specifically claimed murine CA nucleic acid  
 CC sequence of the invention. Note: The complete sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 92726 BP; 23819 A; 19174 C; 20109 G; 27030 T; 0 U; 2594 Other;  
 XX  
 OY Query Match 72.2%; Score 13; DB 9; Length 92726;  
 Best Local Similarity 92.3%; Pred. No. 5.3e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 CCUGGAGNNNNNN 18  
 Db 155 CCTGGAGNNNNNN 143  
 XX  
 RESULT 13  
 ADB72665/c  
 ID ADB72665 standard; DNA; 92726 BP.  
 XX  
 AC ADB72665;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Mouse Pk3r1 gene.  
 XX  
 KM mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;  
 KM cancer; neoplasm; adenocarcinoma; sarcoma; gene.  
 XX  
 OS Mus sp.  
 XX  
 PN WO2003008583-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 26-DEC-2001; 2001WO-US051291.  
 XX  
 PR 02-MAR-2001; 2001US-00798586.  
 XX  
 PR 23-OCT-2001; 2001US-00004113.  
 XX  
 PR 08-NOV-2001; 2001US-00052482.  
 XX  
 PR 30-NOV-2001; 2001US-00997722.  
 XX  
 PR 20-DEC-2001; 2001US-00034650.  
 XX  
 PA (SAGR-) SAGRES DISCOVERY.  
 XX  
 PI Morris DW, Engelhard EK;  
 XX  
 DR WPI; 2003-239337/23.  
 XX  
 PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,  
 PT cancers, neoplasm, adenocarcinoma, or sarcomas.  
 XX  
 PS Claim 1; SEQ ID NO 493; 2304bp; English.  
 XX  
 CC The invention relates to a novel recombinant nucleic acid comprising a

CC nucleotide sequence selected from any of the 660 sequences fully defined  
 CC in the specification. A polynucleotide of the invention has cytosolic  
 CC activity, and may have a use in gene therapy, or in a vaccine. The  
 CC recombinant nucleic acids and polypeptides are useful for treating  
 CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and  
 CC sarcomas. The present sequence represents a mouse gene of the invention.

XX Sequence 92726 BP; 23819 A; 19174 C; 20109 G; 27030 T; 0 U; 2594 Other;

Query Match 72.2%; Score 13; DB 10; Length 92726;

Best Local Similarity 92.3%; Pred. No. 5.3e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCUGAGAGNNNNNN 18

Db 155 CCTGAGAGNNNNNN 143

RESULT 14

ADC85407/c ID ADC85407 standard; DNA; 92726 BP.

AC ADC85407;

DT 01-JAN-2004 (first entry)

DE Mouse Pk3r1 genomic sequence.

XX Cytosolic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;

KM secreted; transmembrane; intracellular; ds.

XX Mus SP.

PN WO2003045230-A2.

XX 05-JUN-2003.

PF 02-DEC-2002; 2002WO-US038582.

PR 30-NOV-2001; 2001US-00997722.

XX (SAGR-) SAGRES DISCOVERY.

PI Morris DW, Engelhard EK;

XX WPI; 2003-513603/48.

PT New recombinant nucleic acid comprising a nucleotide sequence of any of

PT the carcinoma-associated (CA) genes, useful for screening for drug

PT candidates for diagnosing or treating carcinomas.

XX Claim 1; SEQ ID NO 193; 983pp; English.

CC The invention relates to a recombinant nucleic acid comprising a

CC nucleotide sequence selected from any of the fully defined carcinoma-

CC associated (CA) genes from the 50 tables given in the specification. The

CC CA proteins are secreted, transmembrane or intracellular proteins. The

CC recombinant nucleic acids are useful for screening for drug candidates

CC for diagnosing or treating carcinomas. Sequences given in ADC85215-

CC ADC85514 represent CA genes of the invention.

XX Sequence 92726 BP; 23819 A; 19173 C; 20110 G; 27030 T; 0 U; 2594 Other;

Qy 6 CCUGAGAGNNNNNN 18

Db 155 CCTGAGAGNNNNNN 143

RESULT 15

ADM74522/c ID ADM74522 standard; DNA; 92726 BP.

XX ADM74522;

DT 01-JUL-2004 (first entry)

DE Murine carcinoma associated (CA) nucleic acid #97.

XX Mouse; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;

KM carcinoma associated protein; CAP; carcinoma; leukemia; lymphoma;

XX cytosolic.

OS Mus musculus.

PN US2004072154-A1.

PD 15-APR-2004.

PF 30-NOV-2001; 2001US-00997722.

PR 22-DEC-2000; 2000US-00747377.

PR 02-MAR-2001; 2001US-00798586.

XX (MORR/) MORRIS D W.

PA (ENGE/) ENGELHARD E K.

PI Morris DW, Engelhard EK;

XX WPI; 2004-328562/30.

PT New carcinoma associated gene or protein, useful for preparing a

PT composition for diagnosing or treating carcinoma e.g., leukemia or

PT lymphoma.

XX Claim 1; SEQ ID NO 193; 29pp; English.

CC The invention relates to new recombinant nucleic acids. The invention

CC also relates to a host cell comprising a recombinant nucleic acid or

CC expression vector, an expression vector comprising a recombinant nucleic

CC acid, a recombinant protein, a method of screening for drug candidates, a

CC method of screening for a bioactive agent capable of binding to a

CC carcinoma associated protein (CAP) encoded by a nucleotide sequence, a

CC method of screening for a bioactive agent capable of modulating the

CC activity of a CAP, a method of evaluating the effect of a candidate

CC carcinoma drug, a method of diagnosing carcinomas, a method for inhibiting

CC the activity of a CAP, a method of treating carcinomas, a method of

CC neutralising the effect of a CAP and a method of diagnosing carcinoma or

CC propensity to carcinoma. A method of evaluating the effect of a candidate

CC carcinoma drug comprises administering the drug to a patient, removing a

CC cell sample from the patient and determining alterations in the

CC expression or activation of a gene comprising the nucleotide sequence. A

CC method of diagnosing carcinoma comprises determining the expression of

CC one or more genes comprising the nucleic acid sequence in a first tissue

CC type of a first individual and comparing the expression of the gene from

CC a second normal tissue type from the first individual or a second

CC unaffected individual, where a difference in the expression indicates

CC that the first individual has carcinoma. A method of inhibiting the

CC activity of a CAP comprises binding an inhibitor to the CAP. Treating

CC carcinomas comprises administering to a patient an inhibitor of CAP.

CC Neutralising the effect of a CAP comprises contacting an agent specific

CC for the CAP. The polypeptide specifically binds to the protein encoded by

CC the nucleic acid. It comprises an antibody that specifically binds to the

CC protein encoded by the nucleic acid. The nucleic acids are useful for

CC preparing a composition for diagnosing or treating carcinoma e.g.,

CC leukemia or lymphoma. This sequence represents a murine carcinoma

CC associated (CA) nucleic acid of the invention. Note: The sequence data

CC for this patent did not form part of the printed specification but was

CC obtained in electronic format directly from USPTO at

CC segdata.uspto.gov/sequence.html.

XX Sequence 92726 BP; 23819 A; 19174 C; 20109 G; 27030 T; 0 U; 2594 Other;

```

Query Match      72.2%; Score 13; DB 12; Length 92726;
Best Local Similarity 92.3%; Pred. No. 5.3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCUGGAGNNNNNN 18
      ||:|||||
Db      155 CCTGGAGNNNNNN 143

RESULT 16
ACN44524
ID ACN44524 standard; DNA; 165221 BP.
XX
XX ACN44524;
AC
XX 18-NOV-2004 (first entry)
DT
XX Mouse genomic sequence MCG20599.
DE
XX Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
KM
XX Mus musculus.
OS
XX WO2003073826-A2.
PN
XX 12-SEP-2003.
PD
XX 28-FEB-2003; 2003WO-US006235.
PF
XX 01-MAR-2002; 2002US-00087192.
PR
XX (SAGR-) SAGRES DISCOVERY.
PA
XX Morris DW;
PI
XX WPI; 2003-328604/31.
DR
XX
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
PT
XX
XX Claim 1; SEQ ID NO 1015; Opp; English.
PS
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biolchip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
CC
XX
SQ Sequence 165221 BP; 41378 A; 37617 C; 38634 G; 43338 T; 0 U; 4354 Other;

Query Match      72.2%; Score 13; DB 11; Length 165221;
Best Local Similarity 92.3%; Pred. No. 5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCUGGAGNNNNNN 18
      ||:|||||
Db      59475 CCTGGAGNNNNNN 59487

RESULT 17
ADE82948
ID ADE82948 standard; DNA; 167163 BP.
XX
XX ADE82948;
AC

XX
XX 29-JAN-2004 (first entry)
DT
XX Human PVT1 genomic DNA sequence.
DE
XX
XX human; cancer-associated nucleic acid; screening; cancer; lymphoma;
XX leukemia; breast cancer; gene therapy; vaccine; ds.
KM
XX Homo sapiens.
OS
XX WO2003080808-A2.
PN
XX 02-OCT-2003.
PD
XX 21-MAR-2003; 2003WO-US008919.
PF
XX 21-MAR-2002; 2002US-0367025P.
PR
XX (SAGR-) SAGRES DISCOVERY.
PA
XX Morris DW;
PI
XX WPI; 2003-865119/80.
DR
XX
XX New cancer-associated proteins and nucleic acids, useful for screening
XX for anticancer activity in a potential drug, or for detecting,
XX diagnosing, preventing and treating cancers, e.g. lymphoma, leukemia or
XX breast cancer.
XX
XX Claim 1; SEQ ID NO 32; 248bp; English.
PS
XX
CC The invention comprises human and mouse cancer-associated nucleic acid
CC sequences. The cancer associated nucleic acids of the invention are
CC useful for screening for anticancer activity in a potential drug, as well
CC as detecting, diagnosing, preventing and treating cancers (e.g. lymphoma,
CC leukaemia, or breast cancer). The present sequence represents a cancer-
CC associated nucleic acid of the invention.
CC
XX
SQ Sequence 167163 BP; 39596 A; 36036 C; 39470 G; 45086 T; 0 U; 6975 Other;

Query Match      72.2%; Score 13; DB 10; Length 167163;
Best Local Similarity 92.3%; Pred. No. 5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCUGGAGNNNNNN 18
      ||:|||||
Db      62041 CCTGGAGNNNNNN 62053

RESULT 18
AAT80257
ID AAT80257 standard; DNA; 12 BP.
XX
XX AAT80257;
AC
XX 15-OCT-1997 (first entry)
DT
XX
XX Oligo HCV82 used in luciferase assay.
DE
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
KM
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX modified_base 1..6
XX FT /*tag= a
XX FT /note= "Optionally 2'OME modified"
XX FT modified_base 7..12
XX FT /*tag= b
XX FT /note= "Optionally comprises phosphorothioate linkages"
XX

```



CC and sensitive, reproducible and quantitative detection of one or more  
CC nucleic acids (single or double stranded). The design of primers and  
CC probes is sufficiently flexible to allow many nucleic acids to be  
CC detected in a standardized reaction format using partly the same primers  
CC and probes. Only small amplicons are produced (requiring short  
CC amplification cycles), there is no competition/displacement between the  
CC short counter-strand of the amplicon and the detection probe, and  
CC specificity is high because the relative proportion of the internal  
CC detection region is increased with respect to the total amplicon length,  
CC allowing better differentiation between (viral) subtypes. Also short  
CC amplicons are less likely to undergo non-specific hybridization, so  
CC background is low, and short RNA sequences are more stable, with reduced  
CC tendency to form secondary structures. AAX23968-69 and AAX24035-37 are  
CC PCR primers and probes used in the method of the invention

XX  
SQ Sequence 12 BP; 2 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 12;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUUGAG 12  
Db 12 GGGGTCCTGGAG 1

RESULT 21  
ABS65841  
ID ABS65841 standard; RNA; 12 BP.  
XX  
AC ABS65841;  
XX  
DT 15-NOV-2002 (first entry)

XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #47.

XX  
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KM gene therapy; ss.

XX  
OS Synthetic.

XX  
PN US2002081577-A1.

XX  
PD 27-JUN-2002.

XX  
PF 02-JUL-1997; 97US-00887505.

XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.

XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.

XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
XX WPI; 2002-537132/57.

XX  
PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.

XX  
PS Claim 1; Page 61; 74pp; English.

XX  
CC The invention describes synthetic oligonucleotides complementary to a

CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic oligonucleotide used for inhibiting HCV  
CC replication and expression of HCV

XX  
SQ Sequence 12 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUUGAG 12  
Db 1 GGGGUCUUGAG 12

RESULT 22  
AAQ70177/C  
ID AAQ70177 standard; RNA; 14 BP.  
XX  
AC AAQ70177;  
XX  
DT 16-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 04-OCT-1994 (first entry)

XX  
DE Hepatitis C virus 5'-UTR antisense oligonucleotide target (A).

XX  
KM Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBH;  
KM antisense oligonucleotide; translation inhibition; therapy;  
KM 5'-untranslated region; ss.

XX  
OS Hepatitis C virus; Virus.

XX  
PN WO9405813-A1.

XX  
PD 17-MAR-1994.

XX  
PF 10-SEP-1993; 93MO-JP001293.

XX  
PR 10-SEP-1992; 92US-00945289.  
PR 14-APR-1993; 93JP-00087195.

XX  
PA (MOCH) MOCHIDA PHARM CO LTD.  
PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.  
PA (ISIS-) ISIS PHARM INC.

XX  
PI Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;  
PI Nakatake H, Hamada F, Eto T, Furukawa S;  
XX  
XX WPI; 1994-101217/12.

XX  
PT Anti-sense oligonucleotide(s) complementary to hepatitis C viral genome  
PT - useful for inhibiting HCV replication, to treat related diseases.

XX  
PS Claim 16; Page 71; 91pp; English.

XX  
CC Oligonucleotides which are complementary to part of the hepatitis C virus  
CC genomic or messenger RNA are claimed. AAQ70177 is a preferred target  
CC sequence which is present in the 5'-UTR of the HCV genome. (Updated on 25  
CC -MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS  
CC field)

XX  
SQ Sequence 14 BP; 2 A; 8 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCUCUGAG 12  
 ||||:||||  
 Db 14 GGGGTCCTGAG 3

RESULT 23  
 AA065140  
 ID AA065140 standard; DNA; 15 BP.  
 XX  
 AC AA065140;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 PD 26-FEB-1994.  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 163; 262pp; English.  
 XX  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 15 BP; 1 A; 2 C; 10 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 2; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCUCUGAG 12  
 ||||:||||  
 Db 4 GGGGTCCTGAG 15

RESULT 24  
 ABX01805/c  
 ID ABX01805 standard; RNA; 15 BP.  
 XX  
 AC ABX01805;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Hepatitis C virus (HCV) ribozyme related RNA sequence #74.  
 DE Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 XX  
 KM

KM HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KM liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KM type I interferon; interferon alpha; interferon beta; cytostatic; ss;  
 KM interferon gamma; consensus interferon; hepatotropic; antiinflammatory.  
 XX  
 OS Unidentified.  
 XX  
 PN US2002082225-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 23-MAR-1999; 99US-00274553.  
 XX  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Moswigen JA, Roberts B, Pavco PA, Macejack D;  
 XX  
 DR WPI; 2002-617759/66.  
 XX  
 PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 PT replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 XX  
 PS Disclosure; SEQ ID NO 1587; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of  
 CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more  
 CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a RNA sequence of unknown function. Note: The present  
 CC sequence is given in the sequence data but is not mentioned elsewhere in  
 CC the specification. The complete sequence data for this patent was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdIDentry.html  
 XX  
 SQ Sequence 15 BP; 3 A; 8 C; 3 G; 0 T; 1 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 6; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCUCUGAG 12  
 ||||:||||  
 Db 15 GGGGTCCTGAG 4

RESULT 25  
 AA065141  
 ID AA065141 standard; DNA; 16 BP.  
 XX  
 AC AA065141;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 DE Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.



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XX CA2104649-A.
PN
XX
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX
XX Seki M, Honda Y, Yamada E;
PI
XX
XX WPI; 1994-151836/19.
DR
XX
XX Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 163; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
CC
XX
XX Sequence 16 BP; 2 A; 2 C; 10 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 16;
XX Best Local Similarity 83.3%; Pred. No. 3.5e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGGUCGAG 12
DB 5 GGGGCTCTCGAG 16
XX
XX
XX RESULT 26
XX AA065125
XX ID AA065125 standard; DNA; 16 BP.
XX
XX AA065125;
AC
XX
XX 21-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX
XX CA2104649-A.
PN
XX
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX
XX Seki M, Honda Y, Yamada E;
PI
XX
XX WPI; 1994-151836/19.
DR
XX
XX Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 156; 262pp; English.
PS
```

```
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
CC
XX
XX Sequence 16 BP; 1 A; 2 C; 11 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 16;
XX Best Local Similarity 83.3%; Pred. No. 3.5e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGGUCGAG 12
DB 4 GGGGCTCTCGAG 15
XX
XX
XX RESULT 27
XX AAT90622
XX ID AAT90622 standard; RNA; 16 BP.
XX
XX AAT90622;
AC
XX
XX 07-APR-1998 (first entry)
DT
XX
XX Hepatitis C virus recognition sequence 32 for ribozyme cleavage.
DE
XX
XX Recognition sequence; HCV; ribozyme; 5' untranslated region;
KM nucleocapsid coding region; hairpin ribozyme; RNA cleavage; treatment;
KM HCV infection; HCV contamination; ss.
XX
XX Hepatitis C virus.
OS
XX
XX Key Location/Qualifiers
XX FH 1..4
XX FT misc_feature /*tag= a
XX FT /note= "complementary to the CNR2 ribozyme"
XX FT misc_feature 6
XX FT /*tag= b
XX FT /note= "cleavage site corresponding to position 120 of
XX FT the (-) strand, counting from 3' end"
XX FT misc_feature 9..16
XX FT /*tag= c
XX FT /note= "complementary to the CNR2 ribozyme"
XX
XX WO9732018-A2.
XX
XX 04-SEP-1997.
PD
XX
XX 27-FEB-1997; 97WO-US003304.
PF
XX 29-FEB-1996; 96US-00608862.
PR
XX
XX (IMMU-) IMMUSOL INC.
PA
XX
XX Barber JR, Welch PJ, Tritz R, Yel S, Yu M;
PI
XX
XX WPI; 1997-470461/43.
DR
XX
XX Ribozyme(s) directed against hepatitis C virus - for prevention and
PT treatment of viral infection, and detection of HCV contamination of
PT blood.
XX
XX Example 1; Page 17; 98pp; English.
PS
XX
XX AAT90621-650 represent recognition sequences found in the positive (-)
CC strand of the Hepatitis C virus (HCV) RNA. The sequences are recognised
CC by novel ribozymes which inhibit replication, infectivity or gene
CC expression of HCV. The present sequence is located within the 5' UTR.
CC Hairpin ribozymes of the present invention were designed based on
CC sequences adjacent to the GUC sequence recognition feature. The ribozymes
```

CC are directed against conserved regions of the genome and so should be  
 CC active against many strains of HCV. The ribozymes, when optionally  
 CC expressed from a vector, cleave the RNA of HCV and so are useful for  
 CC treatment and prevention of HCV infection. They can also be used to  
 CC detect HCV contamination of blood or for clinical diagnosis

XX  
 SQ Sequence 16 BP; 1 A; 3 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
 |||||  
 3 GGGGUCUCGAG 14

RESULT 28  
 ID AAA13439 standard; RNA; 16 BP.  
 XX  
 AC AAA13439;  
 XX  
 DT 17-JUL-2000 (first entry)  
 XX

DE Hepatitis C virus hairpin ribozyme recognition sequence SEQ ID NO:39.  
 KW Hepatitis C virus; HCV; hairpin ribozyme; cleavage; recognition site;  
 KM infection; virucide; hepatotropic; antiinflammatory;  
 XX replication inhibitor; gene expression inhibitor; ss.  
 OS Hepatitis C virus.  
 XX

PN US6043077-A.  
 XX  
 PD 28-MAR-2000.  
 XX  
 PF 20-OCT-1997; 97US-00954210.  
 XX  
 PR 29-FEB-1996; 97US-00608862.  
 XX 27-FEB-1997; 97WO-US003304.  
 PA (IMMU-) IMMUSOL INC.  
 XX

PI Tritz R, Yei S, Yu M, Barber JR, Welch PJ;  
 XX  
 DR WPI; 2000-270342/23.

PT Ribozyme capable of inhibiting replication, infectivity or gene  
 expression of hepatitis C virus, useful for treating or preventing  
 PT hepatitis C virus infection.  
 XX

PS Claim 1; Col 13; 57pp; English.

XX The present invention describes ribozymes (I) capable of inhibiting  
 CC replication, infectivity or gene expression of a hepatitis C virus (HCV),  
 CC directed to target sequences AAA13438 to AAA13444, AAA13454 and AAA13465.  
 CC (I) have virucide, hepatotropic and antiinflammatory activities. (I), or  
 CC vectors comprising nucleotide sequences encoding (I), are useful for  
 CC interfering with the replication or gene expression of HCV in a human  
 CC cells. (I) are useful for diagnosis, prevention and treatment of HCV  
 CC infection or disease in a mammals especially humans. Nucleotide sequences  
 CC encoding (I) are useful for preventing hepatitis C viral infection in a  
 CC cell. AAA13401 to AAA13405 represent examples of the briefest  
 CC requirements for hairpin ribozyme; AAA13406 and AAA13407 represent PCR  
 CC primers used in the amplification of the HCV capsid sequence; AAA13408 to  
 CC AAA13467 represent HCV hairpin ribozyme recognition sites; and AAA13468  
 CC to AAA13473 represent oligonucleotides used in the construction of HCV  
 CC hairpin ribozymes, all these sequences are used in the exemplification of  
 CC the present invention

XX Sequence 16 BP; 1 A; 3 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 3; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
 |||||  
 3 GGGGUCUCGAG 14

RESULT 29  
 ID ABX74358 standard; RNA; 16 BP.  
 XX  
 AC ABX74358;  
 XX  
 DT 24-MAR-2003 (first entry)  
 XX

DE Hepatitis C recognition sequence for ribozyme CN2.  
 KW Hairpin ribozyme; ss; hepatitis C infection; HCV; gene therapy; virucide.  
 XX  
 OS Hepatitis C virus.  
 XX

PN US6458567-B1.  
 XX  
 PD 01-OCT-2002.  
 XX  
 PF 01-NOV-1999; 99US-00431419.  
 XX  
 PR 29-FEB-1996; 96US-00608862.  
 XX 20-OCT-1997; 97US-00954210.  
 PA (IMMU-) IMMUSOL INC.  
 XX

PI Barber JR, Welch PJ, Tritz R, Yei S, Yu M;  
 XX  
 DR WPI; 2003-15536/15.

PT New ribozyme having the ability to inhibit replication, infectivity or  
 PT gene expression of a Hepatitis C Virus (HCV), useful for treating or  
 PT preventing HCV infection.  
 XX

PS Example 1; Col 12; 48pp; English.

XX The invention relates to a new ribozyme with the ability to inhibit  
 CC replication, infectivity or gene expression of a Hepatitis C Virus (HCV)  
 CC by cleaving the positive strand genomic RNA of HCV at a sequence having  
 CC 16 bp. Also included are a nucleic acid encoding the ribozyme, a host  
 CC cell containing the ribozyme or vector, a vector comprising a promoter  
 CC operably linked to the nucleic acid, producing a ribozyme, interfering  
 CC with HCV replication or gene expression in a cell infected in a cell  
 CC culture with HCV or a composition comprising the ribozyme and a carrier  
 CC or diluent. The ribozyme is useful for treating or preventing HCV  
 CC infection. The present sequence is an HCV -ve strand recognition sequence  
 CC for a ribozyme of the invention

XX Sequence 16 BP; 1 A; 3 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
 |||||  
 3 GGGGUCUCGAG 14

RESULT 30  
 ID AAO65126 standard; DNA; 17 BP.  
 XX  
 AC AAO65126;  
 XX

XX Sequence 16 BP; 1 A; 3 C; 10 G; 0 T; 2 U; 0 Other;

DT 21-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
FN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 157; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 17 BP; 2 A; 2 C; 11 G; 2 T; 0 U; 0 Other;  
OY  
Query Match 66.7%; Score 12; DB 2; Length 17;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGCCUGAG 12  
Db 5 GGGGTCCTGGAG 16  
RESULT 31  
AA065142  
ID AA065142 standard; DNA; 17 BP.  
XX  
AC AA065142;  
XX  
DT 21-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
FN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX

PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 164; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 17 BP; 2 A; 2 C; 11 G; 2 T; 0 U; 0 Other;  
OY  
Query Match 66.7%; Score 12; DB 2; Length 17;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGCCUGAG 12  
Db 6 GGGGTCCTGGAG 17  
RESULT 32  
AA065111  
ID AA065111 standard; DNA; 17 BP.  
XX  
AC AA065111;  
XX  
DT 21-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
FN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 150; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 17 BP; 1 A; 3 C; 11 G; 2 T; 0 U; 0 Other;  
OY  
Query Match 66.7%; Score 12; DB 2; Length 17;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGCCUGAG 12  
Db 6 GGGGTCCTGGAG 17

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 4 GGGGCTCTGGAG 15

RESULT 33  
 ACD65845  
 ID ACD65845 standard; RNA, 17 BP.  
 AC ACD65845;  
 XX  
 DT 30-SEP-2003 (first entry)  
 DE HCV minus strand DNAzyme substrate sequence #2252.

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;  
 KW amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.

XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.

XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEBP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.

PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.

PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.

PS Claim 1; Page 315; 387pp; English.

CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAses,  
 CC inozymes, zinzymes, amberyzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNAzyme or minus strand DNAzyme sequences disclosed in the present  
 CC invention

XX  
 SQ Sequence 17 BP; 2 A; 2 C; 11 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 6 GGGGCTCTGGAG 17

RESULT 34  
 ACD56830/C  
 ID ACD56830 standard; RNA, 17 BP.  
 AC ACD56830;  
 XX  
 DT 23-SEP-2003 (first entry)  
 DE HCV DNAzyme substrate sequence #26.

XX  
 OS Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;  
 KW amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.

XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.

XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEBP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.

PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.

PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.

PS Claim 1; Page 234; 387pp; English.

CC The present invention relates to nucleic acid molecules which modulate



QY 1 GGGGUCUCCUGAG 12  
 DB 6 GGGGUCUCCUGAG 17

## RESULT 37

AD182780/c  
 ID AD182780 standard; RNA, 17 BP.

AC AD182780;

DT 03-JUN-2004 (first entry)

XX HCV DNAzyme substrate sequence #26.

XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KM HCV infection; type I interferon; DNAzyme.

OS Hepatitis C virus.

PN US2003125270-A1.

PD 03-JUL-2003.

PF 18-DEC-2000; 2000US-00740332.

PR 18-DEC-2000; 2000US-00740332.

PA (BLAT/) BLATT L.

PA (MCSM/) MCSWIGGEN J.

PA (ROBE/) ROBERTS E.

PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

PI Blact L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

DR WPI; 2004-031273/03.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived

PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,

PT especially in combination with type I interferon therapy.

XX Claim 1; SEQ ID NO 26; 198bp; English.

PS The invention relates to an enzymatic nucleic acid molecule which

CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which

CC the binding arms of the enzymatic nucleic acid molecule comprises

CC sequences complementary to any of the defined substrate sequences given

CC in the specification. The nucleic acid molecule may be administered for

CC the treatment of HCV infections, especially in combination with type I

CC interferons. The present sequence represents a HCV DNAzyme substrate

CC sequence.

XX Sequence 17 BP; 2 A; 11 C; 2 G; 0 T; 2 U; 0 Other;

QY Query Match 66.7%; Score 12; DB 12; Length 17;

XX Best Local Similarity 83.3%; Pred. No. 3.5e+03;

XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1 GGGGUCUCCUGAG 12

13 GGGGTCCTCGAG 2

## RESULT 38

AA065127

ID AA065127 standard; DNA, 18 BP.

AC AA065127;

XX 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;

KM inhibition; viral protein precursor; ss.

XX Synthetic.

XX CA2104649-A.

PN 26-FEB-1994.

PD 23-AUG-1993; 93CA-02104649.

PF 25-AUG-1992; 92JP-00248796.

PR 03-MAR-1993; 93JP-00042736.

XX (SEKI/) SEKI M.

XX Seki M, Honda Y, Yamada E;

PI WPI; 1994-151836/19.

DR Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus

XX genome - are useful as antiviral agents.

PT Claim 5; Page 157; 262pp; English.

PS This oligonucleotide is an example of a preferred antisense compound i.e.

XX it has a base sequence of 15-30 bases which is included within the 49

CC bases from G at position 127 to C at position 175 of AA064913 and which

CC contains at least 7 bases from C at position 147 to C at position 153.

CC The antisense oligonucleotide is useful for inhibiting translation of HCV

CC genes

XX Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 U; 0 Other;

SQ Query Match 66.7%; Score 12; DB 2; Length 18;

XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;

XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCCUGAG 12

6 GGGGTCCTCGAG 17.

DB RESULT 39

AA065112

ID AA065112 standard; DNA, 18 BP.

XX AA065112;

AC 21-DEC-1994 (first entry)

XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;

XX inhibition; viral protein precursor; ss.

XX Synthetic.

XX CA2104649-A.

PN 26-FEB-1994.

XX 23-AUG-1993; 93CA-02104649.

XX 25-AUG-1992; 92JP-00248796.

XX 03-MAR-1993; 93JP-00042736.

XX (SEKI/) SEKI M.

XX Seki M, Honda Y, Yamada E;

XX PI

DR WPI; 1994-151836/19.  
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
XX  
PS Claim 5; Page 151; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 18 BP; 2 A; 3 C; 11 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCCUGAG 12  
DB 5 GGGGTCTCGAG 16  
RESULT 40  
AA065098  
ID AA065098 standard; DNA; 18 BP.  
XX  
XX AA065098;  
AC  
XX  
DT 20-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
PN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
XX  
PS Claim 5; Page 144; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 18 BP; 1 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCUGAG 12  
DB 4 GGGGTCTCGAG 15  
RESULT 41  
AA065143  
ID AA065143 standard; DNA; 18 BP.  
XX  
AC AA065143;  
XX  
DT 21-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
PN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
XX  
PS Claim 5; Page 164; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCCUGAG 12  
DB 7 GGGGTCTCGAG 18  
RESULT 42  
AAT80255  
ID AAT80255 standard; DNA; 18 BP.  
XX  
AC AAT80255;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV61, targeted to HCV region +4 to +9.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.

XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..12
FT		/tag= a
FT		/note= "2'Ome modified"
FT	modified_base	13..18
FT		/tag= b
FT		/note= "Phosphorothioate linkages"
PN	WO9639500-A2.	
XX		
PD	12-DEC-1996.	
XX		
PF	04-JUN-1996;	96WO-EPO02427.
XX		
PR	06-JUN-1995;	95US-00471968.
XX		
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.	
PA	(HYBR-) HYBRIDON INC.	
XX		
PI	Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;	
PI	Roberts PC, Walthers DM, Wolfe JL,	
DR	WPI; 1997-043122/04.	
XX		
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in	
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-	
PT	carcinoma.	
PS	Claim 19; Page 31; 100pp; English.	
XX		
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides	
CC	which are complementary to a portion of the 5' untranslated region (UTR)	
CC	of hepatitis C virus (HCV). These sequences may be used in a	
CC	pharmaceutical composition for the control or prevention of HCV	
CC	infection. They may be used to inhibit replication or expression of HCV	
CC	or for detecting the presence of HCV in a sample. They may be used to	
CC	inhibit HCV replication in a cell and are therefore useful in the	
CC	treatment of HCV infections such as chronic and acute hepatitis and	
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine	
CC	whether it binds successfully to its target	
SQ	Sequence 18 BP; 1 A; 4 C; 9 G; 2 T; 2 U; 0 Other;	
	Query Match	66.7%; Score 12; DB 2; Length 18;
	Best Local Similarity	100.0%; Pred.No. 3.4e+03;
	Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GGCGUCGUGAG 12	
DB	1 GGCGUCGUGAG 12	
RESULT 43		
ID	AAT80250	
AC	AAT80250 standard; DNA; 18 BP.	
XX		
AC	AAT80250;	
DT	15-OCT-1997 (first entry)	
XX		
DE	Oligo HCV54, targeted to HCV region -9 to -4.	
XX		
KV	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;	
KW	Inhibition; replication; expression; detection; chronic hepatitis;	
KW	acute hepatitis; hepatocarcinoma; ss.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..6
FT		/tag= b
FT		/note= "Phosphorothioate linkages"

FT	modified_base	7..18
FT	/tag=	a
FT	/note=	"2'OME modified"
PN	WO9639500-A2.	
XX		
XX	12-DEC-1996.	
PD		
XX		
PX	04-JUN-1996;	96MO-BP002427.
PR	06-JUN-1995;	95US-00471968.
XX		
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.	
PA	(HYBR-) HYBRIDON INC.	
XX		
PI	Frank BL, Goodchild J, Hamlin HA, Kilukie RE, Roberts NA;	
PI	Roberts PC, Walther DM, Wolfe JL,	
XX		
DR	WPI, 1997-043122/04.	
XX		
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in	
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-	
PT	carcinoma.	
XX		
PS	Claim 19; Page 31; 100pp; English.	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides	
CC	which are complementary to a portion of the 5' untranslated region (UTR)	
CC	of hepatitis C virus (HCV). These sequences may be used in a	
CC	pharmaceutical composition for the control or prevention of HCV	
CC	infection. They may be used to inhibit replication or expression of HCV	
CC	or for detecting the presence of HCV in a sample. They may be used to	
CC	inhibit HCV replication in a cell and are therefore useful in the	
CC	treatment of HCV infections such as chronic and acute hepatitis and	
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine	
CC	whether it binds successfully to its target	
SQ	Sequence 18 BP; 2 A; 4 C; 10 G; 0 T; 2 U; 0 Other;	
XX		
QY	Query Match	66.7%; Score 12; DB 2; Length 18;
	Best Local Similarity	100.0%; Pred. No. 3.4e+03;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	1 GGGGUCCTCGAG 12	
	7 GGGGUCCTCGAG 18	
DB		
RESULT 44		
AAT80261		
ID	AAT80261 standard; DNA; 18 BP.	
AC	AAT80261;	
XX		
DT	15-OCT-1997 (first entry)	
XX		
DE	Oligo HCV93, targeted to HCV region +1 to +6.	
XX		
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;	
KW	inhibition; replication; expression; detection; chronic hepatitis;	
XX	acute hepatitis; hepatocarcinoma; ss.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..12
FT	/tag=	a
FT	/note=	"2'OME modified"
FT	modified_base	13..18
FT	/tag=	b
XX	/note=	"Phosphothioate linkages"
NN	WO9639500-A2.	



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XX 12-DEC-1996.
PD 04-JUN-1996; 96WO-EP002427.
PF 06-JUN-1995; 95US-00471968.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
PA Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walthers DM, Wolfe JL;
XX WPI; 1997-043122/04.
DR
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
XX Sequence 18 BP; 2 A; 4 C; 8 G; 2 T; 2 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGCGAG 12
DB 1 GGGGUCGCGAG 12

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PR 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
PA Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walthers DM, Wolfe JL;
XX WPI; 1997-043122/04.
DR
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
XX Sequence 18 BP; 2 A; 3 C; 9 G; 2 T; 2 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGCGAG 12
DB 1 GGGGUCGCGAG 12

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RESULT 45
AAT80253
ID AAT80253 standard; DNA; 18 BP.
XX
XX AAT80253;
XX
XX 15-OCT-1997 (first entry)
XX
XX Oligo HCV59, targeted to HCV region -3 to +3.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..12 /*tag= a
XX modified_base 13..18 /*note= "2'OME modified"
XX modified_base 13..18 /*tag= b
XX /*note= "Phosphorothioate linkages"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX
XX

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RESULT 46
AAT80256
ID AAT80256 standard; DNA; 18 BP.
XX
XX AAT80256;
XX
XX 15-OCT-1997 (first entry)
XX
XX Oligo HCV62, targeted to HCV region +4 to +9.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..6 /*tag= b
XX modified_base 7..18 /*note= "Phosphorothioate linkages"
XX modified_base 7..18 /*tag= a
XX modified_base 7..18 /*note= "2'OME modified"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX

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PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
XX	
PS	Claim 19; Page 32; 100pp; English.
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmaceutical composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC	whether it binds successfully to its target
XX	
SQ	Sequence 18 BP, 2 A; 3 C; 8 G; 3 T; 2 U; 0 Other;
Query Match	66.7%; Score 12; DB 2; Length 18;
Best Local Similarity	100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 GGCGUCCUGGAG 12       
Db	7 GGCGUCCUGGAG 18
RESULT 48	
ID	AAT80353
XX	AAT80353 standard; DNA; 18 BP.
AC	
XX	AAT80353;
DJ	
DT	16-OCT-1997 (first entry)
XX	
DE	Oligo HCV-205, targeted to HCV mRNA position +20 to +25.
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	inhibition; replication; expression; detection; chronic hepatitis;
XX	acute hepatitis; hepatocarcinoma; su.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	modified_base 1..6
FT	/*tag= b
FT	/note= "Comprises phosphorothioate linkages"
FT	modified_base 7..18
FT	/*tag= a
FT	/note= "2'-OME RNA"
XX	
PN	WO9639500-A2.
PD	
PD	12-DEC-1996.
XX	
PF	04-JUN-1996; 96MO-BP002427.
PR	
PR	06-JUN-1995; 95US-00471968.
PA	(HOFF ) HOFFMANN IA ROCHE & CO AG F.
PA	(HYBR-) HYBRIDON INC.
PI	Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI	Roberts PC, Walther DM, Wolfe JL;
DR	
WI	WPI; 1997-043122/04.
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
XX	
XX	Claim 20; Page 20; 100pp; English.

XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the  
 CC HCV genome. This sequence is anchored at position -219 to -230 and is  
 CC targeted to position +20 to +25

XX  
 SQ Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 2 U; 0 Other;

QY Query Match 66.7%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGGGUCGCGAG 12  
 7 GGGGUCGCGAG 18

RESULT 49  
 AAT80355  
 ID AAT80355 standard; DNA; 18 BP.  
 XX  
 AC AAT80355;  
 XX  
 DT 16-OCT-1997 (first entry)  
 XX  
 DE Oligo HCV-213, targeted to HCV mRNA position +230 to +235.

XX  
 KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..12  
 FT /\*tag= a  
 FT /note= "2'-Ome RNA"  
 FT modified\_base 13..18  
 FT /\*tag= b  
 FT /note= "Comprises phosphorothioate linkages"

XX  
 PN W09639500-A2.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96WO-EP002427.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 XX  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 DR WPI; 1997-043122/04.  
 XX  
 PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 PT carcinoma.  
 XX  
 PS Claim 20; Page 20; 100pp; English.  
 XX  
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the  
 CC HCV genome. This sequence is anchored at position -219 to -230 and is  
 CC targeted to position +20 to +25

CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the  
 CC HCV genome. This sequence is anchored at position -219 to -230 and is  
 CC targeted to position +230 to +235

XX  
 SQ Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;

QY Query Match 66.7%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGGGUCGCGAG 12  
 1 GGGGUCGCGAG 12

RESULT 50  
 AAT80263  
 ID AAT80263 standard; DNA; 18 BP.  
 XX  
 AC AAT80263;  
 XX  
 DT 15-OCT-1997 (first entry)  
 XX  
 DE Oligo HCV96, targeted to HCV region +7 to +12.

XX  
 KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..12  
 FT /\*tag= a  
 FT /note= "2'-Ome modified"  
 FT modified\_base 13..18  
 FT /\*tag= b  
 FT /note= "Phosphorothioate linkages"

XX  
 PN W09639500-A2.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96WO-EP002427.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 XX  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 DR WPI; 1997-043122/04.  
 XX  
 PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 PT carcinoma.  
 XX  
 PS Claim 19; Page 32; 100pp; English.  
 XX  
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the

CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
SQ Sequence 18 BP; 2 A; 3 C; 8 G; 3 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
DB 1 GGGGUCUCGAG 12  
RESULT 51  
ID AAT80357 standard; DNA; 18 BP.  
AC AAT80357;  
XX 16-OCT-1997 (first entry)  
DT Oligo HCV-219, targeted to HCV mRNA position +240 to +245.  
DE  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..12  
FT /\*tag= a  
FT /note= "2'-Ome RNA"  
FT 13..18  
FT /\*tag= b  
FT /note= "Comprises phosphorothioate linkages"  
XX  
PN MO9639500-A2.  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOF) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 20; Page 20; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the  
CC HCV genome. This sequence is anchored at position -219 to -230 and is  
CC targeted to position +240 to +245  
XX

SQ Sequence 18 BP; 3 A; 2 C; 10 G; 1 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
DB 1 GGGGUCUCGAG 12  
RESULT 52  
ID AAT80254 standard; DNA; 18 BP.  
AC AAT80254;  
XX 15-OCT-1997 (first entry)  
DT Oligo HCV60, targeted to HCV region -3 to +3.  
DE  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..6  
FT /\*tag= b  
FT /note= "Phosphorothioate linkages"  
FT 7..18  
FT /\*tag= a  
FT /note= "2'Ome modified"  
XX  
PN MO9639500-A2.  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOF) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 19; Page 31; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 18 BP; 2 A; 3 C; 9 G; 2 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
 DB 7 GGGGUCGAG 18

## RESULT 53

AA80252 standard; DNA; 18 BP.

AA80252;

15-OCT-1997 (first entry)

Oligo HCV56, targeted to HCV region +10 to +15.

Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 inhibition; replication; expression; detection; chronic hepatitis;  
 acute hepatitis; hepatocarcinoma; ss.

Synthetic.

Key Location/Qualifiers

modified\_base

/tag= b  
 /note= "Phosphorothioate linkages"

modified\_base

/tag= a  
 /note= "2'-Ome modified"

WO9639500-A2.

12-DEC-1996.

04-JUN-1996; 96WO-EP002427.

06-JUN-1995; 95US-00471968.

(HOFF-) HOFFMANN LA ROCHE & CO AG F.

(HYBR-) HYBRIDON INC.

Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;

Roberts PC, Walther DM, Wolfe JL;

WPI; 1997-043122/04.

Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 carcinoma.

Claim 19; Page 31; 100pp; English.

The sequences given in AA80211-382 represent synthetic oligonucleotides  
 which are complementary to a portion of the 5' untranslated region (UTR)  
 of hepatitis C virus (HCV). These sequences may be used in a  
 pharmaceutical composition for the control or prevention of HCV  
 infection. They may be used to inhibit replication or expression of HCV  
 or for detecting the presence of HCV in a sample. They may be used to  
 inhibit HCV replication in a cell and are therefore useful in the  
 treatment of HCV infections such as chronic and acute hepatitis and  
 hepatocarcinoma. This oligo was used in a luciferase assay to determine  
 whether it binds successfully to its target

Sequence 18 BP; 3 A; 2 C; 9 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

DB 7 GGGGUCGAG 18

RESULT 54  
 AA80352 standard; DNA; 18 BP.

AA80352;

16-OCT-1997 (first entry)

Oligo HCV-201, targeted to HCV mRNA position +15 to +20.

Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 inhibition; replication; expression; detection; chronic hepatitis;  
 acute hepatitis; hepatocarcinoma; ss.

Synthetic.

Key Location/Qualifiers

modified\_base

/tag= b  
 /note= "Comprises phosphorothioate linkages"

modified\_base

/tag= a  
 /note= "2'-Ome RNA"

WO9639500-A2.

12-DEC-1996.

04-JUN-1996; 96WO-EP002427.

06-JUN-1995; 95US-00471968.

(HOFF-) HOFFMANN LA ROCHE & CO AG F.

(HYBR-) HYBRIDON INC.

Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;

Roberts PC, Walther DM, Wolfe JL;

WPI; 1997-043122/04.

Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 carcinoma.

Claim 20; Page 20; 100pp; English.

The sequences given in AA80211-382 represent synthetic oligonucleotides  
 which are complementary to a portion of the 5' untranslated region (UTR)  
 of hepatitis C virus (HCV). These sequences may be used in a  
 pharmaceutical composition for the control or prevention of HCV  
 infection. They may be used to inhibit replication or expression of HCV  
 or for detecting the presence of HCV in a sample. They may be used to  
 inhibit HCV replication in a cell and are therefore useful in the  
 treatment of HCV infections such as chronic and acute hepatitis and  
 hepatocarcinoma. This sequence binds to two non-contiguous regions of the  
 HCV genome. This sequence is anchored at position -219 to -230 and is  
 targeted to position +15 to +20

Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

DB 7 GGGGUCGAG 18

## RESULT 55

AA80249 standard; DNA; 18 BP.

```

XX AC AAT80249;
XX XX 15-OCT-1997 (first entry)
XX DE Oligo HCV53, targeted to HCV region -9 to -4.
XX KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KM inhibition; replication; expression; detection; chronic hepatitis;
XX KM acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT modified_base 1..12
XX FT /*tag= a
XX FT /note= "Optionally 2' OMe modified"
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walthers DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 19; Page 31; 100pp; English.
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX CC whether it binds successfully to its target
XX SQ Sequence 18 BP; 2 A; 4 C; 10 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUCUGAG 12
Db 1 GGGGUCUCUGAG 12

```

```

XX KM inhibition; replication; expression; detection; chronic hepatitis;
XX KM acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT modified_base 1..12
XX FT /*tag= a
XX FT /note= "2'-OMe RNA"
XX FT modified_base 13..18
XX FT /*tag= b
XX FT /note= "Comprises phosphorothioate linkages"
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walthers DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 20; Page 20; 100pp; English.
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the
XX CC HCV genome. This sequence is anchored at position -219 to -230 and is
XX CC targeted to position +235 to +240
XX SQ Sequence 18 BP; 2 A; 5 C; 9 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUCUGAG 12
Db 1 GGGGUCUCUGAG 12

```

```

RESULT 56
AAT80356
ID AAT80356 standard; DNA; 18 BP.
XX AAT80356;
XX 16-OCT-1997 (first entry)
XX Oligo HCV-216, targeted to HCV mRNA position +235 to +240.
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX Synthetic.

```

```

RESULT 57
AAT80251
ID AAT80251 standard; DNA; 18 BP.
XX AAT80251;
XX 15-OCT-1997 (first entry)
XX Oligo HCV55, targeted to HCV region +10 to +15.
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX Synthetic.

```

```

XX Key Location/Qualifiers
FH modified_base 1..12
FT /*tag= a
FT /note= "2'Ome modified"
FT modified_base 13..18
FT /*tag= b
FT /note= "Phosphorothioate linkages"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOF ) HOFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX whether it binds successfully to its target
XX
XX Sequence 18 BP; 3 A; 2 C; 9 G; 2 T; 2 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGUGAG 12
Db 1 GGGGUCGUGAG 12
XX
XX RESULT 58
XX AAT80351
XX ID AAT80351 standard; DNA; 18 BP.
XX
XX AAT80351;
XX
XX 16-OCT-1997 (first entry)
XX
XX Oligo HCV-197, targeted to HCV mRNA position -18 to -13.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..6
XX /*tag= b
XX /note= "Comprises phosphorothioate linkages"
FT

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```

FT modified_base 7..18
FT /*tag= a
FT /note= "2'-Ome RNA"
FT
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOF ) HOFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 20; Page 20; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This sequence binds to two non-contiguous regions of the
XX HCV genome. This sequence is anchored at position -219 to -230 and is
XX targeted to position -18 to -13
XX
XX Sequence 18 BP; 4 A; 3 C; 9 G; 0 T; 2 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGUGAG 12
Db 7 GGGGUCGUGAG 18
XX
XX RESULT 59
XX AAT80259
XX ID AAT80259 standard; DNA; 18 BP.
XX
XX AAT80259;
XX
XX 15-OCT-1997 (first entry)
XX
XX Oligo HCV90, targeted to HCV region -1 to -6.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..12
XX /*tag= a
XX /note= "2'Ome modified"
FT
XX modified_base 13..18
XX /*tag= b
XX /note= "Phosphorothioate linkages"
FT

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PN WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX Roberts PC, Walthers DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX whether it binds successfully to its target
XX
XX Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGGUCUCUGAG 12
XX 1 GGGGUCUCUGAG 12
XX
XX Db
XX
XX RESULT 60
XX AAT80260
XX ID AAT80260 standard; DNA; 18 BP.
XX
XX AAT80260;
XX
XX 15-OCT-1997 (first entry)
XX
XX Oligo HCV91, targeted to HCV region -1 to -6.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..6
XX FT /tag= b
XX FT /note= "Phosphorothioate linkages"
XX modified_base 7..18
XX FT /tag= a
XX FT /note= "2'-Ome modified"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.

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XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX Roberts PC, Walthers DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX whether it binds successfully to its target
XX
XX Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGGUCUCUGAG 12
XX 7 GGGGUCUCUGAG 18
XX
XX Db
XX
XX RESULT 61
XX AAT80354
XX ID AAT80354 standard; DNA; 18 BP.
XX
XX AAT80354;
XX
XX 16-OCT-1997 (first entry)
XX
XX Oligo HCV-209, targeted to HCV mRNA position +25 to +30.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..6
XX FT /tag= b
XX FT /note= "Comprises phosphorothioate linkages"
XX modified_base 7..18
XX FT /tag= a
XX FT /note= "2'-Ome RNA"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.

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XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 20; Page 20; 100pp; English.
XX
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the
CC HCV genome. This sequence is anchored at position -219 to -230 and is
CC targeted to position +25 to +30
XX
SQ Sequence 18 BP; 1 A; 3 C; 7 G; 5 T; 2 U; 0 Other;

Query Match      66.7%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GGGGUCCTGGAG 12
        |||||
Db       7 GGGGUCCTGGAG 18

RESULT 62
AAT80262
ID AAT80262 standard; DNA; 18 BP.
XX
AC AAT80262;
XX
DT 15-OCT-1997 (first entry)
XX
DE Oligo HCV94, targeted to HCV region +1 to +6.
XX
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KM inhibition; replication; expression; detection; chronic hepatitis;
KM acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..6
FT /*tag= b
FT /note= "Phosphorochioate linkages"
FT modified_base 7..18
FT /*tag= a
FT /note= "2 Ome modified"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOPF ) HOFEMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX

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```

DR WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
XX
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
SQ Sequence 18 BP; 2 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match      66.7%; Score 12; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 GGGGUCCTGGAG 12
        |||||
Db       7 GGGGTCTCTGGAG 18

RESULT 63
ABS65834
ID ABS65834 standard; DNA; 18 BP.
XX
AC ABS65834;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #40.
XX
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KM non-B hepatitis; acute hepatitis; chronic hepatitis;
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KM gene therapy; ss; DNA-RNA hybrid.
XX
OS Synthetic.
XX
FH US2002081577-A1.
XX
PD 27-JUN-2002.
XX
XX 02-JUL-1997; 97US-00887505.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX 02-JUL-1996; 96US-0021104P.
XX
XX (KILK/) KILKUSKIE R L.
XX PA (FRAN/) FRANK B L.
XX PA (GOOD/) GOODCHILD J.
XX PA (WOLFE/) WOLFE J L.
XX PA (ROBE/) ROBERTS P C.
XX PA (HAML/) HAMLIN H A.
XX PA (ROBE/) ROBERTS N A.
XX PA (WALT/) WALTHER D M.
XX
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
XX
XX WPI; 2002-537132/57.
XX
PT Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.

```

XX PS Claim 22; Page 10; 74pp; English.

XX CC The invention describes synthetic oligonucleotides complementary to a

XX CC portion of the 5' untranslated region of hepatitis C virus. The

XX CC oligonucleotides may be used in methods for controlling, preventing, and

XX CC treating hepatitis C virus infection, in antisense technology and gene

XX CC therapy, and of detecting the presence of hepatitis C virus in a sample.

XX CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded

XX CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non

XX CC -B, acute and chronic hepatitis, and has been associated with

XX CC hepatocellular carcinoma. The invention describes methods and kits for

XX CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic

XX CC acid and protein, and for treating HCV infections. This sequence

XX CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting

XX CC HCV replication and expression of HCV

XX SQ Sequence 18 BP; 2 A; 4 C; 10 G; 0 T; 2 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTUGAG 12

DB 7 GGGGUCCTUGAG 18

RESULT 64

ABS65838

ID ABS65838 standard; DNA; 18 BP.

XX AC ABS65838;

XX DT 15-NOV-2002 (first entry)

XX DE Inhibitory oligonucleotide specific for hepatitis C virus #44.

XX KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

XX KW non-B hepatitis; acute hepatitis; chronic hepatitis;

XX KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX KW gene therapy; ss; DNA-RNA hybrid.

XX OS Synthetic.

XX PN US2002081577-A1.

XX PD 27-JUN-2002.

XX PF 02-JUL-1997; 97US-00887505.

XX PR 06-JUN-1995; 95US-00471968.

XX PR 02-JUL-1996; 96US-0021104P.

XX PA (KILK/) KILKUSKIE R L.

XX PA (FRAN/) FRANK B L.

XX PA (GOOD/) GOODCHILD J.

XX PA (WOLF/) WOLFE J L.

XX PA (ROBE/) ROBERTS P C.

XX PA (HAML/) HAMLIN H A.

XX PA (ROBE/) ROBERTS N A.

XX PA (WALT/) WALTHER D M.

XX PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

XX PI Hamlin HA, Roberts NA, Walther DM;

XX DR WPI; 2002-537132/57.

XX PT Synthetic oligonucleotides complementary to a portion of the 5'

XX PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and

XX PT treating HCV infections and hepatocellular carcinoma.

XX PS Claim 22; Page 10; 74pp; English.

XX CC The invention describes synthetic oligonucleotides complementary to a

XX CC portion of the 5' untranslated region of hepatitis C virus. The

XX CC oligonucleotides may be used in methods for controlling, preventing, and

XX CC treating hepatitis C virus infection, in antisense technology and gene

XX CC therapy, and of detecting the presence of hepatitis C virus in a sample.

XX CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded

XX CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non

XX CC -B, acute and chronic hepatitis, and has been associated with

XX CC hepatocellular carcinoma. The invention describes methods and kits for

XX CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic

XX CC acid and protein, and for treating HCV infections. This sequence

XX CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting

XX CC HCV replication and expression of HCV

XX SQ Sequence 18 BP; 2 A; 3 C; 9 G; 2 T; 2 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTUGAG 12

DB 7 GGGGUCCTUGAG 18

RESULT 65

ABS65840

ID ABS65840 standard; DNA; 18 BP.

XX AC ABS65840;

XX DT 15-NOV-2002 (first entry)

XX DE Inhibitory oligonucleotide specific for hepatitis C virus #46.

XX KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

XX KW non-B hepatitis; acute hepatitis; chronic hepatitis;

XX KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX KW gene therapy; ss; DNA-RNA hybrid.

XX OS Synthetic.

XX PN US2002081577-A1.

XX PD 27-JUN-2002.

XX PF 02-JUL-1997; 97US-00887505.

XX PR 06-JUN-1995; 95US-00471968.

XX PR 02-JUL-1996; 96US-0021104P.

XX PA (KILK/) KILKUSKIE R L.

XX PA (FRAN/) FRANK B L.

XX PA (GOOD/) GOODCHILD J.

XX PA (WOLF/) WOLFE J L.

XX PA (ROBE/) ROBERTS P C.

XX PA (HAML/) HAMLIN H A.

XX PA (ROBE/) ROBERTS N A.

XX PA (WALT/) WALTHER D M.

XX PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

XX PI Hamlin HA, Roberts NA, Walther DM;

XX DR WPI; 2002-537132/57.

XX PT Synthetic oligonucleotides complementary to a portion of the 5'

XX PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and

XX PT treating HCV infections and hepatocellular carcinoma.

XX PS Claim 22; Page 10; 74pp; English.

XX CC The invention describes synthetic oligonucleotides complementary to a

CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV

SO Sequence 18 BP; 1 A; 4 C; 9 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGCGAG 12  
Db 7 GGGGUCGCGAG 18

RESULT 66  
ABS65837  
ID ABS65837 standard; DNA; 18 BP.  
AC ABS65837;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #43.  
XX  
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
DR WPI; 2002-537132/57.  
XX  
PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
PS Claim 22; Page 10; 74pp; English.  
XX  
CC The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and

CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV

SO Sequence 18 BP; 2 A; 3 C; 9 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGCGAG 12  
Db 1 GGGGUCGCGAG 12

RESULT 67  
ABS65847  
ID ABS65847 standard; DNA; 18 BP.  
AC ABS65847;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #53.  
XX  
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
DR WPI; 2002-537132/57.  
XX  
PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
PS Claim 22; Page 11; 74pp; English.  
XX  
CC The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.

CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV  
XX  
SQ Sequence 18 BP; 2 A; 3 C; 8 G; 3 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3,4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12

## RESULT 68

AB865941  
ID AB865941 standard; DNA; 18 BP.  
XX  
AC AB865941;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #147.  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
XX non-B hepatitis; acute hepatitis; chronic hepatitis;  
XX hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
XX gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walthers DM;  
XX  
DR WPI; 2002-537132/57.  
XX  
PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
PS  
XX

Claim 23; Page 7; 74pp; English.

CC The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non

CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV  
XX  
SQ Sequence 18 BP; 3 A; 2 C; 10 G; 1 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3,4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12

## RESULT 69

AB865845  
ID AB865845 standard; DNA; 18 BP.  
XX  
AC AB865845;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #51.  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
XX non-B hepatitis; acute hepatitis; chronic hepatitis;  
XX hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
XX gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walthers DM;  
XX  
DR WPI; 2002-537132/57.  
XX  
PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
PS  
XX

Claim 22; Page 11; 74pp; English.

CC The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for

CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV

XX Sequence 18 BP; 2 A; 4 C; 8 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

Db 1 GGGGUCGAG 12

RESULT 70

AB85839

ID AB85839 standard; DNA; 18 BP.

XX ABS65839;

DT 15-NOV-2002 (first entry)

DE Inhibitory oligonucleotide specific for hepatitis C virus #45.

KM Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;

KM non-B hepatitis; acute hepatitis; chronic hepatitis;

KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

KM gene therapy; ss; DNA-RNA hybrid.

XX Synthetic.

OS US2002081577-A1.

PN 27-JUN-2002.

PD 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

PR 02-JUL-1996; 96US-0021104P.

XX (KILK/) KILKUSKIE R L.

PA (FRAN/) FRANK B L.

PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.

PA (ROBE/) ROBERTS N A.

PA (WALT/) WALTHER D M.

PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

PI Hamlin HA, Roberts NA, Walther DM;

DR WPI; 2002-537132/57.

PT Synthetic oligonucleotides complementary to a portion of the 5' untranslated region of hepatitis C virus (HCV), useful for diagnosing and treating HCV infections and hepatocellular carcinoma.

PS Claim 22; Page 10; 74pp; English.

XX The invention describes synthetic oligonucleotides complementary to a portion of the 5' untranslated region of hepatitis C virus. The oligonucleotides may be used in methods for controlling, preventing, and treating hepatitis C virus infection, in antisense technology and gene therapy, and of detecting the presence of hepatitis C virus in a sample. Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded RNA virus which infects hepatocytes. HCV is the major cause of non-A, non-B, acute and chronic hepatitis, and has been associated with hepatocellular carcinoma. The invention describes methods and kits for inhibiting replication of HCV, inhibiting the expression of HCV nucleic acid and protein, and for treating HCV infections. This sequence

CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV

XX Sequence 18 BP; 1 A; 4 C; 9 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

Db 1 GGGGUCGAG 12

RESULT 71

AB85936

ID AB85936 standard; DNA; 18 BP.

XX ABS65936;

DT 15-NOV-2002 (first entry)

DE Inhibitory oligonucleotide specific for hepatitis C virus #142.

KM Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;

KM non-B hepatitis; acute hepatitis; chronic hepatitis;

KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

KM gene therapy; ss; DNA-RNA hybrid.

XX Synthetic.

OS US2002081577-A1.

PN 27-JUN-2002.

PD 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

PR 02-JUL-1996; 96US-0021104P.

XX (KILK/) KILKUSKIE R L.

PA (FRAN/) FRANK B L.

PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.

PA (ROBE/) ROBERTS N A.

PA (WALT/) WALTHER D M.

PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

PI Hamlin HA, Roberts NA, Walther DM;

DR WPI; 2002-537132/57.

PT Synthetic oligonucleotides complementary to a portion of the 5' untranslated region of hepatitis C virus (HCV), useful for diagnosing and treating HCV infections and hepatocellular carcinoma.

PS Claim 23; Page 7; 74pp; English.

XX The invention describes synthetic oligonucleotides complementary to a portion of the 5' untranslated region of hepatitis C virus. The oligonucleotides may be used in methods for controlling, preventing, and treating hepatitis C virus infection, in antisense technology and gene therapy, and of detecting the presence of hepatitis C virus in a sample. Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded RNA virus which infects hepatocytes. HCV is the major cause of non-A, non-B, acute and chronic hepatitis, and has been associated with hepatocellular carcinoma. The invention describes methods and kits for inhibiting replication of HCV, inhibiting the expression of HCV nucleic acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV

```
XX Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 2 U; 0 Other;
SQ
Query Match 66.7%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGUCUCGAG 12
Db 7 GGGGUCUCGAG 18

RESULT 72
ABS65835
ID ABS65835 standard; DNA; 18 BP.
AC ABS65835;
XX
XX 15-NOV-2002 (first entry)
DT
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #41.
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
XX
XX Synthetic.
OS
XX US2002081577-A1.
FN
XX 27-JUN-2002.
PD
XX 02-JUL-1997; 97US-00887505.
PF
XX 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
XX
XX WPI; 2002-537132/57.
DR
XX
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
XX Claim 22; Page 10; 74pp; English.
PS
XX
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 18 BP; 3 A; 2 C; 9 G; 2 T; 2 U; 0 Other;
```

```
XX Query Match 66.7%; Score 12; DB 6; Length 18;
SQ Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGUCUCGAG 12
Db 1 GGGGUCUCGAG 12

RESULT 73
ABS65846
ID ABS65846 standard; DNA; 18 BP.
AC ABS65846;
XX
XX 15-NOV-2002 (first entry)
DT
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #52.
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KW gene therapy; ss.
XX
XX Synthetic.
OS
XX US2002081577-A1.
FN
XX 27-JUN-2002.
PD
XX 02-JUL-1997; 97US-00887505.
PF
XX 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
XX
XX WPI; 2002-537132/57.
DR
XX
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
XX Claim 22; Page 11; 74pp; English.
PS
XX
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic oligonucleotide used for inhibiting HCV
CC replication and expression of HCV
XX
SQ Sequence 18 BP; 2 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
```

Query Match

66.7%; Score 12; DB 6; Length 18;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
Db 7 GGGGUCUUGAG 18

## RESULT 74

AB565935  
ID ABS65935 standard; DNA, 18 BP.

XX AC ABS65935;

XX DT 15-NOV-2002 (first entry)

XX DE Inhibitory oligonucleotide specific for hepatitis C virus #141.

XX KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX KW gene therapy; ss; DNA-RNA hybrid.

XX OS Synthetic.

XX PN US2002081577-A1.

XX PD 27-JUN-2002.

XX PF 02-JUL-1997; 97US-00887505.

XX PR 06-JUN-1995; 95US-00471968.

XX PR 02-JUL-1996; 96US-0021104P.

XX PA (KILK/) KILKUSKIE R L.

PA (FRAN/) FRANK B L.

PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.

PA (ROBE/) ROBERTS N A.

PA (WALT/) WALTHER D M.

XX PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

PI Hamlin HA, Roberts NA, Walther DM;

XX DR WPI; 2002-537132/57.

XX PT Synthetic oligonucleotides complementary to a portion of the 5'

PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and

PT treating HCV infections and hepatocellular carcinoma.

XX PS Claim 23; Page 7; 74pp; English.

XX CC The invention describes synthetic oligonucleotides complementary to a

CC portion of the 5' untranslated region of hepatitis C virus. The

CC oligonucleotides may be used in methods for controlling, preventing, and

CC treating hepatitis C virus infection, in antisense technology and gene

CC therapy, and of detecting the presence of hepatitis C virus in a sample.

CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded

CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non

CC -B, acute and chronic hepatitis, and has been associated with

CC hepatocellular carcinoma. The invention describes methods and kits for

CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic

CC acid and protein, and for treating HCV infections. This sequence

CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting

CC HCV replication and expression of HCV

XX SQ Sequence 18 BP; 4 A; 3 C; 9 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12

Db 7 GGGGUCUUGAG 18

## RESULT 75

AB565937  
ID ABS65937 standard; DNA, 18 BP.

XX AC ABS65937;

XX DT 15-NOV-2002 (first entry)

XX DE Inhibitory oligonucleotide specific for hepatitis C virus #143.

XX KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

KW non-B hepatitis; acute hepatitis; chronic hepatitis;

KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX KW gene therapy; ss; DNA-RNA hybrid.

XX OS Synthetic.

XX PN US2002081577-A1.

XX PD 27-JUN-2002.

XX PF 02-JUL-1997; 97US-00887505.

XX PR 06-JUN-1995; 95US-00471968.

XX PR 02-JUL-1996; 96US-0021104P.

XX PA (KILK/) KILKUSKIE R L.

PA (FRAN/) FRANK B L.

PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.

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PA (WALT/) WALTHER D M.

XX PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

PI Hamlin HA, Roberts NA, Walther DM;

XX DR WPI; 2002-537132/57.

XX PT Synthetic oligonucleotides complementary to a portion of the 5'

PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and

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CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non

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CC hepatocellular carcinoma. The invention describes methods and kits for

CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic

CC acid and protein, and for treating HCV infections. This sequence

CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting

CC HCV replication and expression of HCV

XX SQ Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12

Db 7 GGGGUCUGAG 18

RESULT 76  
ABS65938  
ID ABS65938 standard; DNA; 18 BP.  
AC ABS65938;  
XX  
XX 15-NOV-2002 (first entry)  
DT  
DE Inhibitory oligonucleotide specific for hepatitis C virus #144.  
XX  
XX Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;  
KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.  
XX  
XX Synthetic.  
OS  
XX US2002081577-A1.  
XX  
XX 27-JUN-2002.  
PD  
XX 02-JUL-1997; 97US-00887505.  
PF  
XX 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
XX (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
XX WPI; 2002-537132/57.  
DR  
XX Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
XX Claim 23; Page 7; 74pp; English.  
PS  
XX The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
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CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV  
XX  
XX Sequence 18 BP; 1 A; 3 C; 7 G; 5 T; 2 U; 0 Other;  
SQ  
Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 77  
ABS65848  
ID ABS65848 standard; DNA; 18 BP.  
AC ABS65848;  
XX  
XX 15-NOV-2002 (first entry)  
DT  
DE Inhibitory oligonucleotide specific for hepatitis C virus #54.  
XX  
XX Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;  
KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.  
XX  
XX Synthetic.  
OS  
XX US2002081577-A1.  
XX  
XX 27-JUN-2002.  
PD  
XX 02-JUL-1997; 97US-00887505.  
PF  
XX 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
XX (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
XX WPI; 2002-537132/57.  
DR  
XX Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
XX Claim 22; Page 11; 74pp; English.  
PS  
XX The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV  
XX  
XX Sequence 18 BP; 2 A; 3 C; 8 G; 3 T; 2 U; 0 Other;  
SQ  
Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

RESULT 78
ABSS5939
ID      ABS565939 standard; DNA; 18 BP.
XX
XX AC      ABS565939;
XX
XX DT      15-NOV-2002 (first entry)
XX
DE      Inhibitory oligonucleotide specific for hepatitis C virus #145.
XX
XX      Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
XX      non-B hepatitis; acute hepatitis; chronic hepatitis;
XX      hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
XX      gene therapy; ss; DNA-RNA hybrid.
XX
XX OS      Synthetic.
XX
XX PN      US2002081577-A1.
XX
XX PD      27-JUN-2002.
XX
XX PF      02-JUL-1997; 97US-00887505.
XX
XX PR      06-JUN-1995; 95US-00471968.
XX      02-JUL-1996; 96US-0021104P.
XX
XX PA      (KILK/) KILKUSKIE R L.
XX      (FRAN/) FRANK B L.
XX      (GOOD/) GOODCHILD J.
XX      (MOLE/) MOLEFE J L.
XX      (ROBE/) ROBERTS P C.
XX      (HAML/) HAMLIN H A.
XX      (ROBE/) ROBERTS N A.
XX      (WALT/) WALTHER D M.
XX
XX PI      Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
XX      Hamlin HA, Roberts NA, Walther DM;
XX
XX DR      WPI: 2002-537132/57.
XX
XX PT      Synthetic oligonucleotides complementary to a portion of the 5'
XX      untranslated region of hepatitis C virus (HCV), useful for diagnosing and
XX      treating HCV infections and hepatocellular carcinoma.
XX
XX PS      Claim 23; Page 7; 74pp; English.
XX
XX      The invention describes synthetic oligonucleotides complementary to a
XX      portion of the 5' untranslated region of hepatitis C virus. The
XX      oligonucleotides may be used in methods for controlling, preventing, and
XX      treating hepatitis C virus infection, in antisense technology and gene
XX      therapy, and of detecting the presence of hepatitis C virus in a sample.
XX      Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
XX      RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
XX      -B, acute and chronic hepatitis, and has been associated with
XX      hepatocellular carcinoma. The invention describes methods and kits for
XX      inhibiting replication of HCV, inhibiting the expression of HCV nucleic
XX      acid and protein, and for treating HCV infections. This sequence
XX      represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
XX      HCV replication and expression of HCV
XX
XX SQ      Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;
XX
XX      Query Match      66.7%; Score 12; DB 6; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX      1 GGGGUCUCUGAG 12
XX      |||||
XX      1 GGGGUCUCUGAG 12

```

ID	AB865836 standard; DNA; 18 BP.
XX	
AC	AB865836;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Inhibitory oligonucleotide specific for hepatitis C virus #42.
XX	
KW	Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW	non-B hepatitis; acute hepatitis; chronic hepatitis;
KW	hepatocellular carcinoma; viraemia; cytosolic; antisense therapy;
KW	gene therapy; see, DNA-RNA hybrid.
XX	
OS	Synthetic.
XX	
PN	US2002081577-A1.
XX	
PD	27-JUN-2002.
XX	
PF	02-JUL-1997; 97US-00887505.
XX	
PR	06-JUN-1995; 95US-00471968.
XX	
PR	02-JUL-1996; 96US-0021104P.
XX	
PA	(KILK/) KILKUSKIE R L.
PA	(FRAN/) FRANK B L.
PA	(GOOD/) GOODCHILD J.
PA	(WOLF/) WOLFE J L.
PA	(ROBE/) ROBERTS P C.
PA	(HAML/) HAMLIN H A.
PA	(ROBE/) ROBERTS N A.
PA	(WALT/) WALTHER D M.
PI	KilKuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI	Hamlin HA, Roberts NA, Walther DM;
XX	
WP	2002-537132/57.
XX	
PT	Synthetic oligonucleotides complementary to a portion of the 5'
XX	untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT	treating HCV infections and hepatocellular carcinoma.
XX	
PS	Claim 22; Page 10; 74p; English.
XX	
CC	The invention describes synthetic oligonucleotides complementary to a
CC	portion of the 5' untranslated region of hepatitis C virus. The
CC	oligonucleotides may be used in methods for controlling, preventing, and
CC	treating hepatitis C virus infection, in antisense technology and gene
CC	therapy, and of detecting the presence of hepatitis C virus in a sample.
CC	Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC	RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC	-B, acute and chronic hepatitis, and has been associated with
CC	hepatocellular carcinoma. The invention describes methods and kits for
CC	inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC	acid and protein, and for treating HCV infections. This sequence
CC	represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC	HCV replication and expression of HCV
XX	
SO	Sequence 18 BP; 3 A; 2 C; 9 G; 2 T; 2 U; 0 Other;
XX	
Query Match	66.7%; Score 12; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GGGGUCUUGGAG 12
DB	7 GGGGUCUUGGAG 18
	-
RESULT 80	
AB865843	
ID	AB865843 standard; DNA; 18 BP.
XX	

AC ABS65843;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #49.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 22; Page 11; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
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 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis. HCV is the major cause of non-A, non  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;  
 XX  
 QY Query Match 66.7%; Score 12; DB 6; Length 18;  
 Db Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCUCUGAG 12  
 Db 1 GGGGUCUCUGAG 12  
 XX  
 RESULT 81  
 ID ABS65844  
 XX ABS65844 standard; DNA; 18 BP.  
 AC ABS65844;  
 XX

DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #50.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
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 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;  
 XX  
 QY Query Match 66.7%; Score 12; DB 6; Length 18;  
 Db Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCUCUGAG 12  
 Db 7 GGGGUCUCUGAG 18  
 XX  
 RESULT 82  
 ID ABS65833  
 XX ABS65833 standard; DNA; 18 BP.  
 AC ABS65833;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX

DE Inhibitory oligonucleotide specific for hepatitis C virus #39.  
 XX Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;  
 KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KM gene therapy; ss; DNA-RNA hybrid.  
 XX Synthetic.  
 OS  
 XX US2002081577-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX 02-JUL-1997; 97US-00887505.  
 PF  
 XX 06-JUN-1995; 95US-00471968.  
 PR  
 XX 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
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 PS Claim 22; Page 10; 74pp; English.  
 XX  
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 CC oligonucleotides may be used in methods for controlling, preventing, and  
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 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 18 BP; 2 A; 4 C; 10 G; 0 T; 2 U; 0 Other;  
 XX  
 QY Query Match 66.7%; Score 12; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCUGAG 12  
 |||||  
 Db 1 GGGGUCCUGAG 12  
 |||||  
 RESULT 83  
 ID A865940 standard; DNA; 18 BP.  
 XX A865940;  
 AC A865940;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #146.  
 XX

KM Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;  
 KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KM gene therapy; ss; DNA-RNA hybrid.  
 XX Synthetic.  
 OS  
 XX US2002081577-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX 02-JUL-1997; 97US-00887505.  
 PF  
 XX 06-JUN-1995; 95US-00471968.  
 PR  
 XX 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 23; Page 7; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 18 BP; 2 A; 5 C; 9 G; 0 T; 2 U; 0 Other;  
 XX  
 QY Query Match 66.7%; Score 12; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCUGAG 12  
 |||||  
 Db 1 GGGGUCCUGAG 12  
 |||||  
 RESULT 84  
 ID AA065099 standard; DNA; 19 BP.  
 XX AA065099;  
 AC AA065099;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.

```
XX OS Synthetic.
XX PS CA2104649-A.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 145; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 19 BP; 2 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGGGUCCTCGAG 12
Db 5 GGGGTCTCTGAG 16
XX
XX RESULT 85
XX AAQ65086
XX ID AAQ65086 standard; DNA; 19 BP.
XX AC AAQ65086;
XX XX
XX DT 20-DEC-1994 (first entry)
XX XX
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX XX
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX KM inhibition; viral protein precursor; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN CA2104649-A.
XX XX
XX PD 26-FEB-1994.
XX XX
XX PF 23-AUG-1993; 93CA-02104649.
XX XX
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX XX
XX PA (SEKI/) SEKI M.
XX XX
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
```

```
XX PS Claim 5; Page 139; 262pp; English.
XX XX
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGGGUCCTCGAG 12
Db 4 GGGGTCTCTGAG 15
XX
XX RESULT 86
XX AAQ65128
XX ID AAQ65128 standard; DNA; 19 BP.
XX AC AAQ65128;
XX XX
XX DT 21-DEC-1994 (first entry)
XX XX
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX XX
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX KM inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX XX
XX PN CA2104649-A.
XX XX
XX PD 26-FEB-1994.
XX XX
XX PF 23-AUG-1993; 93CA-02104649.
XX XX
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX XX
XX PA (SEKI/) SEKI M.
XX XX
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX XX
XX PS Claim 5; Page 158; 262pp; English.
XX XX
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 19 BP; 2 A; 2 C; 13 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGGGUCCTCGAG 12
Db 7 GGGGTCTCTGAG 18
```

```
RESULT 87
AA065144
ID AA065144 standard; DNA; 19 BP.
XX
AC AA065144;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
genome - are useful as antiviral agents.
XX
PS Claim 5; Page 165; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 19 BP; 2 A; 2 C; 13 G; 2 T; 0 U; 0 Other;
Query Match 66.7%; Score 12; DB 2; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
DB 8 GGGGTCTCTGGAG 19
RESULT 88
AA065100
ID AA065100 standard; DNA; 19 BP.
XX
AC AA065100;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
```

```
PF 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
genome - are useful as antiviral agents.
XX
PS Claim 5; Page 145; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 19 BP; 2 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 12; DB 2; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
DB 5 GGGGTCTCTGGAG 16
```

```
RESULT 89
AA065113
ID AA065113 standard; DNA; 19 BP.
XX
AC AA065113;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
genome - are useful as antiviral agents.
XX
PS Claim 5; Page 151; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
```

CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 19 BP; 2 A; 3 C; 12 G; 2 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
|||:|||||  
DB 6 GGGGTCCTGGAG 17  
|||:|||||  
RESULT 90  
AA299225  
ID AA299225 standard; DNA; 19 BP.  
XX  
AC AA299225;  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Primer for primer-specific and mispair extension analysis of HCV.  
XX  
KM Primer-specific and mispair extension assay; PSMEA;  
KM genotype determination; HCV; gene variation; PCR primer; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200009745-A1.  
XX  
PD 24-FEB-2000.  
XX  
PF 09-AUG-1999; 99WO-CA000733.  
XX  
PR 13-AUG-1998; 98CA-02245039.  
XX  
PA (CABL-) CANADIAN BLOOD SERVICES.  
PA (HEMA-) HEMA-QUEBEC.  
XX  
PI Hu Y;  
XX  
DR WPI; 2000-224367/19.  
XX  
PT Primer-specific and mispair extension assay for identifying gene  
PT variations, comprises specific primer amplification of unknown nucleic  
PT acid sequences of patients using incomplete dNTP sets.  
XX  
PS Disclosure; Page 13; 65pp; English.  
XX  
CC AA299212-26 represent PCR primers used in a primer-specific and mispair  
CC extension assay (PSMEA) for genotype determination of Hepatitis C virus  
CC (HCV). The method comprises extending an unknown nucleic acid sequence  
CC (from a patient) using a primer specific for particular genotype and  
CC incomplete set of dNTPs under suitable conditions followed by  
CC characterizing and comparing the extension products with known nucleic  
CC acid sequences of various genotypes. The present primers are used for  
CC detecting nucleotide variations in the 5' untranslated region of the HCV  
CC genome. PSMEA is capable of accurately detecting heterozygotes and  
CC nucleotide mutations in a nucleic acid sequence. The PSMEA is useful for  
CC identifying gene variations such as in different genotypes or subtypes  
CC a given genotype, especially Hepatitis C virus genotypes and subtypes  
XX  
SQ Sequence 19 BP; 1 A; 3 C; 10 G; 5 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 3; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
|||:|||||  
DB 2 GGGGTCCTGGAG 13  
|||:|||||

RESULT 91  
ADF52572  
ID ADF52572 standard; RNA; 19 BP.  
XX  
AC ADF52572;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siRNA antisense strand SeqID1162.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187P.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
PI Mcswiggen J, Belgelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 1162; 183pp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virulence, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA. By RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX  
SQ Sequence 19 BP; 2 A; 2 C; 13 G; 0 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
|||:|||||

Db 7 GGGGUCGAG 18

RESULT 92

ID ADF51877/c

AC ADF51877 standard; RNA; 19 BP.

XX ADF51877;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus short interfering nucleic acid sense strand SeqID467.

XX

XX short interfering nucleic acid; siNA; virus replication inhibition;

KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;

KM hepatocellular cancer; cirrhosis; ss.

XX

OS Hepatitis C virus.

PN WO2003070750-A2.

PD 28-AUG-2003.

XX

PF 20-FEB-2003; 2003WO-US005043.

XX

PR 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-036782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX

PA (SIRN-) SIRNA THERAPEUTICS INC.

PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX

DR WPI; 2003-689778/65.

XX

PT New double-stranded short interfering nucleic acid comprises sugar-

PT modified pyrimidine bases useful for treating infection with hepatitis C

PT virus.

XX

PS Example 3; SEQ ID NO 467; 183bp; English.

XX

XX This invention relates to novel double-stranded short interfering nucleic

CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where

CC one strand is an antisense strand (ASS) that is complementary to (part

CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to

CC ASS, and where most of the pyrimidine nucleotides comprise a sugar

CC modification. The invention may allow development of compounds with

CC virucide, antiinflammatory, hepatotropic or cytostatic activities by

CC modulation (inhibition) of expression or activity of HCV RNA, by RNA

CC interference. The siNA's of the invention may be used to inhibit

CC replication of HCV, in cells, tissue explants or organisms, for treating

CC HCV infection and its consequences (liver failure; hepatocellular cancer

CC and cirrhosis), and also for drug screening, diagnosis, target

CC identification and validation, genetic engineering, pharmacogenomics,

CC studying gene function and gene mapping (for example of single-nucleotide

CC polymorphisms). The chemical modification improves stability, activity,

CC cellular uptake and/or binding affinity. The siNA can be directed to

CC conserved regions of HCV genes, so are active against many different

CC strains.

XX

XX Sequence 19 BP; 2 A; 13 C; 2 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12

Db 12 GGGGUCGAG 1

RESULT 93

ID ADF51948/c

AC ADF51948 standard; RNA; 19 BP.

XX ADF51948;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus short interfering nucleic acid sense strand SeqID538.

XX

XX short interfering nucleic acid; siNA; virus replication inhibition;

KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;

KM hepatocellular cancer; cirrhosis; ss.

XX

OS Hepatitis C virus.

PN WO2003070750-A2.

PD 28-AUG-2003.

XX

PF 20-FEB-2003; 2003WO-US005043.

XX

PR 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-036782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX

PA (SIRN-) SIRNA THERAPEUTICS INC.

PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX

DR WPI; 2003-689778/65.

XX

PT New double-stranded short interfering nucleic acid comprises sugar-

PT modified pyrimidine bases useful for treating infection with hepatitis C

PT virus.

XX

PS Example 3; SEQ ID NO 538; 183bp; English.

XX

XX This invention relates to novel double-stranded short interfering nucleic

CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where

CC one strand is an antisense strand (ASS) that is complementary to (part

CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to

CC ASS, and where most of the pyrimidine nucleotides comprise a sugar

CC modification. The invention may allow development of compounds with

CC virucide, antiinflammatory, hepatotropic or cytostatic activities by

CC modulation (inhibition) of expression or activity of HCV RNA, by RNA

CC interference. The siNA's of the invention may be used to inhibit

CC replication of HCV, in cells, tissue explants or organisms, for treating

CC HCV infection and its consequences (liver failure; hepatocellular cancer

CC and cirrhosis), and also for drug screening, diagnosis, target

CC identification and validation, genetic engineering, pharmacogenomics,

CC studying gene function and gene mapping (for example of single-nucleotide

CC polymorphisms). The chemical modification improves stability, activity,

CC cellular uptake and/or binding affinity. The siNA can be directed to

CC conserved regions of HCV genes, so are active against many different

CC strains.

XX

XX Sequence 19 BP; 3 A; 10 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCUUGAG 12  
18 GGGGCTCTGAG 7  
Db 3 GGGGUCUUGAG 14

RESULT 94  
ID ADF52651 standard; RNA; 19 BP.  
AC ADF52651;  
XX  
XX  
XX 12-FEB-2004 (first entry)  
DE Hepatitis C virus siNA antisense strand SegID1241.  
XX  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005043.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
XX  
XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
XX Example 3; SEQ ID NO 1241; 183pp; English.

This invention relates to novel double-stranded short interfering nucleic acids (siNA) that inhibits replication of hepatitis C virus (HCV), where one strand is an antisense strand (ASS) that is complementary to (part of) an HCV RNA (portion) and a sense strand (SS) that is complementary to ASS, and where most of the pyrimidine nucleotides comprise a sugar modification. The invention may allow development of compounds with virucide, antiinflammatory, hepatotropic or cytostatic activities by modulation (inhibition) of expression or activity of HCV RNA, by RNA interference. The siNA's of the invention may be used to inhibit replication of HCV, in cells, tissue explants or organisms, for treating HCV infection and its consequences (liver failure; hepatocellular cancer and cirrhosis), and also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single-nucleotide polymorphisms). The chemical modification improves stability, activity, cellular uptake and/or binding affinity. The siNA can be directed to conserved regions of HCV genes, so are active against many different strains.

Sequence 19 BP; 1 A; 4 C; 11 G; 0 T; 3 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCUUGAG 12  
3 GGGGUCUUGAG 14  
Db 3 GGGGUCUUGAG 14

RESULT 95  
ID ADF52606 standard; RNA; 19 BP.  
AC ADF52606;  
XX  
XX  
XX 12-FEB-2004 (first entry)  
DE Hepatitis C virus siNA antisense strand SegID1196.  
XX  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
XX  
XX PN WO2003070750-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005043.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
XX  
XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
XX Example 3; SEQ ID NO 1196; 183pp; English.

This invention relates to novel double-stranded short interfering nucleic acids (siNA) that inhibits replication of hepatitis C virus (HCV), where one strand is an antisense strand (ASS) that is complementary to (part of) an HCV RNA (portion) and a sense strand (SS) that is complementary to ASS, and where most of the pyrimidine nucleotides comprise a sugar modification. The invention may allow development of compounds with virucide, antiinflammatory, hepatotropic or cytostatic activities by modulation (inhibition) of expression or activity of HCV RNA, by RNA interference. The siNA's of the invention may be used to inhibit replication of HCV, in cells, tissue explants or organisms, for treating HCV infection and its consequences (liver failure; hepatocellular cancer and cirrhosis), and also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single-nucleotide polymorphisms). The chemical modification improves stability, activity, cellular uptake and/or binding affinity. The siNA can be directed to conserved regions of HCV genes, so are active against many different strains.



SQ Sequence 19 BP; 2 A; 3 C; 12 G; 0 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
|||  
Db 6 GGGGUCCUGAG 17  
RESULT 96  
ADFS2644  
ID ADFS2644 standard; RNA; 19 BP.  
XX  
AC ADFS2644;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siRNA antisense strand SeqID1234.  
XX  
KM short interfering nucleic acid; siRNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatocellular cancer; cytostatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-669778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 1234; 183bp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acid (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different

CC strains.  
XX  
SQ Sequence 19 BP; 2 A; 4 C; 10 G; 0 T; 3 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
|||  
Db 2 GGGGUCCUGAG 13  
RESULT 97  
ADFS1912/C  
ID ADFS1912 standard; RNA; 19 BP.  
XX  
AC ADFS1912;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID502.  
XX  
KM short interfering nucleic acid; siRNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatocellular cancer; cytostatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-669778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 502; 183bp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acid (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,

CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX  
SQ Sequence 19 BP; 3 A; 11 C; 3 G; 0 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 15 GGGGTCTCTGAG 4  
RESULT 98  
ADFS1876/c  
ID ADFS1876 standard; RNA; 19 BP.  
XX  
AC ADFS1876;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID466.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; viraemia; antiinflammatory;  
KM hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
PI WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 466; 183bp; English.  
XX  
PS This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASs) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASs, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC viraemic, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,

CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX  
SQ Sequence 19 BP; 2 A; 13 C; 2 G; 0 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 13 GGGGTCTCTGAG 2  
RESULT 99  
ADFS1910/c  
ID ADFS1910 standard; RNA; 19 BP.  
XX  
AC ADFS1910;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID500.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; viraemia; antiinflammatory;  
KM hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
PI WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 500; 183bp; English.  
XX  
PS This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASs) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASs, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC viraemic, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer

CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.

XX  
SQ Sequence 19 BP; 2 A; 12 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGCGAG 12  
Db 14 GGGGTCCTGGAG 3  
||||:|||||

RESULT 100  
ADFS1954/C  
ID ADFS1954 standard; RNA; 19 BP.  
XX  
AC ADFS1954;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID544.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatocellular carcinoma; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-036782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Meswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 544; 183bp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (AS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC AS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit

CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure, hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.

XX  
SQ Sequence 19 BP; 3 A; 9 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGCGAG 12  
Db 19 GGGGTCCTGGAG 8  
||||:|||||

RESULT 101  
ADFS2650  
ID ADFS2650 standard; RNA; 19 BP.  
XX  
AC ADFS2650;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siNA antisense strand SeqID1240.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatocellular carcinoma; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-036782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Meswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 1240; 183bp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (AS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC AS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by

CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
SQ Sequence 19 BP; 2 A; 5 C; 9 G; 0 T; 3 U; 0 Other;  
XX  
XX  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12  
RESULT 102  
ADF52573  
ID ADF52573 standard; RNA; 19 BP.  
XX  
AC ADF52573;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siRNA antisense strand SeqID1163.  
XX  
XX short interfering nucleic acid; siRNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
PI WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
XX virus.  
XX  
PS Example 3; SEQ ID NO 1163; 183bp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar

CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
SQ Sequence 19 BP; 2 A; 2 C; 13 G; 0 T; 2 U; 0 Other;  
XX  
XX  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
1 GGGGUCCUGAG 12  
Db 8 GGGGUCCUGAG 19  
RESULT 103  
ADF51908/C  
ID ADF51908 standard; RNA; 19 BP.  
XX  
AC ADF51908;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID498.  
XX  
XX short interfering nucleic acid; siRNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
PI WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
XX virus.  
XX  
PS Example 3; SEQ ID NO 498; 183bp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part

```
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure, hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX
SQ Sequence 19 BP; 3 A; 12 C; 3 G; 0 T; 1 U; 0 Other;
Query Match 66.7%; Score 12; DB 10; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
Db 16 GGGGTCCTGGAG 5
RESULT 104
ADFS2608
ID ADFS2608 standard; RNA; 19 BP.
XX
AC ADFS2608;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siNA antisense strand SegID1198.
XX
KM short interfering nucleic acid; siNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KM hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-036782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI McSwiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
PS Example 3; SEQ ID NO 1198; 183bp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
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```
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure, hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX
SQ Sequence 19 BP; 2 A; 3 C; 11 G; 0 T; 3 U; 0 Other;
Query Match 66.7%; Score 12; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
Db 5 GGGGUCCTGGAG 16
RESULT 105
ADFS1955/c
ID ADFS1955 standard; RNA; 19 BP.
XX
AC ADFS1955;
XX
DT 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus short interfering nucleic acid sense strand SegID545.
XX
KM short interfering nucleic acid; siNA; virus replication inhibition;
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KM hepatocellular cancer; cirrhosis; ss.
XX
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-036782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI McSwiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
PS Example 3; SEQ ID NO 545; 183bp; English.
XX
XX
```

XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC antiviral, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure, hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.

SO Sequence 19 BP; 3 A; 11 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 17 GGGGCTCTGAG 6

RESULT 106  
ADFS2604  
ID ADFS2604 standard; RNA; 19 BP.  
XX  
AC ADFS2604;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siNA antisense strand SeqID1194.  
XX  
KW short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatocytic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRNA-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.

XX Example 3; SEQ ID NO 1194; 183bp; English.

PS This invention relates to novel double-stranded short interfering nucleic  
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC antiviral, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure, hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.

SO Sequence 19 BP; 1 A; 3 C; 12 G; 0 T; 3 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 4 GGGGUCGAG 15

RESULT 107  
ADJ53727/c  
ID ADJ53727 standard; DNA; 19 BP.  
XX  
AC ADJ53727;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE HCV specific oligonucleotide #7.  
XX  
KW ss; capture oligonucleotide; HBV; HIV-1; HCV; donated blood screening;  
KW DNA-RNA hybrid.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003106714-A1.  
XX  
PD 24-DEC-2003.  
XX  
PF 13-JUN-2003; 2003WO-US018993.  
XX  
PR 14-JUN-2002; 2002US-0389393P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Linnen JM, Kolk DP, Dockter JM, Getman DK, Yoshimura T;  
XX  
PI Ho-Sing-Loy M, Stringfellow LA;  
XX  
DR WPI; 2004-082210/08.  
XX  
PT Capture oligonucleotide composition useful for detection of hepatitis B  
PT virus (HBV), comprising polynucleotide having HBV-complementary sequence  
PT which is immobilized on solid support.  
XX  
PS Example 7; SEQ ID NO 121; 112bp; English.  
XX  
CC The invention relates to a capture oligonucleotide composition comprising  
CC an hepatitis B virus (HBV)-complementary sequence polynucleotide  
CC immobilised to a solid support. The composition is useful for detecting  
CC nucleic acids of HBV and/of HIV-1 and/or HCV in biological sample such as

CC blood, serum, plasma or other body fluid or tissue to be tested. The  
 CC composition can be used either in diagnostic application or for screening  
 CC donated blood and that products or other tissues that may contain  
 CC infectious particles. The composition facilitates detection of very low  
 CC levels of HBV nucleic acids. The composition allows selective detection  
 CC of nucleic acids of HBV and/or HIV and/or HCV. The present sequence is  
 CC used in the exemplification of the invention.

XX  
 SQ Sequence 19 BP; 3 A; 11 C; 3 G; 1 T; 1 U; 0 Other;

Query Match 66.7%; Score 12; DB 12; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 15 GGGGTCCTGGAG 4

RESULT 108  
 ADR81222/c  
 ID ADR81222 standard; DNA; 19 BP.

XX ADR81222;  
 AC  
 XX 16-DEC-2004 (first entry)  
 DT  
 XX Hepatitis C virus (HCV) oligonucleotide seqid 5721.

DE  
 XX  
 KM antiHepemic; cardiatic; vasotropic; antiarteriosclerotic; antidiabetic;  
 KM cytosaratic; anticonvulsant; nootropic; muscular; anti-HIV;  
 KM RNA interference; iRNA; antisense technology; lipid metabolism;  
 KM cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
 KM coronary artery disease; CAD; coronary heart disease; CHD;  
 KM atherosclerosis; hepatic glucose production;  
 KM glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
 KM colon cancer; lung cancer; neurological disease; Huntington disease;  
 KM spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.

XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2004080406-A2.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 08-MAR-2004; 2004WO-US007070.  
 XX  
 XX 07-MAR-2003; 2003US-0452682P.  
 PR 12-MAR-2003; 2003US-0454265P.  
 PR 13-MAR-2003; 2003US-0454962P.  
 PR 13-MAR-2003; 2003US-0455050P.  
 PR 14-APR-2003; 2003US-0462894P.  
 PR 17-APR-2003; 2003US-0463772P.  
 PR 25-APR-2003; 2003US-0465655P.  
 PR 25-APR-2003; 2003US-0465802P.  
 PR 09-MAY-2003; 2003US-0469612P.  
 PR 08-AUG-2003; 2003US-0493986P.  
 PR 11-AUG-2003; 2003US-0494597P.  
 PR 26-SEP-2003; 2003US-0506341P.  
 PR 09-OCT-2003; 2003US-0510246P.  
 PR 10-OCT-2003; 2003US-0510318P.  
 PR 07-NOV-2003; 2003US-0518453P.  
 XX  
 PA (ALNY-) ALNYLAM PHARM.  
 XX  
 PI Manoharan M, Bumcrot D;  
 XX  
 DR WPI; 2004-677362/66.  
 XX  
 XX  
 PT Interference RNA agent useful for treating dyslipidemia; coronary artery  
 PT disease, diabetes, cancer or neurological disease, comprises sense  
 PT sequence and antisense sequence which has specific modifications.  
 XX

PS Example 5; SEQ ID NO 5721; 378bp; English.

XX  
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a  
 CC sense sequence and an antisense sequence, where the sense sequences have  
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
 CC sequences have one or more asymmetrical phosphorothioate modifications  
 CC and the antisense sequence targets a human gene sequence. Also described  
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100  
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
 CC stabilising (I), involves selecting a sequence with activity and  
 CC introducing one or more asymmetrical modification in the sequence, where  
 CC the modification decreases nucleic acid sensitivity while not decreasing its  
 CC activity; a kit comprising (I) and instruction for its use; and a device  
 CC that can be dispense or administer a composition comprising (I). (I) is  
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels.  
 CC The subject is suffering from a disorder characterised by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
 CC dyslipidemia, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.

XX  
 SQ Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 13; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 19 GGGGTCCTGGAG 8

RESULT 109  
 ADR81223/c  
 ID ADR81223 standard; DNA; 19 BP.

XX ADR81223;  
 AC  
 XX 16-DEC-2004 (first entry)  
 DT  
 XX Hepatitis C virus (HCV) oligonucleotide seqid 5722.

DE  
 XX  
 KM antiHepemic; cardiatic; vasotropic; antiarteriosclerotic; antidiabetic;  
 KM cytosaratic; anticonvulsant; nootropic; muscular; anti-HIV;  
 KM RNA interference; iRNA; antisense technology; lipid metabolism;  
 KM cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
 KM coronary artery disease; CAD; coronary heart disease; CHD;  
 KM atherosclerosis; hepatic glucose production;  
 KM glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
 KM colon cancer; lung cancer; neurological disease; Huntington disease;  
 KM spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.

XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2004080406-A2.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 08-MAR-2004; 2004WO-US007070.  
 XX  
 XX 07-MAR-2003; 2003US-0452682P.  
 PR 12-MAR-2003; 2003US-0454265P.  
 PR 13-MAR-2003; 2003US-0454962P.

PR 13-MAR-2003; 2003US-0455050P.  
 PR 14-APR-2003; 2003US-0462894P.  
 PR 17-APR-2003; 2003US-0463772P.  
 PR 25-APR-2003; 2003US-0465665P.  
 PR 25-MAY-2003; 2003US-0465802P.  
 PR 09-MAY-2003; 2003US-0469612P.  
 PR 08-AUG-2003; 2003US-0493996P.  
 PR 11-AUG-2003; 2003US-0494597P.  
 PR 26-SEP-2003; 2003US-0506341P.  
 PR 09-OCT-2003; 2003US-0510246P.  
 PR 10-OCT-2003; 2003US-0510318P.  
 PR 07-NOV-2003; 2003US-0518453P.  
 XX  
 PA (ALNTV-) ALNTVLM PHARM.  
 XX  
 PI Manoharan M, Bumcrot D;  
 XX  
 DR WPI; 2004-677362/66.  
 XX  
 PT Interference RNA agent useful for treating dyslipidemias, coronary artery  
 PT disease, diabetes, cancer or neurological disease, comprises sense  
 PT sequence and antisense sequence which has specific modifications.  
 XX  
 PS Example 5; SEQ ID NO 5722; 378bp; English.  
 XX  
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a  
 CC sense sequence and an antisense sequence, where the sense sequences have  
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
 CC sequences have one or more asymmetrical phosphorothioate modifications  
 CC and the antisense sequence targets a human gene sequence. Also described  
 CC are: a pharmaceutical preparation comprising (II): reducing (MI) apob-100  
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
 CC stabilizing (I); involves selecting a sequence with activity and  
 CC introducing one or more asymmetrical modification in the sequence, where  
 CC the modification decreases nuclease sensitivity while not decreasing its  
 CC activity; a kit comprising (I) and an instruction for its use; and a device  
 CC that can be dispense or administer a composition comprising (I). (I) is  
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels. (MI)  
 CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels.  
 CC The subject is suffering from a disorder characterized by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
 CC dyslipidemias, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.  
 CC  
 SQ Sequence 19 BP; 3 A; 10 C; 4 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 66.7%; Score 12; DB 13; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 DB 18 GGGGTCCTCGAG 7  
 XX  
 RESULT 110  
 ID AA032979/c  
 XX AA032979 standard; DNA; 20 BP.  
 AC AA032979;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 14-MAY-1993 (first entry)

XX  
 DE HCV probe NC (+) (-235- -216).  
 XX  
 KM PCR; amplification; prototype; HCV pt; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9221759-A1.  
 XX  
 PD 10-DEC-1992.  
 XX  
 PF 04-JUN-1992; 92MO-FR000501.  
 XX  
 PR 06-JUN-1991; 91FR-00006882.  
 XX  
 PA (INSP) INST PASTEUR.  
 XX  
 PI Brechot C, Kremsdorf D, Porchon C;  
 XX  
 DR WPI; 1992-433657/52.  
 XX  
 PT New nucleotide and peptide sequences - specific for French isolate of  
 PT hepatitis C virus and useful in diagnosing and treating related  
 PT infections.  
 XX  
 PS Disclosure; Page 11; 50pp; French.  
 XX  
 CC RNA was extracted from the serum of an HCV-positive blood donor, subjected  
 CC to reverse transcription and the cDNA formed amplified by PCR.  
 CC Amplification products were cloned, screened with a probe derived from the  
 CC HCV prototype and inserts sequenced. The results showed marked  
 CC conservation in the non-coding region, significant variability in the  
 CC structural region (encoding envelope proteins) and reduced variability in  
 CC the non-structural region. The primer and probe sequences and positions  
 CC correspond to the HCV prototype (HCV pt) (EP-A-O 318 216 and WO-A-  
 CC 90/14436). (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 66.7%; Score 12; DB 2; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 DB 19 GGGGTCCTCGAG 8  
 XX  
 RESULT 111  
 ID AA065145  
 XX AA065145 standard; DNA; 20 BP.  
 AC AA065145;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI) SEKI M.



```
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 165; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AA064913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 U; 0 Other;

Query Match          66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12
   ||||:|||||
   9 GGGCTCTCGAG 20

Db

RESULT 112
AA065075
ID AA065075 standard; DNA; 20 BP.
XX AC AA065075;
XX DT 20-DEC-1994 (first entry)
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX KM Inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 134; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AA064913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 20 BP; 1 A; 4 C; 12 G; 3 T; 0 U; 0 Other;

Query Match          66.7%; Score 12; DB 2; Length 20;
```

```
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12
   ||||:|||||
   4 GGGCTCTCGAG 15

Db

RESULT 113
AA065114
ID AA065114 standard; DNA; 20 BP.
XX AC AA065114;
XX DT 21-DEC-1994 (first entry)
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX KM Inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 151; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AA064913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 U; 0 Other;

Query Match          66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12
   ||||:|||||
   7 GGGCTCTCGAG 18

Db

RESULT 114
AA065129
ID AA065129 standard; DNA; 20 BP.
XX AC AA065129;
XX DT 21-DEC-1994 (first entry)
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX KM Inhibition; viral protein precursor; ss.
```

```

XX OS Synthetic.
XX PS
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 158; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 20 BP; 2 A; 2 C; 14 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTCGAG 12
XX Db 8 GGGGTCTCTGAG 19
XX
XX RESULT 115
XX ID AAQ64918 standard; DNA; 20 BP.
XX AC AAQ64918;
XX AT 19-DEC-1994 (first entry)
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX KM inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX OS CA2104649-A.
XX PN 26-FEB-1994.
XX PD 23-AUG-1993; 93CA-02104649.
XX PF 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.

```

```

XX OS Claim 5; Page 66; 262pp; English.
XX PS
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 140; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTCGAG 12
XX Db 5 GGGGTCTCTGAG 16
XX
XX RESULT 116
XX ID AAQ65087 standard; DNA; 20 BP.
XX AC AAQ65087;
XX AT 20-DEC-1994 (first entry)
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX KM inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX OS CA2104649-A.
XX PN 26-FEB-1994.
XX PD 23-AUG-1993; 93CA-02104649.
XX PF 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 140; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX CC it has a base sequence of 15-30 bases which is included within the 49
XX CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX CC contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX CC genes
XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTCGAG 12
XX Db 5 GGGGTCTCTGAG 16

```

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RESULT 117
AA055282 standard; DNA; 20 BP.
ID AA055282 standard; DNA; 20 BP.
XX
XX
AC AA055282;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
XX CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Antisense oligonucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Disclosure; Page 225; 262pp; English.
XX
CC This oligonucleotide is an example of an antisense compound designed to
CC hybridise to a hepatitis C virus sequence. Such antisense
CC oligonucleotides are useful for inhibiting translation of HCV genes. (The
CC patent specification does not contain any references to this sequence)
XX
SQ Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12
   |||:|||||
Db 2 GGGGCTCTGGAG 13

RESULT 118
AA058400
ID AA058400 standard; DNA; 20 BP.
XX
AC AA058400;
XX
XX
DT 25-MAR-2003 (revised)
DT 04-OCT-1994 (first entry)
XX
DE Antisense oligonucleotide CAS-104 to HCV 5'-untranslated region.
XX
KM Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;
KM antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;
KM 5'-untranslated region; loop C; ss.
XX
OS Synthetic.
XX
XX WO9405813-A1.
XX
PD 17-MAR-1994.
XX

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```

PF 10-SEP-1993; 93WO-JP001293.
XX
XX 10-SEP-1992; 92US-00945289.
PR 14-APR-1993; 93JP-00087195.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PA (ISIS-) ISIS PHARM INC.
XX
XX Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;
PI Nakatake H, Hamada F, Eto T, Furukawa S;
XX
DR WPI; 1994-101217/12.
XX
PT Antisense oligonucleotide(s) complementary to hepatitis C viral genome
PT - useful for inhibiting HCV replication, to treat related diseases.
XX
XX Claim 28; Page 24; 91pp; English.
XX
CC Antisense oligonucleotides were synthesised which are complementary to
CC target sequences located at 10-nucleotide intervals from nucleotide 1 to
CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to
CC CAS-320), oligonucleotide CAS-110 (AA058403), which is complementary to a
CC portion of loop C, was found to cause greater than 80% inhibition of core
CC protein translation. Antisense oligonucleotides which are complementary
CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong
CC inhibitory activity compared to oligonucleotides complementary to other
CC regions of the 5'-UTR. The oligonucleotides CAS-104, -106 and -108 showed
CC 70% or more inhibition of HCV translation. See AA058388-Q58422, AA044885-
CC Q44892 and AA058383. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12
   |||:|||||
Db 1 GGGGCTCTGGAG 12

RESULT 119
AA058401
ID AA058401 standard; DNA; 20 BP.
XX
AC AA058401;
XX
XX
DT 25-MAR-2003 (revised)
DT 04-OCT-1994 (first entry)
XX
DE Antisense oligonucleotide CAS-106 to HCV 5'-untranslated region.
XX
XX Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;
XX antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;
XX 5'-untranslated region; loop C; ss.
XX
OS Synthetic.
XX
XX WO9405813-A1.
XX
XX
PD 17-MAR-1994.
XX
PF 10-SEP-1993; 93WO-JP001293.
XX
XX 10-SEP-1992; 92US-00945289.
PR 14-APR-1993; 93JP-00087195.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PA (ISIS-) ISIS PHARM INC.
XX
XX Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;
PI

```

PI Nakatake H, Hamada F, Eto T, Furukawa S;  
 XX WPI; 1994-101217/12.  
 DR Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome  
 XX PT - useful for inhibiting HCV replication, to treat related diseases.  
 XX PS Claim 28; Page 24; 91pp; English.  
 CC Antisense oligonucleotides were synthesised which are complementary to  
 CC target sequences located at 10-nucleotide intervals from nucleotide 1 to  
 CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to  
 CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a  
 CC portion of loop C, was found to cause greater than 80% inhibition of core  
 CC protein translation. Antisense oligonucleotides which are complementary  
 CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong  
 CC inhibitory activity compared to oligonucleotides complementary to other  
 CC regions of the 5'-UTR. The oligonucleotides CAS-104, -106 and -108 showed  
 CC 70% or more inhibition of HCV translation. See AAQ58388-Q58422, AAQ44885-  
 CC Q44892 and AAQ58383. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 20 BP; 2 A; 4 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGUGAG 12  
 |||||:  
 Db 3 GGGGTCTGAG 14

RESULT 120  
 AAQ58402  
 ID AAQ58402 standard; DNA; 20 BP.  
 AC AAQ58402;  
 XX 25-MAR-2003 (revised)  
 DT 04-OCT-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide CAS-108 to HCV 5'-untranslated region.  
 XX Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;  
 KW antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;  
 KM 5'-untranslated region; loop C; ss.  
 XX Synthetic.  
 OS  
 PN WO9405813-A1.  
 XX 17-MAR-1994.  
 PD 10-SEP-1993; 93WO-JP001293.  
 XX PF 10-SEP-1992; 92US-00945289.  
 PR 14-APR-1993; 93JP-00087195.  
 XX  
 PA (MOCH) MOCHIDA PHARM CO LTD.  
 PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Anderson KP, Hanecek RC, Hoshiko K, Nozaki C, Nishihara T;  
 PI Nakatake H, Hamada F, Eto T, Furukawa S;  
 XX WPI; 1994-101217/12.  
 DR Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome  
 XX PT - useful for inhibiting HCV replication, to treat related diseases.  
 XX PS Claim 28; Page 24; 91pp; English.  
 CC Antisense oligonucleotides were synthesised which are complementary to

CC target sequences located at 10-nucleotide intervals from nucleotide 1 to  
 CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to  
 CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a  
 CC portion of loop C, was found to cause greater than 80% inhibition of core  
 CC protein translation. Antisense oligonucleotides which are complementary  
 CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong  
 CC inhibitory activity compared to oligonucleotides complementary to other  
 CC regions of the 5'-UTR. The oligonucleotides CAS-104, -106 and -108 showed  
 CC 70% or more inhibition of HCV translation. See AAQ58388-Q58422, AAQ44885-  
 CC Q44892 and AAQ58383. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGUGAG 12  
 |||||:  
 Db 5 GGGGTCTGAG 16

RESULT 121  
 AAQ58406  
 ID AAQ58406 standard; DNA; 20 BP.  
 AC AAQ58406;  
 XX 25-MAR-2003 (revised)  
 DT 04-OCT-1994 (first entry)  
 XX

DE Antisense oligonucleotide CAS-112 to HCV 5'-untranslated region.

KW Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;  
 KW antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;  
 KM 5'-untranslated region; loop C; ss.

XX Synthetic.

OS  
 PN WO9405813-A1.

XX 17-MAR-1994.

PD 10-SEP-1993; 93WO-JP001293.

XX PF 10-SEP-1992; 92US-00945289.

PR 14-APR-1993; 93JP-00087195.

XX  
 PA (MOCH) MOCHIDA PHARM CO LTD.  
 PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.

PA (ISIS-) ISIS PHARM INC.

XX  
 PI Anderson KP, Hanecek RC, Hoshiko K, Nozaki C, Nishihara T;  
 PI Nakatake H, Hamada F, Eto T, Furukawa S;

XX WPI; 1994-101217/12.

DR Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome  
 XX PT - useful for inhibiting HCV replication, to treat related diseases.  
 XX PS Claim 28; Page 24; 91pp; English.

CC Antisense oligonucleotides were synthesised which are complementary to  
 CC target sequences located at 10-nucleotide intervals from nucleotide 1 to  
 CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to  
 CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a  
 CC portion of loop C, was found to cause greater than 80% inhibition of core  
 CC protein translation. Antisense oligonucleotides which are complementary  
 CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong  
 CC inhibitory activity compared to oligonucleotides complementary to other  
 CC regions of the 5'-UTR. See AAQ58388-Q58422, AAQ44885-Q44892 and AAQ58383.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 9 GGGGTCTCTGGAG 20

# RESULT 122

AAQ58403 ID AAQ58403 standard; DNA; 20 BP.

AC AAQ58403;

DT 25-MAR-2003 (revised)

DT 04-OCT-1994 (first entry)

DE Antisense oligonucleotide CAS-110 to HCV 5'-untranslated region.

XX Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;

KM Antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;

KM 5'-untranslated region; loop C; ss.

XX Synthetic.

OS WO9405813-A1.

PN 17-MAR-1994.

PD 10-SEP-1993; 93WO-JP001293.

PR 10-SEP-1992; 92US-00945289.

PR 14-APR-1993; 93JP-00087195.

XX (MOCH) MOCHIDA PHARM CO LTD.

PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.

PA (ISIS-) ISIS PHARM INC.

XX Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;

PI Nakatake H, Hamada F, Eco T, Furukawa S;

PI WPI; 1994-101217/12.

DR WPI; 1994-101217/12.

XX Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome

PT - useful for inhibiting HCV replication, to treat related diseases.

XX Claim 28; Page 24; 91pp; English.

PS Antisense oligonucleotides were synthesised which are complementary to

CC target sequences located at 10-nucleotide intervals from nucleotide 1 to

CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to

CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a

CC portion of loop C, was found to cause greater than 80% inhibition of core

CC protein translation. Antisense oligonucleotides which are complementary

CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong

CC inhibitory activity compared to oligonucleotides complementary to other

CC regions of the 5'-UTR. See AAQ58388-Q58422, AAQ44885-Q44892 and AAQ58383.

# RESULT 123

AAT39734/C ID AAT39734 standard; DNA; 20 BP.

AC AAT39734;

DT 09-APR-1997 (first entry)

XX Hepatitis C virus PCR primer IN2, based on nucleotides 88-97.

XX Hepatitis C virus; HCV; polymerase chain reaction; amplification;

KM replication; non-lymphoblastoid cell; monkey kidney cell; ss.

XX Synthetic.

OS WO9624662-A1.

PN 15-AUG-1996.

PD 10-FEB-1995; 95WO-IT000016.

PR 10-FEB-1995; 95WO-IT000016.

PR (CMR) CONSIGLIO NAZ DELLE RICERCHE.

PA Ravagnan G, Battaglia M, Carloni G, Ponzetto A, Iacovacci S;

PI WPI; 1996-384435/38.

DR Replication of hepatitis C virus in non-lymphoblastoid mammalian cells -

XX useful for studies of HCV replication, prodn. of vaccines or viral

PT antigens, etc.

PS Disclosure; Page 8; 25pp; English.

XX Hepatitis C virus can be replicated in non-lymphoblastoid mammalian cells

CC by first incubating an HCV sample with the cells until an infecting

CC amount of HCV has been absorbed. Infected cells are then washed and

CC incubated under growth conditions. In an example, the presence of HCV in

CC culture medium of monkey kidney cells inoculated with HCV-infected serum

CC was verified by PCR amplification using two external primers (OU1 and

CC OU2, see AAT39731 and AAT39732) and two internal primers (IN1 and IN2,

CC see AAT39733 and AAT39734). The amplified products were identified by

CC hybridisation to labelled probe SI (see AAT39735). Small amounts of virus

CC were shown to be released into the culture medium from secondary

CC cultures. Control (non-inoculated) cells were negative for presence of

CC viral genome

XX Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 19 GGGGTCTCTGGAG 8

RESULT 124  
AAT80229 ID AAT80229 standard; DNA; 20 BP.

AC AAT80229;

DT 15-OCT-1997 (first entry)

DE Oligo HCV42, targeted to HCV mRNA RNase sensitive region B.

XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;

KM inhibition; replication; expression; detection; chronic hepatitis;

KM acute hepatitis; hepatocarcinoma; ss.

```

OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /note= "Comprises phosphorothioate linkages"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX PD
XX
XX PF 04-JUN-1996; 96WO-EP002427.
XX
XX PR 06-JUN-1995; 95US-00471968.
XX
XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX PI Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;
XX PI Roberts PC, Walthers DM, Wolfe JL;
XX
XX DR WPI; 1997-043122/04.
XX
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX
XX PS Disclosure; Page 25; 100pp; English.
XX
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This oligo was used in an RNase H assay to determine
XX CC whether it binds successfully to its target. Three regions of HCV mRNA
XX CC were investigated as RNase sensitive sites. This oligo binds to position
XX CC -237 to -218
XX
XX SQ Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCUCCUGAG 12
XX ||||:|||||
XX 2 GGGGTCTCTGGAG 13
XX
XX Db
XX
XX RESULT 125
XX AAT80230
XX ID AAT80230 standard; DNA; 20 BP.
XX
XX AC AAT80230;
XX
XX DT 15-OCT-1997 (first entry)
XX
XX DE Oligo HCV43, targetted to HCV mRNA RNase sensitive region B.
XX
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KW inhibition; replication; expression; detection; chronic hepatitis;
XX KW acute hepatitis; hepatocarcinoma; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /note= "Comprises phosphorothioate linkages"

```

```

XX
XX PN WO9639500-A2.
XX
XX PD 12-DEC-1996.
XX
XX PF 04-JUN-1996; 96WO-EP002427.
XX
XX PR 06-JUN-1995; 95US-00471968.
XX
XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX PI Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;
XX PI Roberts PC, Walthers DM, Wolfe JL;
XX
XX DR WPI; 1997-043122/04.
XX
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX
XX PS Disclosure; Page 25; 100pp; English.
XX
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This oligo was used in an RNase H assay to determine
XX CC whether it binds successfully to its target. Three regions of HCV mRNA
XX CC were investigated as RNase sensitive sites. This oligo binds to position
XX CC -233 to -214
XX
XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCUCCUGAG 12
XX ||||:|||||
XX 6 GGGGTCTCTGGAG 17
XX
XX Db
XX
XX RESULT 126
XX AAX84019/C
XX ID AAX84019 standard; cDNA; 20 BP.
XX
XX AC AAX84019;
XX
XX DT 27-AUG-2003 (revised)
XX DT 26-AUG-1999 (first entry)
XX
XX DE Probe for HCV EI coding sequence.
XX
XX KW HCV EI region; monoclonal antibody; diagnosis; HCV EI-specific antigen;
XX KW probe; ss.
XX
XX OS Synthetic.
XX
XX PN US5919454-A.
XX
XX PD 06-JUL-1999.
XX
XX PF 07-JUN-1995; 95US-00487231.
XX
XX PR 18-MAR-1993; 93US-00965285.
XX
XX PA (INSP) INST PASTEUR.

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XX Porchon C, Brechot C, Kremendorf D;
XX WPI; 1999-394595/33.
XX Nucleotides and peptides from hepatitis C virus isolate for detecting EI-
XX specific antigens.
XX PS Disclosure; Col 5; 45pp; English.
XX This sequence represents a probe for DNA encoding a hepatitis C virus
XX (HCV) E1 region protein. The invention relates to human or murine
XX monoclonal antibodies directed against a HCV E1 protein sequence. The
XX CC monoclinal antibodies and their fragments are useful for the in vitro
XX CC diagnosis of HCV E1-specific antigens. (Updated on 27-AUG-2003 to correct
XX OS field.)
XX Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGAG 12
Db 19 GGGCTCTGAG 8

```

RESULT 127  
AA16776/c  
ID AA16776 standard; DNA; 20 BP.

AC AA16776;  
XX  
XX 27-APR-1999 (first entry)  
XX  
XX Hepatitis C virus probe NC, bases -235 to -216.  
XX  
XX  
XX E1 region; French Hepatitis C virus; HCV; immunogen; antibody; detection;  
XX Immunassay; probe; hybridisation; ss.  
XX  
XX Synthetic.  
XX Hepatitis C virus.  
XX  
XX  
XX US5866139-A.  
XX  
XX 02-FEB-1999.  
XX  
XX 07-JUN-1995; 95US-00483695.  
XX  
XX 18-MAR-1993; 93US-00965285.  
XX  
XX (INSP ) INST PASTEUR.  
XX  
XX Porchon C, Kremendorf D, Brechot C;  
XX WPI; 1999-141865/12.  
XX  
XX New isolated and purified Hepatitis C virus E1 peptides - useful for  
XX vaccine production or diagnostic purposes.  
XX  
XX  
XX Disclosure; Col 5-6; 45pp; English.  
XX  
XX Probes AA16773-X16777 were used to screen for sequences in the E1, NS1,  
XX CC NS2, NS3 and NS4 regions from a French Hepatitis C virus (HCV) isolate.  
XX CC The protein or peptides derived from these regions (see AA16758-X16761)  
XX CC can be: (i) conjugated to a carrier protein and used as immunogens for  
XX CC eliciting protective antibodies; or (ii) labelled, and used as  
XX CC immunassay reagents for detecting antibodies specific for HCV E1  
XX  
XX Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 20;

```

Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGAG 12
Db 19 GGGCTCTGAG 8

```

RESULT 128  
AA52565  
ID AA52565 standard; DNA; 20 BP.  
XX  
XX AA52565;  
XX  
XX 27-SEP-2000 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO:3, complementary to HCV RNA bases 97-116.  
XX  
XX Oligonucleotide; HCV genomic RNA; detection; amplification;  
XX reverse transcription inhibition; translation inhibition; antiviral;  
XX gene therapy; antisense; reverse transcription-PCR; RT-PCR primer; probe;  
XX ss.  
XX  
XX Hepatitis C virus.  
XX  
XX  
XX Key Location/Qualifiers  
XX FT masc\_binding 1..20 /\*tag= a  
XX FT /bound\_molecy= "HCV genomic RNA, bases 97-116"  
XX  
XX EP1002878-A2.  
XX  
XX 24-MAY-2000.  
XX  
XX 18-NOV-1999; 99EP-00122092.  
XX  
XX 19-NOV-1998; 98JP-00329874.  
XX  
XX (TOYT ) TOSOH CORP.  
XX  
XX  
XX Toshiki T, Takahiko I, Juichi S;  
XX WPI; 2000-352431/31.  
XX  
XX  
XX Hepatitis C virus RNA-binding single-stranded oligo DNAs useful as  
XX reagents for gene diagnosis involving cleavage, amplification and  
XX detection of RNA and as an inhibitory drugs.  
XX  
XX  
XX Claim 3; Page 12; 21pp; English.  
XX  
XX The invention relates to single-stranded antisense oligodeoxynucleotides  
XX CC (AA52563-A52568) which bind to various sites on the hepatitis C virus  
XX CC (HCV) RNA genome, and to sense oligodeoxynucleotides (AA52569-A52571)  
XX CC corresponding to sites on the HCV genome. The oligonucleotides are useful  
XX CC as primers in RT-PCR (reverse transcription-PCR) and the sense  
XX CC oligonucleotides may also be used as promoter primers. The antisense  
XX CC oligonucleotides may be used to inhibit translation or reverse  
XX CC transcription of HCV RNA and may be used as probes for detection of HCV  
XX CC RNA. Additionally, the antisense oligos may be linked to an RNA-cleaving  
XX CC cleavage. The invention also encompasses methods of identifying and  
XX CC preparing single-stranded oligodeoxynucleotides which bind to target  
XX CC RNAs. The single-stranded oligodeoxynucleotides are useful as reagents  
XX CC for genetic diagnosis involving cleavage, amplification and detection of  
XX CC HCV RNA (as primers and probes), and as inhibitors of reverse  
XX CC transcription or translation of HCV RNA. Sequences AA52563-A52568  
XX CC represent the antisense oligodeoxynucleotides of the invention. The  
XX CC present sequence is complementary to bases 97-116 of HCV genomic RNA  
XX  
XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|||||  
Db 6 GGGGTCTCGAG 17

## RESULT 129

AAA52566  
ID AAA52566 standard; DNA; 20 BP.

AAA52566;

DT 27-SEP-2000 (first entry)

DE Oligonucleotide SEQ ID NO:4, complementary to HCV RNA bases 95-114.

KM Oligonucleotide; HCV genomic RNA; detection; amplification;

KM reverse transcription inhibition; translation inhibition; antiviral;

KW gene therapy; antisense; reverse transcription-PCR; RT-PCR primer; probe;

ss.

OS Hepatitis C virus.

XX

Key Location/Qualifiers

FT misc\_binding 1..20

FT /tag= a /bound\_moiety= "HCV genomic RNA, bases 95-114"

PN EP1002878-A2.

PD 24-MAY-2000.

PF 18-NOV-1999; 99EP-00122092.

PR 19-NOV-1998; 98UP-00329874.

XX (TOYU ) TOSOH CORP.

XX

XX

PI Toshiko T, Takahiko I, Juichi S;

DR WPI; 2000-352431/31.

XX

XX

PT Hepatitis C virus RNA-binding single-stranded oligo DNAs useful as

PT reagents for gene diagnosis involving cleavage, amplification and

PT detection of RNA and as an inhibitory drugs.

PS Claim 4; Page 13; 21pp; English.

XX

XX

CC The invention relates to single-stranded antisense oligodeoxynucleotides

CC (AAA52563-A52568) which bind to various sites on the hepatitis C virus

CC (HCV) RNA genome, and to sense oligodeoxynucleotides (AAA52569-A52571)

CC corresponding to sites on the HCV genome. The oligonucleotides are useful

CC as primers in RT-PCR (reverse transcription-PCR) and the sense

CC oligonucleotides may also be used as promoter primers. The antisense

CC oligonucleotides may be used to inhibit translation or reverse

CC transcription of HCV RNA and may be used as probes for detection of HCV

CC RNA. Additionally, the antisense oligos may be linked to an RNA-cleaving

CC moiety to target single-stranded RNA cleavage or RNA heteroduplex

CC cleavage. The invention also encompasses methods of identifying and

CC preparing single-stranded oligodeoxynucleotides which bind to target

CC RNAs. The single-stranded oligodeoxynucleotides are useful as reagents

CC for genetic diagnosis involving cleavage, amplification and detection of

CC HCV RNA (as primers and probes), and as inhibitors of reverse

CC transcription or translation of HCV RNA. Sequences AAA42563-A52568

CC represent the antisense oligodeoxynucleotides of the invention. The

CC present sequence is complementary to bases 95-114 of HCV genomic RNA

XX

XX

Qy 1 GGGGUCCUGAG 12  
|||:|||||  
Db 4 GGGGTCTCGAG 15

RESULT 130

AAA52564  
ID AAA52564 standard; DNA; 20 BP.

AAA52564;

DT 27-SEP-2000 (first entry)

DE Oligonucleotide SEQ ID NO:2, complementary to HCV RNA bases 99-118.

KM Oligonucleotide; HCV genomic RNA; detection; amplification;

KM reverse transcription inhibition; translation inhibition; antiviral;

KW gene therapy; antisense; reverse transcription-PCR; RT-PCR primer; probe;

ss.

OS Hepatitis C virus.

XX

Key Location/Qualifiers

FT misc\_binding 1..20

FT /tag= a /bound\_moiety= "HCV genomic RNA, bases 99-118"

PN EP1002878-A2.

PD 24-MAY-2000.

PF 18-NOV-1999; 99EP-00122092.

PR 19-NOV-1998; 98UP-00329874.

XX (TOYU ) TOSOH CORP.

XX

XX

PI Toshiko T, Takahiko I, Juichi S;

DR WPI; 2000-352431/31.

XX

XX

PT Hepatitis C virus RNA-binding single-stranded oligo DNAs useful as

PT reagents for gene diagnosis involving cleavage, amplification and

PT detection of RNA and as an inhibitory drugs.

PS Claim 2; Page 12; 21pp; English.

XX

XX

CC The invention relates to single-stranded antisense oligodeoxynucleotides

CC (AAA52563-A52568) which bind to various sites on the hepatitis C virus

CC (HCV) RNA genome, and to sense oligodeoxynucleotides (AAA52569-A52571)

CC corresponding to sites on the HCV genome. The oligonucleotides are useful

CC as primers in RT-PCR (reverse transcription-PCR) and the sense

CC oligonucleotides may also be used as promoter primers. The antisense

CC oligonucleotides may be used to inhibit translation or reverse

CC transcription of HCV RNA and may be used as probes for detection of HCV

CC RNA. Additionally, the antisense oligos may be linked to an RNA-cleaving

CC moiety to target single-stranded RNA cleavage or RNA heteroduplex

CC cleavage. The invention also encompasses methods of identifying and

CC preparing single-stranded oligodeoxynucleotides which bind to target

CC RNAs. The single-stranded oligodeoxynucleotides are useful as reagents

CC for genetic diagnosis involving cleavage, amplification and detection of

CC HCV RNA (as primers and probes), and as inhibitors of reverse

CC transcription or translation of HCV RNA. Sequences AAA42563-A52568

CC represent the antisense oligodeoxynucleotides of the invention. The

CC present sequence is complementary to bases 99-118 of HCV genomic RNA

XX

XX

Sequence 20 BP; 2 A; 2 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 3; Length 20;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



OY 1 GGGGUCUCGAG 12  
 |||||:  
 DB 8 GGGGTCCTCGAG 19

RESULT 131  
 ID AAK52663/C  
 ABK52663 standard; DNA; 20 BP.

XX AC ABK52663;

XX DT 27-AUG-2002 (first entry)

XX DE Hepatitis C virus DNA real time PCR probe.

XX KM Human; hepatitis C virus; HCV probe; PCR, real-time PCR; antiviral;

XX KM viral replication inhibitor; mitochondrial toxicity; ss.

XX OS Hepatitis C virus.

XX FT Key Location/Qualifiers

FT modified\_base 1

FT /tag= a  
 /note= "FAM (6-carboxy fluorescein) labelled"

FT modified\_base 20

FT /tag= b  
 /note= "TAMRA (6-carbo tetramethyl rhodamine) labelled"

XX PN WO200233128-A2.

XX PD 25-APR-2002.

XX PF 18-OCT-2001; 2001WO-US047223.

XX PR 18-OCT-2000; 2000US-0241488P.

XX PR 15-DEC-2000; 2000US-0256067P.

XX PR 06-APR-2001; 2001US-0282156P.

XX PA (PHAR-) PHARMASSET LTD.

XX PI Stuyver L, Watanabe KA;

XX DR WPI; 2002-454613/48.

XX PT Identifying a viral replication inhibitor comprises contacting nucleic  
 acids from a virus infected host with an amplification mixture of two  
 PT primers and/or probes that provide detectable signals during a polymerase  
 PT chain reaction.

XX PS Example 16; Page 36; 95pp; English.

XX CC This invention relates to a novel method for identifying an inhibitor of  
 CC viral replication by contacting nucleic acids from a virus infected host  
 CC with an amplification mixture having 2 primers and/or probes that provide  
 CC detectable signals during a polymerase chain reaction. The method of the  
 CC invention is useful for identifying a compound that inhibits viral  
 CC replication. Another new method is useful for assessing the toxicity of  
 CC an anti-viral compound. The method of the invention is economic, non-  
 CC radioactive, rapid, accurate, reproducible and amenable to large  
 CC throughput. The second method of the invention is a sensitive and  
 CC accurate method for determining mitochondrial toxicity of a compound. The  
 CC present sequence represents a hepatitis C virus (HCV) real time PCR probe  
 CC used in the method of the invention

XX SQ Sequence 20 BP; 2 A; 14 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUCGAG 12  
 |||||:  
 DB 13 GGGGTCCTCGAG 2

RESULT 132

XX ID AAD33151 standard; DNA; 20 BP.

XX AC AAD33151;

XX DT 01-JUL-2002 (first entry)

XX DE GsuI enzyme recognition sequence #2.

XX KM Restriction endonuclease; altered specificity; recognition sequence;  
 KM GsuI; enzyme; de.

XX OS Unidentified.

XX OS EPI179596-A1.

XX PD 13-FEB-2002.

XX PF 06-JUL-2001; 2001EP-00305859.

XX PR 10-AUG-2000; 2000GB-00019744.

XX PA (FERM-) FERMENTAS AB.

XX PI Janulaitis A, Rimseleiene R, Lubys A;

XX DR WPI; 2002-229927/29.

XX PT Producing DNA encoding restriction endonuclease with altered specificity,  
 PT comprises mutagenizing DNA encoding the enzyme and isolating DNA encoding  
 PT mutated enzyme with specificity for an altered sequence.

XX PS Example; Page 5; 44pp; English.

XX CC The invention relates to a method of producing a polynucleotide encoding  
 CC a restriction endonuclease with altered specificity. The method involves  
 CC mutagenizing a polynucleotide encoding restriction endonuclease with  
 CC specificity for a recognition sequence to produce mutated polynucleotides  
 CC and isolating from them a polynucleotide encoding mutated restriction  
 CC endonuclease with specificity for an altered recognition sequence by  
 CC selecting a polynucleotide expressing a restriction endonuclease with  
 CC methylase specificity for the altered recognition sequence. The method is  
 CC useful for producing a polynucleotide encoding a restriction endonuclease  
 CC comprising Eco571, BcgI, HaeIII or AclI, with an altered specificity. The  
 CC method allows selection of mutant variants recognising new sequences that  
 CC differ not only in single nucleotide from wild type enzyme but also for  
 CC mutants that recognise degenerate sequences or sequences differing in  
 CC several nucleotides, especially if mutants of altered specificity are  
 CC taken into the next round of mutagenesis and digestion-selection. The  
 CC present sequence is recognition sequence of GsuI restriction enzyme

XX SQ Sequence 20 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 14 Other;

Query Match 66.7%; Score 12; DB 6; Length 20;  
 Best Local Similarity 91.7%; Pred. No. 3.4e+03;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CTGGAGNNNNNN 18  
 |||||:  
 DB 1 CTGGAGNNNNNN 12

RESULT 133

XX ID ABO78212 standard; DNA; 20 BP.

XX AC ABO78212;

XX DT 22-OCT-2002 (first entry)

DE Probe complementary to HCV 5' untranslated region.  
 XX  
 KW Flavivirus; Orthomyxovirus; Paramyxovirus; viral infection;  
 KW cellular proliferation; beta-D nucleoside; beta-L nucleoside;  
 KW Hepatitis C virus; HCV; bovine viral diarrhoea virus; BVDV;  
 KW respiratory syncytial virus; RSV; pneumonia virus; psoriasis; eczema;  
 KW turkey rhinotracheitis virus; hyperproliferation; atopic dermatitis;  
 KW lichen planus; wart; pemphigus vulgaris; actinic keratosis; carcinoma;  
 KW blood vessel proliferation disorder; fibrotic disorder;  
 KW autoimmune disorder; graft-versus-host rejection; tumour; cancer;  
 KW atherosclerosis; retinopathy; atherosclerosis; angiogenic disorder;  
 KW vasculogenic disorder; hepatic cirrhosis; glomerulonephritis;  
 KW mesangial proliferation cell disorder; renal disease;  
 KW diabetic nephropathy; malignant nephrosclerosis; transplant rejection;  
 KW thrombotic microangiopathy syndrome; glomerulangiopathy syndrome;  
 KW rheumatoid arthritis; Bachel's syndrome; leukemia; inflammation;  
 KW acquired immune deficiency syndrome; vasculitis; lipid histiocytosis;  
 KW septic shock; probe; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /note= "6-Fam attached"  
 FT modified\_base 28  
 FT /\*tag= b  
 FT /note= "TAMRA attached"  
 FT  
 PN WO200232920-A2.  
 XX  
 PD 25-APR-2002.  
 PF 18-OCT-2001; 2001WO-US046113.  
 XX  
 PR 18-OCT-2000; 2000US-0241488P.  
 PR 06-APR-2001; 2001US-0282156P.  
 XX  
 PA (PHAR-) PHARMASSET LTD.  
 XX  
 PI Stuyver L, Watanabe KA;  
 XX  
 DR MPI; 2002-590431/63.  
 PT Use of beta-D and beta-L nucleosides in the treatment of a virus  
 PT belonging to the Flaviviridae, Orthomyxoviridae or Paramyxoviridae  
 PT family.  
 PS  
 PS Example 52; Page 181; 230pp; English.  
 XX  
 CC The specification describes a method for the treatment or prophylaxis of  
 CC a host exhibiting a Flaviviridae, Orthomyxoviridae or Paramyxoviridae  
 CC viral infection or abnormal cellular proliferation. The method involves  
 CC administering a beta-D or beta-L nucleoside, of formulas given in the  
 CC specification, to the host. The method is useful for the treatment of a  
 CC Flaviviridae, Orthomyxoviridae and/or Paramyxoviridae viral infection,  
 CC and abnormal cellular proliferation. The Flaviviridae viral infection  
 CC includes hepatitis C virus (HCV) and bovine viral diarrhoea virus (BVDV).  
 CC The Orthomyxoviridae viral infection includes respiratory syncytial virus  
 CC (RSV) e.g. bovine RSV, ovine RSV, caprine RSV, pneumonia virus of mice  
 CC and turkey rhinotracheitis virus. The abnormal cellular proliferation  
 CC includes hyperproliferation e.g. psoriasis, chronic eczema, atopic  
 CC dermatitis, lichen planus, wart, pemphigus vulgaris, actinic keratosis,  
 CC basal cell carcinoma and squamous cell carcinoma, blood vessel  
 CC proliferation disorders, fibrotic disorders, autoimmune disorders, graft-  
 CC versus-host rejection, tumours and cancers. The blood vessel  
 CC proliferation disorders e.g. restenosis, retinopathy and atherosclerosis  
 CC include angiogenic and vasculogenic disorders, the fibrotic disorders  
 CC include hepatic cirrhosis and mesangial proliferation cell disorders  
 CC include human renal diseases e.g. glomerulonephritis, diabetic  
 CC nephropathy, malignant nephrosclerosis, thrombotic microangiopathy  
 CC syndromes, transplant rejection and glomerulangiopathy syndromes. The  
 CC method is also useful for treating rheumatoid arthritis, Bachel's

CC syndrome, leukemia, acquired immune deficiency syndrome, vasculitis,  
 CC lipid histiocytosis, septic shock and inflammation. The present sequence  
 CC represents a probe complementary to the HCV 5' untranslated region, which  
 CC is used in the course of the invention  
 XX  
 SQ Sequence 20 BP; 2 A; 14 C; 2 G; 2 T; 0 U; 0 Other;  
 QY 1 GGGGUCUGGAG 12  
 Db 13 GGGGUCUGGAG 2  
 Query Match 66.7%; Score 12; DB 6; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 134  
 ABS65813  
 ID ABS65813 standard; DNA; 20 BP.  
 XX  
 AC ABS65813;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #19.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR MPI; 2002-537132/57.  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 PS  
 PS Disclosure; Page 8; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non-  
 CC B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence

CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV  
 XX  
 SQ Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 6; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 2 GGGGTCTGTGAG 13  
 ||||:||||  
 RESULT 135  
 ABS55814  
 ID ABS55814 standard; DNA; 20 BP.  
 XX  
 AC ABS55814;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #20.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 PT  
 PS Disclosure; Page 8; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV

XX  
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 6; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 6 GGGGTCTGTGAG 17  
 ||||:||||  
 RESULT 136  
 AAQ65101  
 ID AAQ65101 standard; DNA; 21 BP.  
 XX  
 AC AAQ65101;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KW inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 PT  
 PS Claim 5; Page 146; 262pp; English.  
 XX  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AAQ64913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 21 BP; 2 A; 3 C; 13 G; 3 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 2; Length 21;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 7 GGGGTCTGTGAG 18  
 ||||:||||  
 RESULT 137  
 AAQ64923  
 ID AAQ64923 standard; DNA; 21 BP.  
 XX  
 AC AAQ64923;  
 XX  
 DT 19-DEC-1994 (first entry)  
 XX

```

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 68; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 16-24 bases which is included within the 24
CC bases from G at position 127 to C at position 150 of AAQ64913 and which
CC contains at least 16 bases from C at position 131 to A at position 146.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
SQ Sequence 21 BP; 3 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 12; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
Db 1 GGGGTCCTGGAG 12
XX
RESULT 138
AAQ65088
ID AAQ65088 standard; DNA; 21 BP.
XX
XX AAQ65088;
AC
XX
XX 20-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX
XX CA2104649-A.
PN
XX
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
XX
XX

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DR WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 140; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
SQ Sequence 21 BP; 2 A; 3 C; 13 G; 3 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 12; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
Db 6 GGGGTCCTGGAG 17
XX
RESULT 139
AAQ65130
ID AAQ65130 standard; DNA; 21 BP.
XX
XX AAQ65130;
AC
XX
XX 21-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX
XX CA2104649-A.
PN
XX
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 158; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
SQ Sequence 21 BP; 2 A; 3 C; 14 G; 2 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 12; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 GGGGUCGAG 12  
 ||||:||||  
 Db 9 GGGGTCTGGAG 20

## RESULT 140

AA065115  
 ID AA065115 standard; DNA; 21 BP.

XX AA065115;

XX 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.

XX Synthetic.

XX CA2104649-A.

XX 26-FEB-1994.

XX 23-AUG-1993; 93CA-02104649.

XX 25-AUG-1992; 92JP-00248796.

XX 03-MAR-1993; 93JP-00042736.

XX (SEKI/) SEKI M.

XX Seki M, Honda Y, Yamada E;

XX WPI; 1994-151836/19.

PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 genome - are useful as antiviral agents.

XX Claim 5; Page 152; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 it has a base sequence of 15-30 bases which is included within the 49  
 bases from G at position 127 to C at position 175 of AA064913 and which  
 contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 genes

SO Sequence 21 BP; 2 A; 3 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 21;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
 ||||:||||  
 Db 8 GGGGTCTGGAG 19

## RESULT 141

AA065076  
 ID AA065076 standard; DNA; 21 BP.

XX AA065076;

XX 20-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.

XX Synthetic.

PN CA2104649-A.

XX 26-FEB-1994.

XX 23-AUG-1993; 93CA-02104649.

XX 25-AUG-1992; 92JP-00248796.

XX 03-MAR-1993; 93JP-00042736.

XX (SEKI/) SEKI M.

XX Seki M, Honda Y, Yamada E;

XX WPI; 1994-151836/19.

PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 genome - are useful as antiviral agents.

XX Claim 5; Page 135; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 it has a base sequence of 15-30 bases which is included within the 49  
 bases from G at position 127 to C at position 175 of AA064913 and which  
 contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 genes

SO Sequence 21 BP; 2 A; 4 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 21;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
 ||||:||||  
 Db 5 GGGGTCTGGAG 16

## RESULT 142

AA065146  
 ID AA065146 standard; DNA; 21 BP.

XX AA065146;

XX 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.

XX Synthetic.

XX CA2104649-A.

XX 26-FEB-1994.

XX 23-AUG-1993; 93CA-02104649.

XX 25-AUG-1992; 92JP-00248796.

XX 03-MAR-1993; 93JP-00042736.

XX (SEKI/) SEKI M.

XX Seki M, Honda Y, Yamada E;

XX WPI; 1994-151836/19.

PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 genome - are useful as antiviral agents.

XX Claim 5; Page 165; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes

XX Sequence 21 BP; 2 A; 5 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 21;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:  
 DB 10 GGGGTCCTGGAG 21

## RESULT 143

AA065065  
 ID AA065065 standard; DNA; 21 BP.

AC AA065065;

DT 20-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.

XX Synthetic.

XX CA2104649-A.

XX 26-FEB-1994.

PF 23-AUG-1993; 93CA-02104649.

PR 25-AUG-1992; 92JP-00248796.

PR 03-MAR-1993; 93JP-00042736.

PA (SEKI/) SEKI M.

PI Seki M, Honda Y, Yamada E;

PI WPI; 1994-151836/19.

PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.

PS Claim 5; Page 130; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.

CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes

XX Sequence 21 BP; 2 A; 4 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 21;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:  
 DB 4 GGGGTCCTGGAG 15

## RESULT 144

AA072991

ID AAA72991 standard; DNA; 21 BP.

AC AAA72991;

DT 24-NOV-2000 (first entry)

DE Hepatitis C virus antisense oligonucleotide HCV123.

KM Hepatitis C virus; HCV; antisense oligonucleotide; leuciferinase;  
 KM luciferase; HepG2; medicine; ss.

OS Hepatitis C virus.

PN CN1253138-A.

PD 17-MAY-2000.

PF 09-NOV-1998; 98CN-00124388.

PR 09-NOV-1998; 98CN-00124388.

(RAD-) RADIOMEDICINE ACAD MILITARY MEDICAL SCI.

PI Wang S, Wang X, Zhu B;

PI WPI; 2000-46526/41.

PT Structure and usage of antisense oligonucleotide for treating diseases  
 PT correlative to hepatitis C virus.

PS Claim 1; Page 1; 20pp; Chinese.

CC The present invention describes antisense oligonucleotides which are  
 CC designed and synthesised on the basis of the gene structure of hepatitis  
 CC C virus (HCV) and can be used to suppress the expression of HCV gene. The  
 CC non-coding region 5' of HCV gene is used to regulate the instantaneous  
 CC expression system of leuciferinase gene in HepG2 cells and the transgenic  
 CC cell model HepG2.9706 of luciferase gene. The 15 antisense  
 CC oligonucleotides (AA07298 to AA07302) which are complementary to the  
 CC non-coding region 5' and translational initiation region of HCV are  
 CC actively screened and evaluated to discover for the first time the  
 CC oligonucleotides HCV279, HCV349, HCV363, HCV65 and HCV 313 and their  
 CC chemical modified objects for suppressing the expression of HCV gene.  
 CC Thus, the present invention relates to the new medicine for treating the  
 CC diseases associated with HCV

XX Sequence 21 BP; 3 A; 5 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 3; Length 21;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:  
 DB 1 GGGGTCCTGGAG 12

## RESULT 145

ADD67935/C

ID ADD67935 standard; DNA; 21 BP.

AC ADD67935;

DT 15-JAN-2004 (first entry)

DE Hepatitis C virus detection probe seq id 7.

KM antiviral; hepatitis C virus; HCV; viral replication inhibitor;  
 KM replication competent HCV; 3' non-translated region; probe; ss.

OS Hepatitis C virus.

PN US2003125541-A1.

```
XX 03-JUL-2003.
PD
XX
PF 27-SEP-2002; 2002US-00259275.
XX
PR 23-DEC-1999; 99US-0171909P.
PR 23-DEC-2000; 2000US-00747419.
PR 27-SEP-2001; 2001US-0325236P.
PR 13-NOV-2001; 2001US-0338123P.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Lemon SM, Y1 M;
XX
DR WPI; 2003-811006/76.
XX
XX
PT Identifying a compound that inhibits replication of a hepatitis C virus
PT (HCV) RNA comprises contacting a cell comprising a replication competent
PT HCV RNA containing a heterologous polynucleotide encoding a
PT transactivator, with a compound.
XX
XX Example 2; SEQ ID NO 7; 95bp; English.
XX
PS The invention describes a method of identifying a compound that inhibits
CC replication of a hepatitis C virus (HCV) RNA. The method comprises
CC contacting a cell comprising a replication competent HCV RNA containing a
CC heterologous polynucleotide having a first coding sequence encoding a
CC transactivator, with a compound. The method is useful for identifying a
CC compound that inhibits replication of HCV RNA. The kit is useful for
CC detecting replication competent HCV RNA. This sequence represents a probe
CC used to detect DNA encoding HCV in order to detect the production of the
CC virus by chimpanzee.
XX
SQ Sequence 21 BP; 3 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 12; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTCGAG 12
Db 21 GGGGCTCTCGAG 10
RESULT 146
ABX10607/c
ID ABX10607 standard; DNA; 21 BP.
XX
AC ABX10607;
XX
DT 11-APR-2003 (first entry)
XX
DE Light Cycler red PCR probe used to detect HCV.
XX
XX PCR; probe; ss; replication competent; hepatitis C virus; HCV;
KM 3' non-translated RNA; 3'NTR; chronic viral hepatitis; hepatic fibrosis;
KM cirrhosis; hepatocellular carcinoma.
XX
XX Hepatitis C virus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= labelled with Light Cycler Red 640 dye"
XX
XX US2002155582-A1.
XX
XX 24-OCT-2002.
XX
XX 23-DEC-2000; 2000US-00747419.
XX
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PR 23-DEC-1999; 99US-0171909P.
XX
XX (LEMO/) LEMON S M.
PA (Y1M/) Y1 M.
XX
XX Lemon SM, Y1 M;
XX
DR WPI; 2003-182640/18.
XX
XX
PT Novel replication competent hepatitis C virus for producing infectious
PT viral particles and as antigen for detecting hepatitis C virus
PT antibodies, comprises hepatitis C virus genome and heterologous
PT polynucleotide.
XX
XX Example 2; Page 12; 37bp; English.
XX
PS The invention discloses a replication competent hepatitis C virus (HCV)
CC comprising a HCV virus genome and a heterologous polynucleotide, where
CC the HCV genome comprises a 3' non-translated RNA and the heterologous
CC polynucleotide is present in the 3' non-translated RNA. HCV is a cause of
CC chronic viral hepatitis, hepatic fibrosis, cirrhosis and/or the
CC development of hepatocellular carcinoma. A cell comprising the HCV is
CC useful for selecting or detecting a replication competent HCV, for
CC identifying a compound that inhibits replication of HCV, for producing
CC infectious viral particles which are useful as a source of virus
CC particles for various assays, including evaluating methods for
CC inactivating particles, excluding particles from serum, identifying a
CC neutralizing compound and as an antigen for use in detecting anti-HCV
CC antibodies in an animal. The cell comprising the HCV is also useful for
CC identifying a variant HCV. An HCV particle is useful as an antigen, as a
CC positive-control in assays that test for the presence of anti-HCV
CC antibodies, to produce antibodies to detect the presence of viral
CC particles in biological samples (e.g. blood products and cell-free blood
CC products) and as a source of viral antigen to measure the presence and
CC amount of antibody present in an animal. The sequence presented is the
CC Light Cycler PCR red probe which was used to detect HCV
XX
SQ Sequence 21 BP; 3 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 12; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTCGAG 12
Db 21 GGGGCTCTCGAG 10
RESULT 147
AA065116
ID AA065116 standard; DNA; 22 BP.
XX
AC AA065116;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
XX
XX 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
```

XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.  
XX PS Claim 5; Page 152; 262pp; English.  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes.  
XX SQ Sequence 22 BP; 2 A; 4 C; 14 G; 2 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 22;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 9 GGGGTCTGTGAG 20  
RESULT 148  
AA065102  
ID AA065102 standard; DNA; 22 BP.  
XX AC AA065102;  
XX DT 21-DEC-1994 (first entry)  
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX KW inhibition; viral protein precursor; ss.  
XX OS Synthetic.  
XX PN CA2104649-A.  
XX PD 26-FEB-1994.  
XX PF 23-AUG-1993; 93CA-02104649.  
XX PR 25-AUG-1992; 92JP-00248796.  
XX PR 03-MAR-1993; 93JP-00042736.  
XX PA (SEKI/) SEKI M.  
XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.  
XX PS Claim 5; Page 146; 262pp; English.  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes.  
XX SQ Sequence 22 BP; 2 A; 3 C; 14 G; 3 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 22;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 8 GGGGTCTGTGAG 19  
RESULT 149  
AA065131  
ID AA065131 standard; DNA; 22 BP.  
XX AC AA065131;  
XX DT 21-DEC-1994 (first entry)  
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX KW inhibition; viral protein precursor; ss.  
XX OS Synthetic.  
XX PN CA2104649-A.  
XX PD 26-FEB-1994.  
XX PF 23-AUG-1993; 93CA-02104649.  
XX PR 25-AUG-1992; 92JP-00248796.  
XX PR 03-MAR-1993; 93JP-00042736.  
XX PA (SEKI/) SEKI M.  
XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.  
XX PS Claim 5; Page 159; 262pp; English.  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes.  
XX SQ Sequence 22 BP; 2 A; 4 C; 14 G; 2 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 22;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 10 GGGGTCTGTGAG 21  
RESULT 150  
AA065066  
ID AA065066 standard; DNA; 22 BP.  
XX AC AA065066;  
XX DT 20-DEC-1994 (first entry)  
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX KW inhibition; viral protein precursor; ss.



XX OS Synthetic.  
XX PN CA2104649-A.  
XX PD 26-FEB-1994.  
XX PF 23-AUG-1993; 93CA-02104649.  
XX PR 25-AUG-1992; 92JP-00248796.  
XX PR 03-MAR-1993; 93JP-00042736.  
XX PA (SEKI/) SEKI M.  
XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.  
XX PS Claim 5; Page 130; 262pp; English.  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
XX it has a base sequence of 15-30 bases which is included within the 49  
XX bases from G at position 127 to C at position 175 of AA064913 and which  
XX contains at least 7 bases from C at position 147 to C at position 153.  
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
XX genes  
XX SQ Sequence 22 BP; 3 A; 4 C; 12 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 66.7%; Score 12; DB 2; Length 22;  
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 GGGGUCCTGGAG 12  
XX Db 5 GGGGTCTCTGGAG 16  
XX  
XX RESULT 151  
XX AA065056  
XX ID AA065056 standard; DNA; 22 BP.  
XX AC AA065056;  
XX XX  
XX DT 20-DEC-1994 (first entry)  
XX XX  
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX inhibition; viral protein precursor; ss.  
XX OS Synthetic.  
XX PN CA2104649-A.  
XX PD 26-FEB-1994.  
XX PF 23-AUG-1993; 93CA-02104649.  
XX PR 25-AUG-1992; 92JP-00248796.  
XX PR 03-MAR-1993; 93JP-00042736.  
XX PA (SEKI/) SEKI M.  
XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.

XX PS Claim 5; Page 126; 262pp; English.  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
XX it has a base sequence of 15-30 bases which is included within the 49  
XX bases from G at position 127 to C at position 175 of AA064913 and which  
XX contains at least 7 bases from C at position 147 to C at position 153.  
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
XX genes  
XX SQ Sequence 22 BP; 2 A; 5 C; 12 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 66.7%; Score 12; DB 2; Length 22;  
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 GGGGUCCTGGAG 12  
XX Db 4 GGGGTCTCTGGAG 15  
XX  
XX RESULT 152  
XX AA065077  
XX ID AA065077 standard; DNA; 22 BP.  
XX AC AA065077;  
XX DT 20-DEC-1994 (first entry)  
XX XX  
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX inhibition; viral protein precursor; ss.  
XX OS Synthetic.  
XX PN CA2104649-A.  
XX PD 26-FEB-1994.  
XX PF 23-AUG-1993; 93CA-02104649.  
XX PR 25-AUG-1992; 92JP-00248796.  
XX PR 03-MAR-1993; 93JP-00042736.  
XX PA (SEKI/) SEKI M.  
XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.  
XX PS Claim 5; Page 135; 262pp; English.  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
XX it has a base sequence of 15-30 bases which is included within the 49  
XX bases from G at position 127 to C at position 175 of AA064913 and which  
XX contains at least 7 bases from C at position 147 to C at position 153.  
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
XX genes  
XX SQ Sequence 22 BP; 2 A; 4 C; 13 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 66.7%; Score 12; DB 2; Length 22;  
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 GGGGUCCTGGAG 12  
XX Db 6 GGGGTCTCTGGAG 17

```

RESULT 153
AAQ65088
ID AAQ65089 standard; DNA; 22 BP.
XX
XX
AC AAQ65089;
XX
XX
DT 20-DEC-1994 (first entry)
XX
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX
XX
OS Inhibition; viral protein precursor; ss.
XX
XX
OS Synthetic.
XX
XX
PN CA2104649-A.
XX
XX
PD 26-FEB-1994.
XX
XX
PF 23-AUG-1993; 93CA-02104649.
XX
XX
PR 25-AUG-1992; 92JP-00248796.
XX
XX
PR 03-MAR-1993; 93JP-00042736.
XX
XX
PA (SEKI/) SEKI M.
XX
XX
PI Seki M, Honda Y, Yamada E;
XX
XX
DR WPI; 1994-151836/19.
XX
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX
XX
PT genome - are useful as antiviral agents.
XX
XX
PS Claim 5; Page 140; 262pp; English.
XX
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX
XX
CC it has a base sequence of 15-30 bases which is included within the 49
XX
XX
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX
XX
CC contains at least 7 bases from C at position 147 to C at position 153.
XX
XX
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX
XX
CC genes
XX
XX
SQ Sequence 22 BP; 2 A; 3 C; 14 G; 3 T; 0 U; 0 Other;
XX
XX
Query Match 66.7%; Score 12; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUUGAG 12
Db 7 GGGGTCCTGAG 18

```

```

RESULT 154
AAQ65147
ID AAQ65147 standard; DNA; 22 BP.
XX
XX
AC AAQ65147;
XX
XX
DT 21-DEC-1994 (first entry)
XX
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX
XX
OS Inhibition; viral protein precursor; ss.
XX
XX
OS Synthetic.
XX
XX
PN CA2104649-A.
XX
XX
PD 26-FEB-1994.
XX
XX
PF 23-AUG-1993; 93CA-02104649.
XX
XX
PR 25-AUG-1992; 92JP-00248796.
XX
XX
PR 03-MAR-1993; 93JP-00042736.
XX
XX
PA (SEKI/) SEKI M.
XX
XX
PI Seki M, Honda Y, Yamada E;
XX
XX
DR WPI; 1994-151836/19.
XX
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX
XX
PT genome - are useful as antiviral agents.
XX
XX
PS Claim 5; Page 166; 262pp; English.
XX
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX
XX
CC it has a base sequence of 15-30 bases which is included within the 49
XX
XX
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX
XX
CC contains at least 7 bases from C at position 147 to C at position 153.
XX
XX
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX
XX
CC genes
XX
XX
SQ Sequence 22 BP; 2 A; 5 C; 13 G; 2 T; 0 U; 0 Other;
XX
XX
Query Match 66.7%; Score 12; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUUGAG 12
Db 11 GGGGTCCTGAG 22

```

CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 CC XX  
 SQ Sequence 22 BP; 3 A; 6 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 2; Length 22;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCUUGAG 12  
 Db 1 GGGGUCUUGAG 12  
 1 GGGGUCUUGAG 12  
 RESULT 156  
 AAD3107  
 ID AAD3107 standard; DNA; 22 BP.  
 AC AAD3107;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Gsui enzyme recognition sequence #1.  
 XX  
 KM Restriction endonuclease; altered specificity; recognition sequence;  
 KM Gsui; enzyme; ds.  
 OS  
 OS Unidentified.  
 XX  
 PN EPI179596-A1.  
 XX  
 PD 13-FEB-2002.  
 XX  
 PF 06-JUL-2001; 2001EP-00305859.  
 XX  
 PR 10-AUG-2000; 2000GB-00019744.  
 XX  
 PA (FERM-) FERMENTAS AB.  
 XX  
 PI Janulaitis A, Rimseleiene R, Ludyas A;  
 DR WPI; 2002-229927/29.  
 XX  
 PT Producing DNA encoding restriction endonuclease with altered specificity;  
 PT comprises mutagenizing DNA encoding the enzyme and isolating DNA encoding  
 PT mutated enzyme with specificity for an altered sequence.  
 XX  
 PS Example; Page 5; 44pp; English.  
 XX  
 CC The invention relates to a method of producing a polynucleotide encoding  
 CC a restriction endonuclease with altered specificity. The method involves  
 CC mutagenizing a polynucleotide encoding restriction endonuclease with  
 CC specificity for a recognition sequence to produce mutated polynucleotides  
 CC and isolating from them a polynucleotide encoding mutated restriction  
 CC endonuclease with specificity for an altered recognition sequence by  
 CC selecting a polynucleotide expressing a restriction endonuclease with  
 CC methylease specificity for the altered recognition sequence. The method is  
 CC useful for producing a polynucleotide encoding a restriction endonuclease  
 CC comprising Eco571, BcgI, HaeIII or A101, with an altered specificity. The  
 CC method allows selection of mutant variants recognising new sequences that  
 CC differ not only in single nucleotide from wild type enzyme but also for  
 CC mutants that recognise degenerate sequences or sequences differing in  
 CC several nucleotides, especially if mutants of altered specificity are  
 CC taken into the next round of mutagenesis and digestion-selection. The  
 CC present sequence is recognition sequence of Gsui restriction enzyme  
 CC XX  
 SQ Sequence 22 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 16 Other;  
 Query Match 66.7%; Score 12; DB 6; Length 22;  
 Best Local Similarity 91.7%; Pred. No. 3.4e+03;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 CUGAGNNNNNN 18

Db 1 CUGAGNNNNNN 12  
 1 CUGAGNNNNNN 12  
 RESULT 157  
 ADI45772  
 ID ADI45772 standard; DNA; 22 BP.  
 AC ADI45772;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Single stranded nucleic acid cleavage method related nucleotide #205.  
 XX  
 KM ss; single-stranded nucleic acid cleavage; restriction endonuclease;  
 KM complementation; genetic package; bacteriophage display library;  
 KM antibody fragment.  
 XX  
 OS Unidentified.  
 OS  
 OS W0200179481-A2.  
 XX  
 PN 25-OCT-2001.  
 XX  
 PD 17-APR-2001; 2001WO-US012454.  
 XX  
 PF 17-APR-2000; 2000US-0198069P.  
 XX  
 PR (DYAX-) DYAX CORP.  
 XX  
 PA Ladner RC, Cohen EH, Nastri HG, Rookley KL, Hoet R;  
 PI WPI; 2002-011131/01.  
 DR  
 XX  
 PT Selective cleavage of single-stranded nucleic acid, useful for preparing  
 PT display libraries of proteins and peptides, by hybridization with  
 PT oligonucleotide and enzymatic restriction.  
 XX  
 PS Disclosure; SEQ ID NO 223; 190pp; English.  
 XX  
 CC The invention relates to a method of cleaving single-stranded (ss)  
 CC nucleic acid (I) at a selected location, using an oligonucleotide (ON)  
 CC that is complementary to (I) in the target region and a restriction  
 CC endonuclease (RE). The ON forms, with its complement in (I), an RE  
 CC recognition site that ensures cleavage only at the selected location.  
 CC Contact between (I) and ON, and treatment with RE, are done at a  
 CC temperature at which (I) (I) is maintained in substantially ss form and  
 CC (II) RE is active. ON is (I) single stranded, and includes a sequence  
 CC that forms, with its complement in (I), the RE site or (II) has a double-  
 CC stranded (ds) region that includes a recognition site for a type IIS RE  
 CC that cleaves at a remote site formed by complementation of (I) and the ss  
 CC region of ON. The method is used to construct libraries of genetic  
 CC packages (phages) that display diverse families of (poly)peptides and  
 CC proteins (A), especially human Fab or other antibody fragments. The  
 CC libraries are screened to identify (A) for possible therapeutic use. The  
 CC method is not biased to DNAs containing native sequences complementary to  
 CC amplification primers and allows any sequences that may be deleterious to  
 CC expression to be removed before cloning and display. DNAs are cut only at  
 CC a single (constant) site, without the need to build an RE site into the  
 CC or primers used for reverse transcription or amplification, and any natural  
 CC or synthetic site can be used for cleavage. The use of a partially ds ON  
 CC allows cleavage at sites where no restriction sites occur naturally or  
 CC can be created. Both methods allow use of 5' and 3' primers for maximum  
 CC diversity. This sequence represents a sequence used in the invention.  
 CC XX  
 SQ Sequence 22 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 16 Other;  
 Query Match 66.7%; Score 12; DB 6; Length 22;  
 Best Local Similarity 91.7%; Pred. No. 3.4e+03;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 CUGAGNNNNNN 18  
 1 CUGAGNNNNNN 18

Db 1 CTGAGANNNNNN 12

# RESULT 158

ABT15975  
ID ABT15975 standard; DNA; 22 BP.

AC ABT15975;

DT 28-MAR-2003 (first entry)

DE HCV variant detection related PCR primer SEQ ID No 4.

KM Primer extension chain reaction; reverse; forward; target nucleic acid;

OS variant; HIV; HCV; HBV; Parvovirus B19; PCR primer; ss.

OS Hepatitis C virus.

OS Synthetic.

PN WO200283927-A2.

PD 24-OCT-2002.

PF 17-APR-2002; 2002WO-US012035.

PR 17-APR-2001; 2001US-0284334P.

PA (NYBL-) NEW YORK BLOOD CENT INC.

PI Andrus L, Nichols CN;

DR WPI; 2003-103374/09.

PT Detecting presence of target nucleic acid molecule e.g. human

PT immunodeficiency virus, hepatitis B or C virus in a sample, by using a

PT universal multi-variant detection system.

PS Example; Page 25; 63pp; English.

XX The invention relates to a novel method for a primer extension chain

CC reaction for determining presence of a target nucleic acid molecule in a

CC sample, where the nucleotide at 3' end of the reverse primer hybridises

CC with nucleotide at 5' end of the forward primer extension product or a

CC nucleotide separated from the nucleotide at 5' end of the forward primer

CC extension product by a gap comprising a highly conserved nucleotide

CC sequence. The method is useful for determining presence of a target

CC nucleic acid molecule known to have variant sequences, in a sample. The

CC target nucleic acid is preferably a virus including human

CC immunodeficiency virus (HIV), hepatitis C virus (HCV), hepatitis B virus

CC (HBV) or Parvovirus B19. This polynucleotide sequence represents a PCR

CC primer used in the primer extension chain reaction method of the

CC invention

XX SQ Sequence 22 BP; 2 A; 5 C; 13 G; 2 T; 0 U; 0 Other;

QY Query Match 66.7%; Score 12; DB 8; Length 22;

XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;

XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGGGCTCTGGAG 22

XX Tandem tag; concatenated tag; human; ds.

XX Homo sapiens.

OS US2003190618-A1.

PN 09-OCT-2003.

PD 06-MAR-2002; 2002US-00092885.

PF 06-MAR-2002; 2002US-00092885.

PA (SAMA/) SAMA B.

PA (LIYY/) Li Y.

PA (HERM/) HERMIDA L C.

PA (HOPP/) HOPPA N L.

PA (JOHE/) JOHE K K.

PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;

PI WPI; 2003-831617/77.

PT Generating five prime biased tandem tag libraries of cDNAs by isolating a

PT sample of mRNAs, amplifying the released tags, concatenating the

PT amplified tags to form concatenated tags, amplifying and isolating the

PT concatenated tags.

PS Disclosure; Page 9; 0pp; English.

XX The present invention discloses a method for generating five prime biased

CC tandem tag libraries of cDNAs. The step involves isolating a sample of

CC mRNAs, amplifying the released tags, concatenating the amplified tags to

CC form concatenated tags, amplifying and isolating the concatenated tags.

CC The present sequence is human tandem tag DNA

XX SQ Sequence 22 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 16 Other;

QY Query Match 66.7%; Score 12; DB 10; Length 22;

XX Best Local Similarity 91.7%; Pred. No. 3.4e+03;

XX Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 7 CTGAGANNNNNN 18

QY 1 CTGAGANNNNNN 12

Db 1 CTGAGANNNNNN 12

RESULT 160

AB237284

ID AB237284 standard; DNA; 22 BP.

XX AB237284;

AC 18-FEB-2003 (first entry)

XX Type II restriction enzyme recognition sequence Gauri SEQ ID NO:375.

DE Library; cleavage; display; diverse family; ss.

OS Synthetic.

OS WO200283872-A2.

PN 24-OCT-2002.

PD 17-APR-2002; 2002WO-US012405.

PF 17-APR-2001; 2001US-00837306.

PR 24-OCT-2001; 2001US-00000516.

PR 25-OCT-2001; 2001US-00045674.

XX (LADN/) LADNER R C.

PA (COHE/) COHEN E H.

PF	24-SEP-2003; 2003WO-KR001951.
XX	
PR	27-SEP-2002; 2002KR-00058712.
PR	06-NOV-2002; 2002KR-00068496.
XX	
PA	(GENE-) GENEXINE INC.
PA	(POST-) POSTECH FOUND.
PA	(DONG-) DONG-A PHARM CO LTD.
PA	(DAEW-) DAEWOO CO LTD.
PA	(POSC-) POSCO.
XX	
PI	Sung YC, Youn U, Yang S, Park S, Lee CG;
DR	WPI; 2004-305120/28.
XX	
PT	New DNA vaccine comprising plasmid containing 2-6 kb of the total antigen
PT	gene of hepatitis C virus (HCV), useful in treating or preventing HCV
PT	infection.
XX	
PS	Example 16; SEQ ID NO 37; 165bp; English.
XX	
CC	The present invention describes a DNA vaccine which comprises a plasmid
CC	containing 2-6 kb of the total antigen gene of hepatitis C virus (HCV).
CC	Also described: (1) a recombinant adenovirus vaccine including an
CC	adenovirus containing 2-6 Kb of total antigen gene of HCV; (2) a vaccine
CC	administering method; and (3) a method for treating or preventing HCV
CC	infection. The DNA vaccine has virucide activity. The DNA vaccine is
CC	useful in treating or preventing HCV infection. The present sequence
CC	represents a PCR primer for HCV, which is used in an example from the
CC	present invention.
XX	
SQ	Sequence 22 BP; 2 A; 5 C; 13 G; 2 T; 0 U; 0 Other;
QY	
Query Match	66.7%; Score 12; DB 12; Length 22;
Best Local Similarity	83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative	2; Mismatches 0; Indels 0; Gaps 0
DB	1 GGAGUCUGGAG 12      : 11 GGAGTCTCGAG 22
RESULT 162	
AAO65090	
ID	AAO65090 standard; DNA; 23 BP.
AC	AAO65090;
XX	
DT	20-DEC-1994 (first entry)
XX	
DE	Antisense oligonucleotide complementary to Hepatitis C Virus genome.
KM	Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KW	Inhibition; viral protein precursor; ss.
XX	
OS	Synthetic.
XX	
PN	CA2104649-A.
XX	
PD	26-FEB-1994.
XX	
PF	23-AUG-1993; 93CA-02104649.
XX	
PR	25-AUG-1992; 93JP-00248796.
PR	03-MAR-1993; 93JP-00042736.
XX	
PA	(SEKI/) SEKI M.
XX	
PI	Seki M, Honda Y, Yamada E;
XX	
DR	WPI; 1994-151836/19.
TX	Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus



```
XX 23-AUG-1993; 93CA-02104649.
PF 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
PI Seki M, Honda Y, Yamada E;
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 147; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC gene.
XX
SQ Sequence 23 BP; 2 A; 4 C; 14 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCUGAG 12
Db 9 GGGGTCTCGAG 20

RESULT 166
AA065067
ID AA065067 standard; DNA; 23 BP.
XX
AC AA065067;
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
PI Seki M, Honda Y, Yamada E;
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 131; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
```

```
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC gene.
XX
SQ Sequence 23 BP; 3 A; 4 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCUGAG 12
Db 6 GGGGTCTCGAG 17

RESULT 167
AA065117
ID AA065117 standard; DNA; 23 BP.
XX
AC AA065117;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
PI Seki M, Honda Y, Yamada E;
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 153; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC gene.
XX
SQ Sequence 23 BP; 2 A; 5 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCUGAG 12
Db 10 GGGGTCTCGAG 21

RESULT 168
AA065057
ID AA065057 standard; DNA; 23 BP.
XX
AC AA065057;
```

```

XX 20-DEC-1994 (first entry)
DT
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 127; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 23 BP; 3 A; 5 C; 12 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 23;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUUGAG 12
DB 5 GGGGTCTTGAG 16
XX
XX RESULT 169
XX AAQ65048
XX ID AAQ65048 standard; DNA; 23 BP.
XX
XX AAQ65048;
AC
XX
XX 20-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA

```

```

XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 123; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 23 BP; 2 A; 5 C; 13 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 23;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUUGAG 12
DB 4 GGGGTCTTGAG 15
XX
XX RESULT 170
XX AAQ64933
XX ID AAQ64933 standard; DNA; 23 BP.
XX
XX AAQ64933;
AC
XX
XX 19-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 72; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 16-24 bases which is included within the 24
CC bases from G at position 127 to C at position 150 of AAQ64913 and which
CC contains at least 16 bases from C at position 131 to A at position 146.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 23;

```



Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 1 GGGGTCTGTGAG 12

## RESULT 171

AA043906 standard; DNA; 23 BP.

AA043906;

14-NOV-2002 (first entry)

Bpm I restriction endonuclease recognition motif.

Single stranded polynucleotide tag; cleavage agent; gene expression;

restriction endonuclease; ds.

Unidentified.

Key Location/Qualifiers

misc\_feature 22..23  
/\*tag= a  
/note= "Nicking site"

MO200259357-A2.

01-AUG-2002.

24-JAN-2002; 2002MO-DK000052.

24-JAN-2001; 2001DK-00000126.

12-FEB-2001; 2001US-0267704P.

(GENO-) GENOMIC EXPRESSION APS.

Pederesen ML;

WPI: 2002-636542/68.

Obtaining single stranded polynucleotide tags from a biological sample,  
for analyzing gene expression or diagnosing clinical conditions,  
comprises employing nicking endonucleases that cleave complementary  
strands.

Disclosure; Page 88; 302pp; English.

The invention relates to a method for obtaining a single stranded  
polynucleotide tag from a biological sample by cleaving one of the  
complementary strands of a double stranded polynucleotide with a cleavage  
agent capable of recognising a double stranded polynucleotide comprising  
complementary strands and cleaving only one of the strands of the  
polynucleotide in the process of generating a single stranded  
polynucleotide tag. The method is useful for separating, analyzing,  
quantifying or obtaining single stranded polynucleotides comprising tags  
originating partly, and preferably wholly from a source of DNA and/or RNA  
in a sample comprising biological cells. The method is particularly for  
analyzing gene expression (expression profiling or differential gene  
expression), or in diagnosing clinical conditions. The present sequence  
is Bpm I restriction endonuclease recognition motif. This sequence is  
used to illustrate the method of the invention

Sequence 23 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 17 Other;

Query Match 66.7%; Score 12; DB 6; Length 23;

Best Local Similarity 91.7%; Pred. No. 3.4e+03;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
7 CUGAGGNNNNNN 18  
|:|||||

Db 1 CTGAGGNNNNNN 12

## RESULT 172

AA065133 standard; DNA; 24 BP.

AA065133;

21-DEC-1994 (first entry)

Antisense oligonucleotide complementary to Hepatitis C Virus genome.

Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;

inhibition; viral protein precursor; ss.

Synthetic.

CA2104649-A.

26-FEB-1994.

23-AUG-1993; 93CA-02104649.

25-AUG-1992; 92JP-00248796.

03-MAR-1993; 93JP-00042736.

(SEKI/) SEKI M.

Seki M, Honda Y, Yamada E;

WPI: 1994-151836/19.

Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus  
genome - are useful as antiviral agents.

Claim 5; Page 160; 262pp; English.

This oligonucleotide is an example of a preferred antisense compound i.e.  
it has a base sequence of 15-30 bases which is included within the 49  
bases from G at position 127 to C at position 175 of AA064913 and which  
contains at least 7 bases from C at position 147 to C at position 153.  
The antisense oligonucleotide is useful for inhibiting translation of HCV  
genes

Sequence 24 BP; 2 A; 5 C; 14 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 12 GGGGTCTGTGAG 23

## RESULT 173

AA065104 standard; DNA; 24 BP.

AA065104;

21-DEC-1994 (first entry)

Antisense oligonucleotide complementary to Hepatitis C Virus genome.

Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;

inhibition; viral protein precursor; ss.

Synthetic.

CA2104649-A.

```

PD 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 147; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 24 BP; 2 A; 5 C; 14 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
XX |||:|:|:|:|
Db 10 GGGGTCTGGAG 21

RESULT 174
AAQ65091
ID AAQ65091 standard; DNA; 24 BP.
XX
XX AAQ65091;
XX
XX 20-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 141; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49

```

```

CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 24 BP; 2 A; 4 C; 15 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
XX |||:|:|:|:|
Db 9 GGGGTCTGGAG 20

RESULT 175
AAQ65118
ID AAQ65118 standard; DNA; 24 BP.
XX
XX AAQ65118;
XX
XX 21-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 153; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 24 BP; 2 A; 6 C; 14 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
XX |||:|:|:|:|
Db 11 GGGGTCTGGAG 22

RESULT 176
AAQ65049
ID AAQ65049 standard; DNA; 24 BP.
XX

```

AC AA065049;  
 XX  
 DT 20-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 XX inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 DT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 123; 262pp; English.  
 XX  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 24 BP; 3 A; 5 C; 13 G; 3 T; 0 U; 0 Other;  
 XX  
 QY Query Match 66.7%; Score 12; DB 2; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 GGGGUCCTGGAG 12  
 5 GGGGTCTCTGGAG 16  
 XX  
 RESULT 177  
 AA065068  
 ID AA065068 standard; DNA; 24 BP.  
 XX  
 AC AA065068;  
 XX  
 DT 20-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 XX inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX

PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 DT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 131; 262pp; English.  
 XX  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 24 BP; 3 A; 4 C; 14 G; 3 T; 0 U; 0 Other;  
 XX  
 QY Query Match 66.7%; Score 12; DB 2; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 GGGGUCCTGGAG 12  
 7 GGGGTCTCTGGAG 18  
 XX  
 RESULT 178  
 AA065149  
 ID AA065149 standard; DNA; 24 BP.  
 XX  
 AC AA065149;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 XX inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 DT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 167; 262pp; English.  
 XX  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;

```

Query Match          66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
        |||:|||||
        13 GGGCTCTGGAG 24

Db

RESULT 179
AAQ65058
ID      AAQ65058 standard; DNA; 24 BP.
XX
AC      AAQ65058;
XX
DT      20-DEC-1994 (first entry)
XX
DE      Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM      Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KW      Inhibition; viral protein precursor; ss.
XX
OS      Synthetic.
XX
PN      CA2104649-A.
XX
PD      26-FEB-1994.
XX
PF      23-AUG-1993; 93CA-02104649.
XX
PR      25-AUG-1992; 92JP-00248796.
PR      03-MAR-1993; 93JP-00042736.
XX
PA      (SEKI/) SEKI M.
XX
PI      Seki M, Honda Y, Yamada E;
XX
DR      WPI; 1994-151836/19.
XX
PT      Antisense oligonucleotide(s) complementary to the hepatitis C virus
PT      genome - are useful as antiviral agents.
XX
PS      Claim 5; Page 127; 262pp; English.
XX
CC      This oligonucleotide is an example of a preferred antisense compound i.e.
CC      it has a base sequence of 15-30 bases which is included within the 49
CC      bases from G at position 127 to C at position 175 of AAQ64913 and which
CC      contains at least 7 bases from C at position 147 to C at position 153.
CC      The antisense oligonucleotide is useful for inhibiting translation of HCV
CC      genes
XX
SQ      Sequence 24 BP; 3 A; 5 C; 13 G; 3 T; 0 U; 0 Other;

Query Match          66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
        |||:|||||
        6 GGGCTCTGGAG 17

Db

RESULT 180
AAQ65041
ID      AAQ65041 standard; DNA; 24 BP.
XX
AC      AAQ65041;
XX
DT      20-DEC-1994 (first entry)
XX
DE      Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW      Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;

```

```

KM      Inhibition; viral protein precursor; ss.
XX
OS      Synthetic.
XX
PN      CA2104649-A.
XX
PD      26-FEB-1994.
XX
PF      23-AUG-1993; 93CA-02104649.
XX
PR      25-AUG-1992; 92JP-00248796.
PR      03-MAR-1993; 93JP-00042736.
XX
PA      (SEKI/) SEKI M.
XX
PI      Seki M, Honda Y, Yamada E;
XX
DR      WPI; 1994-151836/19.
XX
PT      Antisense oligonucleotide(s) complementary to the hepatitis C virus
PT      genome - are useful as antiviral agents.
XX
PS      Claim 5; Page 120; 262pp; English.
XX
CC      This oligonucleotide is an example of a preferred antisense compound i.e.
CC      it has a base sequence of 15-30 bases which is included within the 49
CC      bases from G at position 127 to C at position 175 of AAQ64913 and which
CC      contains at least 7 bases from C at position 147 to C at position 153.
CC      The antisense oligonucleotide is useful for inhibiting translation of HCV
CC      genes
XX
SQ      Sequence 24 BP; 3 A; 5 C; 13 G; 3 T; 0 U; 0 Other;

Query Match          66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
        |||:|||||
        4 GGGCTCTGGAG 15

Db

RESULT 181
AAQ65079
ID      AAQ65079 standard; DNA; 24 BP.
XX
AC      AAQ65079;
XX
DT      20-DEC-1994 (first entry)
XX
DE      Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW      Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KW      Inhibition; viral protein precursor; ss.
XX
OS      Synthetic.
XX
PN      CA2104649-A.
XX
PD      26-FEB-1994.
XX
PF      23-AUG-1993; 93CA-02104649.
XX
PR      25-AUG-1992; 92JP-00248796.
PR      03-MAR-1993; 93JP-00042736.
XX
PA      (SEKI/) SEKI M.
XX
PI      Seki M, Honda Y, Yamada E;
XX
DR      WPI; 1994-151836/19.
XX
PT      Antisense oligonucleotide(s) complementary to the hepatitis C virus

```

PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 136; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064933 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 24 BP; 2 A; 4 C; 15 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GGGGUCCTGGAG 12  
Db 8 GGGCTCTGGAG 19  
XX  
RESULT 182  
AA064938  
ID AA064938 standard; DNA; 24 BP.  
XX  
AC AA064938;  
XX  
DT 19-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX  
KW inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
PN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 75; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 16-24 bases which is included within the 24  
CC bases from G at position 127 to C at position 150 of AA064913 and which  
CC contains at least 16 bases from C at position 131 to A at position 146.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 24 BP; 4 A; 7 C; 10 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GGGGUCCTGGAG 12  
Db 1 GGGCTCTGGAG 12

RESULT 183  
AAT1277/C  
ID AAT1277 standard; RNA; 24 BP.  
XX  
AC AAT1277;  
XX  
DT 26-JUN-1996 (first entry)  
XX  
DE Hepatitis C virus 5'-UTR PCR primer AS33.  
XX  
KM Antisense; therapy; complementary; HCV; 5'-untranslated region;  
KM Hepatitis C virus; inhibition; infection; treatment; stem-loop;  
KM clone 2-1; ss.  
XX  
OS Synthetic.  
XX  
PN JP07303485-A.  
XX  
PD 21-NOV-1995.  
XX  
PF 13-MAY-1994; 94JP-00124609.  
XX  
PR 13-MAY-1994; 94JP-00124609.  
XX  
PA (TOFU) TONEN CORP.  
XX  
DR WPI; 1996-035187/04.  
XX  
PT Hepatitis C virus (HCV) anti:sense RNA - inhibits HCV structural gene  
PT expression in vivo for treatment of HCV infection.  
XX  
PS Example 1; Page 4; 12pp; Japanese.  
XX  
CC The present sequence is that of amplification primer AS33 which was used  
CC for amplifying partial 5'-UTR sequences from the HCV genome. Clone 2-1  
CC (Journal of Virology: 66, 1476-1483 (1992)) was used as the template for  
CC PCR. The amplified fragments were transcribed to produce antisense RNA  
CC which is useful for inhibiting expression of HCV structural genes and  
CC thereby inhibiting viral replication in vivo. The antisense therapy can  
CC be used in addition to conventional interferon treatment of HCV  
CC infections  
XX  
SQ Sequence 24 BP; 5 A; 10 C; 5 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GGGGUCCTGGAG 12  
Db 23 GGGCTCTGGAG 12  
XX  
RESULT 184  
AAT80269  
ID AAT80269 standard; DNA; 24 BP.  
XX  
AC AAT80269;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV104, targeted to HCV region -3 to +9.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1.24

```

FT      /*tag= a
XX      /note= "Phosphorothioate linkages"
XX      PN      WO9639500-A2.
XX      PD      12-DEC-1996.
XX      PF      04-JUN-1996; 96WO-EP002427.
XX      PR      06-JUN-1995; 95US-00471968.
XX      PA      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      PI      (HYBR-) HYBRIDON INC.
XX      PI      Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX      PI      Roberts PC, Walthers DM, Wolfe JL;
XX      DR      WPI; 1997-043122/04.
XX      PT      Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX      PT      the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX      PT      carcinoma.
XX      PS      Claim 19; Page 32; 100pp; English.
XX      CC      The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX      CC      which are complementary to a portion of the 5' untranslated region (UTR)
XX      CC      of hepatitis C virus (HCV). These sequences may be used in a
XX      CC      pharmaceutical composition for the control or prevention of HCV
XX      CC      infection. They may be used to inhibit replication or expression of HCV
XX      CC      or for detecting the presence of HCV in a sample. They may be used to
XX      CC      inhibit HCV replication in a cell and are therefore useful in the
XX      CC      treatment of HCV infections such as chronic and acute hepatitis and
XX      CC      hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX      CC      whether it binds successfully to its target.
XX      SQ      Sequence 24 BP; 2 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
XX      QY      Query Match 66.7%; Score 12; DB 2; Length 24;
XX      QY      Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX      QY      Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX      DB      1 GGGGUCCTCGAG 12
XX      DB      13 GGGGTCCTCGAG 24
XX      RESULT 185
XX      ID      AAT80359 standard; DNA; 24 BP.
XX      AC      AAT80359;
XX      DT      16-OCT-1997 (first entry)
XX      DE      Oligo HCV-199, tripartite non-contiguous HCV targeting oligomer.
XX      KW      Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX      KW      inhibition; replication; expression; detection; chronic hepatitis;
XX      KW      acute hepatitis; hepatocarcinoma; ss.
XX      OS      Synthetic.
XX      XX      Key Location/Qualifiers
XX      FH      modified_base 1..6
XX      FT      /*tag= b
XX      FT      /note= "Comprises phosphorothioate linkages"
XX      FT      modified_base 7..24
XX      FT      /*tag= a
XX      FT      /note= "2'-OMe RNA"
XX      PN      WO9639500-A2.

```

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PD      12-DEC-1996.
XX      PF      04-JUN-1996; 96WO-EP002427.
XX      PR      06-JUN-1995; 95US-00471968.
XX      PA      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      PI      (HYBR-) HYBRIDON INC.
XX      PI      Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX      PI      Roberts PC, Walthers DM, Wolfe JL;
XX      DR      WPI; 1997-043122/04.
XX      PT      Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX      PT      the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX      PT      carcinoma.
XX      PS      Claim 21; Page 21; 100pp; English.
XX      CC      The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX      CC      which are complementary to a portion of the 5' untranslated region (UTR)
XX      CC      of hepatitis C virus (HCV). These sequences may be used in a
XX      CC      pharmaceutical composition for the control or prevention of HCV
XX      CC      infection. They may be used to inhibit replication or expression of HCV
XX      CC      or for detecting the presence of HCV in a sample. They may be used to
XX      CC      inhibit HCV replication in a cell and are therefore useful in the
XX      CC      treatment of HCV infections such as chronic and acute hepatitis and
XX      CC      hepatocarcinoma. This sequence binds to three non-contiguous regions of
XX      CC      the HCV genome. This sequence is targeted to the 5' target region, +10
XX      CC      to +15, the internal sequence target, -230 to -219 and the 3' target
XX      CC      region, +1 to +6
XX      SQ      Sequence 24 BP; 4 A; 4 C; 10 G; 2 T; 4 U; 0 Other;
XX      QY      Query Match 66.7%; Score 12; DB 2; Length 24;
XX      QY      Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX      QY      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      DB      1 GGGGUCCTCGAG 12
XX      DB      7 GGGGUCCTCGAG 18
XX      RESULT 186
XX      ID      AAT80363 standard; DNA; 24 BP.
XX      AC      AAT80363;
XX      DT      16-OCT-1997 (first entry)
XX      DE      Oligo HCV-207, tripartite non-contiguous HCV targeting oligomer.
XX      KW      Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX      KW      inhibition; replication; expression; detection; chronic hepatitis;
XX      KW      acute hepatitis; hepatocarcinoma; ss.
XX      OS      Synthetic.
XX      XX      Key Location/Qualifiers
XX      FH      modified_base 1..6
XX      FT      /*tag= b
XX      FT      /note= "Comprises phosphorothioate linkages"
XX      FT      modified_base 7..24
XX      FT      /*tag= a
XX      FT      /note= "2'-OMe RNA"
XX      PN      WO9639500-A2.
XX      PD      12-DEC-1996.
XX      PF      04-JUN-1996; 96WO-EP002427.

```

XX 06-JUN-1995; 95US-00471968.  
PR (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX WPI; 1997-043122/04.  
DR  
XX  
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
XX Claim 21; Page 21; 100pp; English.  
PS  
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence binds to three non-contiguous regions of  
CC the HCV genome. This sequence is targeted to the 5' target region, +20  
CC to +25; the internal sequence target, +1 to +6 and the 3' target region,  
CC -230 to -219  
XX  
SQ Sequence 24 BP; 3 A; 4 C; 10 G; 3 T; 4 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3,4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 13 GGGGUCCTGGAG 24  
RESULT 187  
AAT80272  
ID AAT80272 standard; DNA; 24 BP.  
XX  
AC AAT80272;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV109, targeted to HCV region -11 to +1.  
XX  
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..12  
FT /\*tag= a  
FT /note= "Optionally 2' Ome modified"  
FT modified\_base 13..24  
FT /\*tag= b  
FT /note= "Phosphorothioate linkages"  
XX  
XX WO9639500-A2.  
XX  
XX 12-DEC-1996.  
XX  
XX 04-JUN-1996; 96WO-EP002427.  
XX  
XX 06-JUN-1995; 95US-00471968.  
XX

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX WPI; 1997-043122/04.  
DR  
XX  
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
XX Claim 19; Page 32; 100pp; English.  
PS  
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 24 BP; 2 A; 5 C; 12 G; 5 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3,4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 1 GGGGCTCTGGAG 12  
RESULT 188  
AAT80367  
ID AAT80367 standard; DNA; 24 BP.  
XX  
AC AAT80367;  
XX  
DT 16-OCT-1997 (first entry)  
XX  
DE Oligo HCV-217, tripartite non-contiguous HCV targeting oligomer.  
XX  
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..18  
FT /\*tag= a  
FT /note= "2'-Ome RNA"  
FT modified\_base 19..24  
FT /\*tag= b  
FT /note= "Comprises phosphorothioate linkages"  
XX  
XX WO9639500-A2.  
XX  
XX 12-DEC-1996.  
XX  
XX 04-JUN-1996; 96WO-EP002427.  
XX  
XX 06-JUN-1995; 95US-00471968.  
XX  
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;

XX	WP1; 1997-043122/04.
DR	
XX	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
XX	
PS	Claim 21; Page 21; 100pp; English.
XX	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmaceutical composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma. This sequence binds to three non-contiguous regions of
CC	the HCV genome. This sequence is targeted to the 5' target region, +1 to
CC	+6, the internal sequence target, -230 to -219 and the 3' target region,
CC	+235 to +240
XX	
XX	Sequence 24 BP; 3 A; 7 C; 10 G; 0 T; 4 U; 0 Other;
SO	
	Query Match 66.7%; Score 12; DB 2; Length 24;
	Best Local Similarity 100.0%; Pred. No. 3.4e+03;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GGGGCHCUGGAG 12
DB	7 GGGGUCUGGAG 18
RESULT 189	
ID	AAT80276
AC	AAT80276 standard; DNA; 24 BP.
XX	
DT	AAT80276;
XX	
DT	15-OCT-1997 (first entry)
XX	
DE	Oligo HCV125, targeted to HCV region -4 to -15.
XX	
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	inhibition; replication; expression; detection; chronic hepatitis;
XX	acute hepatitis; hepatocarcinoma; ss.
XX	
OS	Synthetic.
XX	
FT	Key
FT	modified_base
FT	Location/Qualifiers
FT	1. .12
FT	/*tag= b
FT	/note= "Optionally phosphorothioate linkages"
FT	modified_base
FT	13. .24
FT	/*tag= a
FT	/note= "Optionally 2' OMe modified"
FN	WO9639500-A2.
XX	
PD	12-DEC-1996.
XX	
PF	04-JUN-1996; 96WO-EP002427.
XX	
FR	06-JUN-1995; 95US-00471968.
XX	
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA	(HYBR-) HYBRIDON INC.
XX	
PI	Frank BL, Goodchild J, Hamlin RA, Kiluskie RE, Roberts NA,
PI	Roberts PC, Maltner DM, Wolfe JU;
XX	
RR	WP1; 1997-043122/04.
XX	

PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in the treatment and detection of HCV infection, esp. hepatitis and hepatocarcinoma.	XX
PS	Claim 19; Page 32-33; 100pp; English.	XX
XX		XX
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides which are complementary to a portion of the 5' untranslated region (UTR) of hepatitis C virus (HCV). These sequences may be used in a	XX
CC	pharmaceutical composition for the control or prevention of HCV infection. They may be used to inhibit replication or expression of HCV	XX
CC	or for detecting the presence of HCV in a sample. They may be used to	XX
CC	inhibit HCV replication in a cell and are therefore useful in the	XX
CC	treatment of HCV infections such as chronic and acute hepatitis and	XX
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine whether it binds successfully to its target	XX
SQ	Sequence 24 BP, 3 A; 6 C; 11 G; 4 T; 0 U; 0 Other;	XX
QY	Query Match 66.7%; Score 12; DB 2; Length 24; Best Local Similarity 83.3%; Pred. NO. 3.4e+03; Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0	XX
Db	1 GGGGUTCCUGAG 12 1 GGGGCTCTGAG 12	XX
RESULT 190		XX
AAT80358		XX
ID	AAT80358 standard; DNA; 24 BP.	XX
AC	AAT80358;	XX
XX		XX
DT	16-OCT-1997 (First entry)	XX
DE	Oligo HCV-198, tripartite non-contiguous HCV targeting oligomer.	XX
XX		XX
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV; inhibition; regulation; expression; detection; chronic hepatitis; acute hepatitis; hepatocarcinoma; ss.	XX
XX		XX
OS	Synthetic.	XX
XX		XX
EH	Key Location/Qualifiers	XX
FT	modified_base 1..6	XX
FT	/*tag= b	XX
FT	/note= "Comprises phosphorothioate linkages"	XX
FT	7..24	XX
FT	/*tag= a	XX
FT	/note= "2'-OME RNA"	XX
XX		XX
EN	WO9639500-A2.	XX
XX		XX
PD	12-DEC-1996.	XX
XX		XX
PF	04-JUN-1996; 96WO-EP002427.	XX
XX		XX
PR	06-JUN-1995; 95US-00471968.	XX
XX		XX
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.	XX
PA	(HYBR-) HYBRIDON INC.	XX
PI	Frank BL, Goodchild J, Hamlin HA, Kilhuskie RE, Roberts NA;	XX
PI	Roberts PC, Walther DW, Wolfe JL;	XX
DR	WPI; 1997-043122/04.	XX
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in the treatment and detection of HCV infection, esp. hepatitis and hepatocarcinoma.	XX
XX		XX
XX	Claim 21; Page 21; 100pp; English.	XX



XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence binds to three non-contiguous regions of  
CC the HCV genome. This sequence is targeted to the 5' target region, -18  
CC to -13, the internal sequence target, -230 to -219 and the 3' target  
CC region, +1 to +6  
XX  
SQ Sequence 24 BP; 5 A; 5 C; 10 G; 0 T; 4 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUUGAG 12  
|||||  
7 GGGGUCUUGAG 18  
Db  
RESULT 191  
AAT80265  
ID AAT80265 standard; DNA; 24 BP.  
XX  
AC AAT80265;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV99, targeted to HCV region +4 to +15.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..24  
FT /\*tag= a  
FT /note= "Phosphorothioate linkages"  
XX  
XX WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilukie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 19; Page 32; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 24 BP; 3 A; 5 C; 9 G; 7 T; 0 U; 0 Other;

CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 24 BP; 3 A; 4 C; 11 G; 6 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUUGAG 12  
|||||  
1 GGGGUCUUGAG 12  
Db  
RESULT 192  
AAT80271  
ID AAT80271 standard; DNA; 24 BP.  
XX  
AC AAT80271;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV107 targeted to HCV region +1 to +12.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..24  
FT /\*tag= a  
FT /note= "Phosphorothioate linkages"  
XX  
XX WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilukie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 19; Page 32; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 24 BP; 3 A; 5 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 |||||  
 Db 13 GGGGTCCTCGAG 24

RESULT 193  
 AAT80366  
 ID AAT80366 standard; DNA; 24 BP.  
 XX  
 AC AAT80366;  
 XX  
 DT 16-OCT-1997 (first entry)  
 XX  
 DE Oligo HCV-214, tripartite non-contiguous HCV targeting oligomer.  
 XX  
 KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FH modified\_base 1..18  
 FT /\*tag= a  
 FT /note= "2'-OME RNA"  
 FT 19..24  
 FT modified\_base  
 FT /\*tag= b  
 FT /note= "Comprises phosphorothioate linkages"  
 XX  
 PN WO639500-A2.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96WO-EP002427.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 DR WPI; 1997-043122/04.  
 XX  
 PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 PT carcinoma.  
 XX  
 PS Claim 21; Page 21; 100pp; English.  
 XX  
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This sequence binds to three non-contiguous regions of  
 CC the HCV genome. This sequence is targeted to the 5' target region, +1 to  
 CC +6, the internal sequence target, -230 to -219 and the 3' target region,  
 CC +230 to +235  
 XX  
 SQ Sequence 24 BP; 3 A; 4 C; 12 G; 1 T; 4 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
 |||||  
 Db 7 GGGGUCCTCGAG 18

RESULT 194  
 AAT80368  
 ID AAT80368 standard; DNA; 24 BP.  
 XX  
 AC AAT80368;  
 XX  
 DT 16-OCT-1997 (first entry)  
 XX  
 DE Oligo HCV-220, tripartite non-contiguous HCV targeting oligomer.  
 XX  
 KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FH modified\_base 1..18  
 FT /\*tag= a  
 FT /note= "2'-OME RNA"  
 FT 19..24  
 FT modified\_base  
 FT /\*tag= b  
 FT /note= "Comprises phosphorothioate linkages"  
 XX  
 PN WO639500-A2.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96WO-EP002427.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 DR WPI; 1997-043122/04.  
 XX  
 PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 PT carcinoma.  
 XX  
 PS Claim 21; Page 21; 100pp; English.  
 XX  
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This sequence binds to three non-contiguous regions of  
 CC the HCV genome. This sequence is targeted to the 5' target region, +1 to  
 CC +6, the internal sequence target, -230 to -219 and the 3' target region,  
 CC +240 to +245  
 XX  
 SQ Sequence 24 BP; 4 A; 4 C; 11 G; 1 T; 4 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 |||||



KM	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	Inhibition; replication; expression; detection; chronic hepatitis;
KX	acute hepatitis; hepatocarcinoma; ss.
OS	Synthetic.
XX	
FH	Key
FT	modified_base
FT	1..24
FT	/tag= a
FT	/note= "phosphorothioate linkages"
PN	
XN	WO9639500-A2.
XX	
PD	12-DEC-1996.
XX	
PF	04-JUN-1996; 96MO-EP002427.
XX	
PR	06-JUN-1995; 95US-00471968.
XX	
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX	(HYBR -) HYBRIDON INC.
PI	
PI	Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;
DR	Roberts PC, Walthier DM, Wolfe JL;
XX	WPI; 1997-043122/04.
PT	
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
PS	
XX	Claim 19; Page 32; 100pp; English.
XX	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmaceutical composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC	whether it binds successfully to its target
SQ	
SQ	Sequence 24 BP; 3 A; 5 C; 9 G; 7 T; 0 U; 0 Other;
	Query Match 66.7%; Score 12; DB 2; Length 24;
	Best Local Similarity 83.3%; Pred. No. 3.4e+03;
	Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
Gy	
	1 GGGGUCUUGAG 12
	:
Db	1 GGGGTCTCGAG 12
	RESULT 198
AAT80275	
ID	AAT80275 standard; DNA; 24 BP.
XX	
AC	AAT80275;
XX	
DT	15-OCT-1997 (first entry)
XX	
DE	Oligo HCV113, targeted to HCV region -6 to +6.
KM	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	Inhibition; replication; expression; detection; chronic hepatitis;
KX	acute hepatitis; hepatocarcinoma; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	modified_base 1..12

FT	/tag= b
FT	/note= "Phosphorothioate linkages"
FT	modified_base 13..24
FT	/tag= a
FT	/note= "Optionally 2' OMe modified"
PN	WO9639500-A2.
PN	
XX	
PD	12-DEC-1996.
XX	
XX	
PR	06-JUN-1995; 95US-00471968.
XX	
XX	
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX	(HYBR-) HYBRIDON INC.
PI	Frank BL, Goodchild J, Hamlin HA, Kilukie RE, Roberts NA,
PI	Roberts PC, Walther DM, Wolfe JL;
DR	WPL, 1997-043122/04.
XX	
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
PS	Claim 19; Page 32; 100pp; English.
XX	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmaceutical composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC	whether it binds successfully to its target
XX	
SQ	Sequence 24 BP; 3 A; 5 C; 11 G; 3 T; 2 U; 0 Other;
Query Match	66.7%; Score 12; DB 2; Length 24;
Best Local Similarity	100.0%; Pred. No. 3 4e+03;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GGGGUCCTUGAG 12     
Db	13 GGGGUCCTUGAG 24
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ID	AAT80365 standard; DNA; 24 BP.
XX	
AC	AAT80365;
XX	
DT	16-OCT-1997 (first entry)
XX	
XX	
OLIGO	Oligo HCV-211, tripartite non-contiguous HCV targeting oligomer.
XX	
KM	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KM	inhibition; replication; expression; detection; chronic hepatitis;
XX	acute hepatitis; hepatocarcinoma; su.
OS	
XX	Synthetic.
Key	
PH	Location/Qualifiers
FT	modified_base 1..6
FT	/tag= b
FT	/note= "Comprises phosphorothioate linkages"
FT	modified_base 7..24
FT	/tag= a
FT	/note= "2'-OMe RNA"
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XX PN W09639500-A2.
XX XX 12-DEC-1996.
XX PD 04-JUN-1996; 96WO-EP002427.
XX PF 06-JUN-1995; 95US-00471968.
XX PR (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 21; Page 21; 100pp; English.
XX XX
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This sequence binds to three non-contiguous regions of
XX CC the HCV genome. This sequence is targeted to the 5' target region, +25
XX CC to +30, the internal sequence target, +1 to +6 and the 3' target region,
XX CC -230 to -219
XX SQ Sequence 24 BP; 2 A; 5 C; 8 G; 5 T; 4 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGCGAG 12
   |||||
Db 13 GGGGUCGCGAG 24

RESULT 200
AAT80258
ID AAT80258 standard; DNA; 24 BP.
XX AC AAT80258;
XX DT 15-OCT-1997 (first entry)
XX DE Oligo HCV88, targeted to HCV -9 to +3.
XX KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KM inhibition; replication; expression; detection; chronic hepatitis;
XX KM acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT 1. .24
XX FT modified_base
XX FT /*tag= a
XX FT /note= "Comprises phosphorothioate linkages"
XX PN W09639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.

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XX ER 06-JUN-1995; 95US-00471968.
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX XX
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX DR
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 19; Page 31; 100pp; English.
XX XX
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX CC whether it binds successfully to its target
XX SQ Sequence 24 BP; 3 A; 5 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGCGAG 12
   |||||
Db 1 GGGGTCTCTGAG 12

Search completed: April 25, 2005, 13:45:37
Job time : 233.053 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:46 ; Search time 1731.32 Seconds  
(without alignments)  
395.743 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18

Sequence: 1 GGGGUCUGAGNNNNNN 18

Scoring table: OLIGO\_NUC

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST: \*  
1: gb\_esc1: \*  
2: gb\_esc2: \*  
3: gb\_hmc: \*  
4: gb\_esc3: \*  
5: gb\_esc4: \*  
6: gb\_esc5: \*  
7: gb\_esc6: \*  
8: gb\_gsa1: \*  
9: gb\_gsa2: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.9	807	9	CL656406	PR10126C
2	83.3	298	7	CN046841	VI_P8_J19
3	83.3	646	3	AV110482	Zea mays
4	83.3	2267	3	AV110086	AV110086 Zea mays
5	83.3	2334	9	AY406052	AY406052 Mus muscu
6	83.3	3643	9	AY406378	AY406378 Pan trogl
7	77.8	295	9	CL605849	CL605849 CH240_183
8	77.8	306	9	CL607685	CL607685 CH240_173
9	77.8	350	6	CB781043	CB781043 AMGNNUC:S
10	77.8	410	6	CB803895	CB803895 AMGNNUC:Y
11	77.8	446	9	CC466788	CC466788 CH240_136
12	77.8	447	4	BG275153	BG275153 NXSI_140
13	77.8	451	9	CG981750	CG981750 CH240_167
14	77.8	503	9	CG608913	CG608913 OST28585
15	77.8	593	6	CB584419	CB584419 AMGNNUC:N
16	77.8	715	9	CL683372	CL683372 PR10136C
17	77.8	745	9	CC923806	CC923806 C071108ba
18	77.8	764	9	CC918669	CC918669 C009611ba
19	77.8	785	9	CL677391	CL677391 PR10120a
20	77.8	789	6	CB897169	CB897169 trico10xa
21	77.8	809	6	CB900187	CB900187 trico21xe
22	77.8	1392	9	AY413964	AY413964 Homo sapi
23	77.8	1392	9	AY413965	AY413965 Homo sapi
24	77.8	1527	9	AY411600	AY411600 Homo sapi

25	14	77.8	1527	9	AY411601	AY411601 Pan trogl
26	14	77.8	2907	3	AY186641	AY186641 Homo sapi
27	14	77.8	5308	3	AY109382	AY109382 Zea mays
28	13	72.2	91	9	CG976547	CG976547 CH240_166
29	13	72.2	122	2	BE242665	BE242665 TCAP1E17
30	13	72.2	166	9	CG918380	CG918380 CH240_144
31	13	72.2	211	9	CG979398	CG979398 CH240_171
32	13	72.2	212	9	CL609827	CL609827 CH240_177
33	13	72.2	221	9	CG986238	CG986238 CH240_156
34	13	72.2	224	9	CL603268	CL603268 CH240_178
35	13	72.2	236	9	CC467061	CC467061 CH240_136
36	13	72.2	250	9	CG989067	CG989067 CH240_146
37	13	72.2	266	9	CG982763	CG982763 CH240_164
38	13	72.2	337	9	CG983959	CG983959 CH240_153
39	13	72.2	332	9	CC470613	CC470613 CH240_144
40	13	72.2	377	9	CL211616	CL211616 W13C04 G
41	13	72.2	392	6	CB774359	CB774359 AMGNNUC:N
42	13	72.2	393	6	CG989457	CG989457 CH240_146
43	13	72.2	412	9	CG980948	CG980948 CH240_161
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47	13	72.2	433	8	BZ759980	BZ759980 622_314_F
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51	13	72.2	497	9	CC467322	CC467322 CH240_137
52	13	72.2	503	8	AQ597630	AQ597630 HS_2065_B
53	13	72.2	504	9	CG986681	CG986681 CH240_157
54	13	72.2	506	9	CL608092	CL608092 CH240_174
55	13	72.2	509	9	CG983697	CG983697 CH240_165
56	13	72.2	526	9	CL608426	CL608426 CH240_175
57	13	72.2	536	9	CG986355	CG986355 CH240_157
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62	13	72.2	606	9	CG992853	CG992853 CH240_152
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65	13	72.2	618	9	AY417454	AY417454 Pan trogl
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68	13	72.2	638	9	CG976913	CG976913 CH240_167
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71	13	72.2	679	8	BZ912643	BZ912643 CH240_111
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73	13	72.2	701	9	CG992790	CG992790 CH240_152
74	13	72.2	716	5	CN035898	CN035898 nm_11_g12
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76	13	72.2	783	7	CN042530	CN042530 v11_p42_o
77	13	72.2	802	3	AY111174	AY111174 Zea mays
78	13	72.2	825	9	AY405397	AY405397 Pan trogl
79	13	72.2	835	5	BQ948650	BQ948650 AGENCOURT
80	13	72.2	858	9	CG921276	CG921276 C047002ba
81	13	72.2	878	5	BU957217	BU957217 AGENCOURT
82	13	72.2	895	3	AY110949	AY110949 Zea mays
83	13	72.2	895	3	AY110949	AY110949 Zea mays
84	13	72.2	903	3	AY110949	AY110949 Zea mays
85	13	72.2	928	3	AY110206	AY110206 Zea mays
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87	13	72.2	1000	5	BQ062584	BQ062584 AGENCOURT
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91	13	72.2	1170	9	AY410560	AY410560 Pan trogl
92	13	72.2	1247	9	AY409438	AY409438 Pan trogl
93	13	72.2	1271	9	AY409437	AY409437 Homo sapi
94	13	72.2	1613	9	AY421522	AY421522 Pan trogl
95	13	72.2	1920	9	AY409605	AY409605 Homo sapi
96	13	72.2	1920	9	AY409606	AY409606 Pan trogl
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C 252	12	66.7	237	1	AI845958	UI-M-AKI-	325	12	66.7	268	2	BS10384
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C 254	12	66.7	237	5	BQ528062	BQ528062 1091055440	327	12	66.7	268	4	BI774348
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C 256	12	66.7	238	1	AA963688	UI-R-El-9	329	12	66.7	268	9	CG543981
C 257	12	66.7	238	6	AI851860	UI-M-BHO-	330	12	66.7	269	2	BE837040
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C 262	12	66.7	242	1	AV127381	AV127381	335	12	66.7	270	2	BF765024
C 263	12	66.7	243	1	AV234199	AV234199	336	12	66.7	270	7	CV342995
C 264	12	66.7	243	1	AV242455	AV242455	337	12	66.7	270	7	N28156
C 265	12	66.7	243	2	BB171141	BB171141	338	12	66.7	270	8	A2956865
C 266	12	66.7	243	2	BM492742	BM492742	339	12	66.7	271	2	AM479994
C 267	12	66.7	243	4	BM446164	BM446164 11L4C9..ab	340	12	66.7	271	2	BB551073
C 268	12	66.7	244	9	CE679091	CE679091 L1gr-g88-	341	12	66.7	271	2	BE717563
C 269	12	66.7	245	1	AA326703	AA326703	342	12	66.7	271	8	BE878816
C 270	12	66.7	245	1	AA357582	AA357582	343	12	66.7	272	2	BE216174
C 271	12	66.7	245	1	BB022056	BB022056	344	12	66.7	272	6	CD542099
C 272	12	66.7	246	2	BF202156	BF202156	345	12	66.7	273	2	BB305567
C 273	12	66.7	247	1	AV205320	AV205320	346	12	66.7	273	8	A2077912
C 274	12	66.7	247	2	BB516760	BB516760	347	12	66.7	274	1	AA376207
C 275	12	66.7	247	6	CD620963	CD620963	348	12	66.7	274	1	CK227223
C 276	12	66.7	247	7	CK227219	CK227219	349	12	66.7	275	1	AA253386
C 277	12	66.7	247	9	CL335852	CL335852 RPCI44_25	350	12	66.7	275	1	AA261297
C 278	12	66.7	248	2	BF560803	BF560803 UI-R-CO-h	351	12	66.7	275	1	AA226091
C 279	12	66.7	248	2	BF929783	BF929783 QV3-NT021	352	12	66.7	275	2	BF370621
C 280	12	66.7	249	9	BF353862	BF353862 IL5-HT070	353	12	66.7	275	2	BB723048
C 281	12	66.7	249	9	CE124814	CE124814 L1gr-g88-	354	12	66.7	275	7	TF22771
C 282	12	66.7	251	7	BB606888	BB606888	355	12	66.7	276	2	BE836978
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C 292	12	66.7	257	2	BB345500	BB345500	365	12	66.7	279	2	BB498881
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C 295	12	66.7	258	9	CE858911	CE858911 L1gr-g88-	368	12	66.7	280	1	AA978208
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C 299	12	66.7	260	5	BP103065	BP103065	372	12	66.7	280	2	BE836994
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C 301	12	66.7	261	7	CN415331	CN415331 170005122	374	12	66.7	280	8	AZ381336
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C 303	12	66.7	261	2	BB837035	BB837035 RC6-FN008	376	12	66.7	281	1	AU075818
C 304	12	66.7	261	4	BG982648	BG982648 IL5-CN006	377	12	66.7	281	1	AV137880
C 305	12	66.7	261	7	CN576464	CN576464 rc65c06.x	378	12	66.7	281	2	BB081511
C 306	12	66.7	261	9	CE317310	CE317310 L1gr-g88-	379	12	66.7	282	1	AA355247
C 307	12	66.7	262	1	AV442031	AV442031	380	12	66.7	282	2	BF371084
C 308	12	66.7	263	2	BF412757	BF412757 UI-R-BT1-	381	12	66.7	282	2	BB310977
C 309	12	66.7	263	2	BF759646	BF759646 CM1-CT060	382	12	66.7	282	2	BB351786
C 310	12	66.7	263	9	CG560120	CG560120 OST180067	383	12	66.7	282	9	CE681986
C 311	12	66.7	264	1	AV268669	AV268669	384	12	66.7	282	9	CG977185
C 312	12	66.7	264	9	CG188511	PUPSD1TD	385	12	66.7	283	2	BF817082
C 313	12	66.7	265	1	AI608577	AI608577 v41c11..x	386	12	66.7	283	2	AM833996
C 314	12	66.7	265	1	AV019951	AV019951	387	12	66.7	283	2	BB126874
C 315	12	66.7	265	2	BF588625	BF588625 7120a06..x	388	12	66.7	283	3	BB154663
C 316	12	66.7	265	2	BB605782	BB605782	389	12	66.7	283	4	BG071262

C 390	12	66.7	283	7	CN372754	170006001	C 463	12	66.7	302	2	BB269914	BB269914
C 391	12	66.7	284	2	BB438340	BB438340	C 464	12	66.7	302	2	BB295403	BB295403
C 392	12	66.7	284	8	CC355492	PUMPT39TB	C 465	12	66.7	302	2	BB322656	BB322656
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## ALIGNMENTS

RESULT 1  
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 ACCESSION CL656406  
 VERSION CL656406.1 GI:50136810  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

CL656406 807 bp DNA linear GSS 09-JUN-2004  
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 GSS.  
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 Pristionchus pacificus  
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 Neodiplogasteridae; Pristionchus.  
 1 (bases 1 to 807)  
 Strinivasan, V., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.  
 Appad: an Acce database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.

## FEATURES

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## Query Match

88.3%; Score 16; DB 9; Length 807;

Best Local Similarity 87.5%; Pred. No. 1,3e+02; Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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 DB 608 GGUCCUGAGNNNNN 623

RESULT 2  
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 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae; Ambystoma.  
 1 (bases 1 to 296)  
 Putta, S., Smith, J. J., Walker, J. A., Ronder, M., Weisrock, D., Monaghan, J., Samuels, A. K., Kump, K., King, D. C., Maness, N. J., Habermann, B., Tanaka, E., Bryant, S. V., Gardiner, D. M., Parichy, D. M. and Voss, S. R.  
 From biomedicine to natural history research: EST resources for ambystomatid salamanders  
 BMC Genomics 5 (1), 54 (2004)  
 Contact: SR Voss  
 Department of Biology  
 University of Kentucky  
 TH Morgan Building, Lexington, KY 40506, USA  
 Tel: 859 257 9888  
 Fax: 859 257 1717  
 Email: srvoos@uky.edu  
 The EST is quality trimmed at the ends with a 20 base window and quality threshold of 15 (phred quality score). Please visit <http://salamander.uky.edu> for any information (trace, quality files etc) regarding this EST.

TITLE  
 JOURNAL  
 COMMENT

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 Location/Qualifiers

## ORIGIN

Query Match 83.3%; Score 15; DB 7; Length 296;  
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 DB 1 GUCCUGAGNNNNN 15

RESULT 3  
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 KEYWORDS  
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 ORGANISM

Zea mays  
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 Hainey, C. F., Dolan, M., Miao, G. H., Vogel, J. M., Whitsitt, M. S., Arthur, L. W., Hanafey, M., Morante, M. and Tingey, S. V.  
 Maize Mapping Project/Dupont Consensus Sequences for Design of

JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 646)  
 AUTHORS Coe,E.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES  
 SOURCE Location/Qualifiers  
 1..646  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="MaizEDB:631545"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Cornsensus Library"  
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN  
 Query Match 83.3%; Score 15; DB 3; Length 646;  
 Best Local Similarity 86.7%; Pred. No. 4.1e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUCCUGAGANNNNNN 18  
 |||:|||||  
 Db 115 GTCTGTGAGNNNNNN 129

RESULT 4  
 LOCUS AY110086 2267 bp mRNA linear HTC 17-OCT-2002  
 DEFINITION Zea mays CL418\_1 mRNA sequence.  
 ACCESSION AY110086  
 VERSION AY110086.1 GI:21214173  
 KEYWORDS HTC.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 2267)  
 Hahney,C.F., DoJan,M., Miao,G.H., Vogel,J.M., Whitstitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
 Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
 JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 2267)  
 AUTHORS Coe,E.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES  
 SOURCE Location/Qualifiers  
 1..2267  
 /organism="Zea mays"  
 /mol\_type="mRNA"

/db\_xref="MaizEDB:630280"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Cornsensus Library"  
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN  
 Query Match 83.3%; Score 15; DB 3; Length 2267;  
 Best Local Similarity 86.7%; Pred. No. 4.1e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUCCUGAGANNNNNN 18  
 |||:|||||  
 Db 339 GTCTGTGAGNNNNNN 325

RESULT 5  
 LOCUS AY406052 2334 bp DNA linear GSS 15-DEC-2003  
 DEFINITION Mus musculus ABLIM1 gene, VIRTUAL TRANSCRIPT, partial sequence.  
 ACCESSION AY406052  
 VERSION AY406052.1 GI:39762026  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.  
 1 (bases 1 to 2334)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
 JOURNAL Location/Qualifiers  
 1..2334  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 <1..>2334  
 /gene="ABLIM1"  
 /locus\_tag="HGM2428"

ORIGIN  
 Query Match 83.3%; Score 15; DB 9; Length 2334;  
 Best Local Similarity 86.7%; Pred. No. 4.1e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUCCUGAGANNNNNN 18  
 |||:|||||  
 Db 886 GTCTGTGAGNNNNNN 900

RESULT 6  
 LOCUS AY406378

LOCUS AY406378 3643 bp DNA linear GSS 12-DEC-2003  
 DEFINITION Pan troglodytes HCM2537 gene, VIRUAL TRANSCRIPT, partial sequence.  
 ACCESSION AY406378  
 VERSION AY406378.1 GI:39762352  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 1 (bases 1 to 3643)  
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering them based on alignment.  
 Location/Qualifiers  
 1. 3643  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 <1..>3643  
 /locus\_tag="HCM2537"

ORIGIN  
 Query Match 83.3%; Score 15; DB 9; Length 3643;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUCCUGAGNNNNN 18  
 ||:|||||  
 DB 85 GTCCTGGAGNNNNN 99

RESULT 7  
 CL605849 295 bp DNA linear GSS 17-JUN-2004  
 LOCUS CH240\_183G18.TJ CHORI-240 Bos taurus genomic clone CH240\_183G18,  
 DEFINITION genomic survey sequence.  
 ACCESSION CL605849  
 VERSION CL605849.1 GI:48873881  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 295)  
 Costa, J.N., Mota, W. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_183G18.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658

FEATURES  
 source  
 Location/Qualifiers  
 1. 295  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_183G18"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN  
 Query Match 77.8%; Score 14; DB 9; Length 295;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGNNNNN 18  
 ||:|||||  
 DB 165 TCTCTGGAGNNNNN 178

RESULT 8  
 CL607685/c 306 bp DNA linear GSS 17-JUN-2004  
 LOCUS CH240\_173D24.TJ CHORI-240 Bos taurus genomic clone CH240\_173D24,  
 DEFINITION genomic survey sequence.  
 ACCESSION CL607685  
 VERSION CL607685.1 GI:48875717  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 306)  
 Costa, J.N., Mota, W. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_173D24.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetaen@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of The International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e tecnologico (CNPq), Brazil  
 Plate: 183 row: G column: 18  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence strop: 295.



(pdejong@mail.chc.org).

Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm).

This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 173 row: D column: 24  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 306.

FEATURES  
source  
1..306  
Location/Qualifiers

/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="Breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_173D24"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBAcl.3; Site 1: MboI; Site 2: MboI;  
Hereford bull l1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 306;  
Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGAGNNNNN 18  
Db 172 TCCTGAGAGNNNNN 159

RESULT 9  
CB781043

LOCUS CB781043 350 bp mRNA linear EST 16-MAY-2003  
DEFINITION AMGNNUC:SRPB2-00120-G1-A srpb2 (10220) Rattus norvegicus cDNA clone  
srpb2-00120-g1 5', mRNA sequence.

ACCESSION CB781043  
VERSION CB781043.1 GI:29869434  
KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 350)

Angen EST Program.  
AUTHORS Angen Rat EST Program  
JOURNAL Unpublished (2003)  
COMMENT Contact: Dan Fitzpatrick  
Angen, Inc

One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00120 row: 9 column: 1.

FEATURES  
source  
1..350  
Location/Qualifiers

/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="srpb2-00120-g1"  
/issue\_type="prostate tissue"  
/clone\_lib="srpb2 (10220)"  
/note="Vector: pSPOR1; Site 1: SalI; Site 2: NotI; rat  
prostate normalized double selected poly(A+) mRNA size  
fraction > 1 kb"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 350;  
Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGAGNNNNN 18  
Db 220 TCCTGAGAGNNNNN 233

RESULT 10  
CB803895

LOCUS CB803895 410 bp mRNA linear EST 16-MAY-2003  
DEFINITION AMGNNUC:YRAPB2-00001-B1-A PLAP-b hypothalamus (10617) Rattus  
norvegicus cDNA clone yrapb2-00001-b1 5', mRNA sequence.

ACCESSION CB803895  
VERSION CB803895.1 GI:29919524  
KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 410)  
AUTHORS Angen EST Program.  
JOURNAL Angen Rat EST Program  
COMMENT Contact: Dan Fitzpatrick  
Angen, Inc

One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00001 row: b column: 1.

FEATURES  
source  
1..410  
Location/Qualifiers

/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="Yrapb2-00001-b1"  
/issue\_type="hypothalamus normal"  
/clone\_lib="PLAP-b hypothalamus (10617)"  
/note="Vector: pCDNA3.1(-)/PLAP-5a; Site 1: XbaI; Site 2:  
NotI"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 410;  
Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGAGNNNNN 18  
Db 244 TCCTGAGAGNNNNN 257

RESULT 11  
CC466788

LOCUS CC466788 446 bp DNA linear GSS 12-JUN-2003  
DEFINITION CH240\_136M10.TV CHORI-240 Bos taurus genomic clone CH240\_136M10,  
genomic survey sequence.

ACCESSION CC466788  
VERSION CC466788.1 GI:31653020  
KEYWORDS GSS.

SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (bases 1 to 446)  
AUTHORS Costa, J.N., Mota, M. and Caetano, A.R.  
JOURNAL Brazil's Contribution to End-Sequencing the Bovine BAC Library  
COMMENT Unpublished (2003)  
Other\_GSSs: CH240\_136M10.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasilia

Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>). Bases shown have phred  
 quality value equal to or higher than 20. Bases with quality value  
 below 20 were masked with 'N'. For BAC library availability, please  
 contact Pieter de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)). Clones may be  
 purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)). This work  
 was undertaken as part of the International Bovine BAC Mapping  
 Consortium (IBMC) by Embrapa Recursos Geneticos e Biotecnologia  
 with financing from Conselho Nacional de Desenvolvimento Cientifico  
 e Tecnologico (CNPq), Brazil  
 Plate: 136 row: M column: 10  
 Seq primer: SP6  
 Clases: BAC ends  
 High quality sequence stop: 446.  
 Location/Qualifiers  
 1..446  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_136M10"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAcl.3; Site\_1: MboI; Site\_2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 446;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 UCCUGAGANNNNNN 18  
 :||:|||||||  
 Db 134 TCCTGAGANNNNNN 147

RESULT 12  
 BG275153 447 bp mRNA linear EST 07-MAY-2003  
 LOCUS NXSI 140 D03 F NXSI (Nef Xylem Side wood inclined) Pinus taeda cDNA  
 DEFINITION A5G02960 unknown protein see  
<http://mips.gsf.de/proj/thal/db/index.html>, mRNA sequence.  
 ACCESSION BG275153 GI:13068180  
 VERSION BG275153.1  
 KEYWORDS EST.  
 SOURCE Pinus taeda (loblolly pine)  
 ORGANISM Pinus taeda  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
 Sederoff, R.  
 1 (bases 1 to 447)  
 TITLE Molecular Basis of Wood Formation in the Pine Megagenome  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Sederoff, Ron  
 Forest Biotechnology  
 North Carolina State University  
 840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
 NC 27695, USA  
 Tel: 919 515 7800  
 Fax: 919 515 7801  
 Email: [ron.sederoff@ncsu.edu](mailto:ron.sederoff@ncsu.edu), [jerry\\_johnson@ncsu.edu](mailto:jerry_johnson@ncsu.edu)  
 Please see <http://web.ahc.unc.edu/biodata/nsfpine/> for further  
 information.  
 Seq primer: T3.  
 Location/Qualifiers  
 1..447

## ORIGIN

Query Match 77.8%; Score 14; DB 4; Length 447;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 UCCUGAGANNNNNN 18  
 :||:|||||||  
 Db 425 TCCTGAGANNNNNN 438

/organism="Pinus taeda"  
 /mol\_type="mRNA"  
 /strain="Coastal plain loblolly pine from North Carolina"  
 /db\_xref="taxon:3352"  
 /clone="NXSI 140 D03"  
 /tissue\_type="Xylem"  
 /cell\_type="Side"  
 /dev\_stage="juvenile"  
 /lab\_host="XLI-Blue"  
 /clone\_lib="NXSI (Nef Xylem Side wood Inclined)"  
 /note="Vector: Bluescript SK, Site\_1: Eco RI; Site\_2:  
 XhoI; The library is from early (spring) wood, taken from  
 three six-year old trees (three different genotypes), in  
 the juvenile phase. These trees were induced to form side  
 wood by bending to a 45 degree angle and tying them to the  
 ground. Differentiating xylem was harvested from the sides  
 of the inclined stems, and a mixture of all three  
 genotypes was used for the library. oligo-dT primed cDNA  
 was directionally cloned into the EcoRI-XhoI Bluescript SK  
 vector arms. NOTE: The sequences contain a 'cDNA adapter'  
 between the EcoRI site and the start of the EST. The  
 adapter sequence is 'AATTCGACGACG'."

RESULT 13  
 CG981750 451 bp DNA linear GSS 15-DEC-2003  
 LOCUS CH240 162B19 TV CHORI-240 Bos taurus genomic clone CH240\_162B19,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG981750 GI:39907529  
 VERSION CG981750.1  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 451)  
 TITLE Costa, V.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: CH240\_162B19.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estrada Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372 70770-900 Brasilia  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have Phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 162 row: B column: 19

Seq primer: SP6  
 Class: BAC ends  
 High quality sequence strip: 451.  
 Location/Qualifiers

# FEATURES

## Source

1. .451  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_162B19"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_1ib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull; Li Domino 993/5; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 451;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNN 18  
 :||:|||||||  
 Db 227 TCCTGAGAGNNNNN 240

RESULT 14  
 CG608913 503 bp mRNA linear GSS 02-OCT-2003  
 LOCUS CG608913/c  
 DEFINITION OST289585 Mus musculus 129SV/Ev Mus musculus cDNA clone OST289585, mRNA sequence.

ACCESSION CG608913  
 VERSION CG608913.1 GI:37432762  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 503)  
 AUTHORS Zambrowicz,B.P., Abuln,A., Ramirez-Solis,R., Richter,L.D., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,C., Key,B.W. Jr., Klipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.  
 Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

TITLE Contact: Zambrowicz BP  
 JOURNAL OmilBank  
 COMMENT Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: materials@lexgen.com

FEATURES  
 Source 1. .503  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129SV/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST289585"  
 /cell\_type="embryonic stem cell"  
 /clone\_1ib="Mus musculus 129SV/Ev"

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 503;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUCUGAGAGNN 15  
 |||:|||||||  
 Db 495 GGCTCTGAGAGNN 482

RESULT 15  
 CB584419 593 bp mRNA linear EST 03-APR-2003  
 LOCUS AMGNNUC:NRH5-00282-F9-A W Rat Hypothalamus (10471) Rattus  
 DEFINITION norvegicus cDNA clone nrh5-00282-f9 5', mRNA sequence.  
 CB584419  
 ACCESSION CB584419 GI:29527870  
 VERSION EST.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 593)  
 AUTHORS Amgen EST Program.  
 TITLE Amgen Rat EST Program  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dan Fitzpatrick  
 Amgen, Inc  
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00282 row: f column: 9.

FEATURES  
 Source 1. .593  
 Location/Qualifiers  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="nrh5-00282-f9"  
 /clone\_1ib="W Rat hypothalamus (10471)"  
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat hypothalamus adult female Wistar rat avg. Insert size 2.3 kb fraction 6 and 7"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 593;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNN 18  
 :||:|||||||  
 Db 105 TCCTGAGAGNNNNN 118

RESULT 16  
 CL683372/c 715 bp DNA linear GSS 09-JUL-2004  
 LOCUS PRI0136C\_G09\_2 - PRI0136C.BR (715) Mixed stage fosmid library of P.  
 DEFINITION Pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL683372.1 GI:50191062  
 VERSION GSS.  
 KEYWORDS Pristionchus pacificus  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus

REFERENCE 1 (bases 1 to 715)  
 AUTHORS Strinvaasen,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.U.  
 TITLE AppDB: an Acedb database for the nematode satellite organism Pristionchus pacificus  
 JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 COMMENT Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.

Seq primer: T7  
Class: fosmid ends.

FEATURES  
source Location/Qualifiers

1..715  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pEpifco-5 Fosmid vector"

# ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 715;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
Db 282 TCCTGAGAGNNNNNN 269

RESULT 17.  
CC923806/c 745 bp DNA linear GSS 08-AUG-2003  
LOCUS t071108ba.f1 TAMB7 Bos taurus genomic clone t071108ba, genomic  
DEFINITION Survey sequence.  
ACCESSION CC923806  
VERSION CC923806.1 GI:33559145  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 745)  
Lin.S., Najjar,F.Z., Adelson,D., Gill,C.A. and Roe,B.A.  
Bovine BAC End Sequences from Library TAMB7  
Unpublished (2003)  
Contact: Bruce A. Roe  
Advanced Center for Genome Technology  
University of Oklahoma Department of Chemistry and Biochemistry  
620 Parrington Oval, Room 208, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Class: BAC ends  
High quality sequence stop: 659.  
Location/Qualifiers

1..745  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="Angus bull T A M U Shoshone Y6 11519666"  
/db\_xref="taxon:9913"  
/clone="t071108ba"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="TAMB7"  
/note="Vector: pBelobAC11, Site 1: HindIII, Site 2:  
HindIII; TAMB7 Bovine BAC library (Male) produced by Texas  
A&M University, Department of Animal Science."

FEATURES  
source Location/Qualifiers

1..745  
/organism="Bos taurus"  
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/strain="Angus bull T A M U Shoshone Y6 11519666"  
/db\_xref="taxon:9913"  
/clone="t071108ba"  
/sex="Male"  
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/clone\_lib="TAMB7"  
/note="Vector: pBelobAC11, Site 1: HindIII, Site 2:  
HindIII; TAMB7 Bovine BAC library (Male) produced by Texas  
A&M University, Department of Animal Science."

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 745;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
Db 38 TCCTGAGAGNNNNNN 25

RESULT 18  
CC918669/c 764 bp DNA linear GSS 08-AUG-2003  
LOCUS t009e11ba.f1 TAMB7 Bos taurus genomic clone t009e11ba, genomic  
DEFINITION Survey sequence.  
ACCESSION CC918669  
VERSION CC918669.1 GI:33549379  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 764)  
Lin.S., Najjar,F.Z., Adelson,D., Gill,C.A. and Roe,B.A.  
Bovine BAC End Sequences from Library TAMB7  
Unpublished (2003)  
Contact: Bruce A. Roe  
Advanced Center for Genome Technology  
University of Oklahoma Department of Chemistry and Biochemistry  
620 Parrington Oval, Room 208, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Class: BAC ends  
High quality sequence start: 6  
High quality sequence stop: 457.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (2003)  
Contact: Bruce A. Roe  
Advanced Center for Genome Technology  
University of Oklahoma Department of Chemistry and Biochemistry  
620 Parrington Oval, Room 208, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Class: BAC ends  
High quality sequence start: 6  
High quality sequence stop: 457.  
Location/Qualifiers

FEATURES  
source Location/Qualifiers

1..764  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="Angus bull T A M U Shoshone Y6 11519666"  
/db\_xref="taxon:9913"  
/clone="t009e11ba"  
/sex="Male"  
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/clone\_lib="TAMB7"  
/note="Vector: pBelobAC11, Site 1: HindIII, Site 2:  
HindIII; TAMB7 Bovine BAC library (Male) produced by Texas  
A&M University, Department of Animal Science."

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 764;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
Db 32 TCCTGAGAGNNNNNN 19

RESULT 19  
CL677391 785 bp DNA linear GSS 09-JUN-2004  
LOCUS PRI0120a.G09.2 - PRI0120a.BR (785) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
ACCESSION CL677391  
VERSION CL677391.1 GI:50183399  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 785)  
Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.U.  
Apadab: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1..785

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"

/note="Vector: pGP1fos-5 Fosmid vector"

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 785;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGGNNNNN 18

Db 369 TCCTGAGGNNNNN 382

## RESULT 20

CB897169/c

LOCUS 789 bp mRNA linear EST 02-JUL-2003

DEFINITION jecorina cDNA clone tric010xa18, mRNA sequence.

ACCESSION CB897169

VERSION CB897169.1 GI:30111827

KEYWORDS EST.

SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)

ORGANISM

REFERENCE

AUTHORS

FOREMAN, P.K., BROWN, D.E., DANKMEYER, L., DEAN, R., DIENER, S.,  
DUNN-COLEMAN, N.S., GOEDEGEBUUR, F., HOUTEK, T.D., ENGLAND, G.J.,  
KELLEY, A.S., MEERMAN, H.J., MITCHELL, T., MITCHINSON, C.,  
OLIVARES, H.A., TEUNISSEN, P.J., YAO, J., and WARD, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Pamela K. Foreman

Genencor Intl.

925 Page Mill Road, Palo Alto, CA 94304, USA

Tel: (650) 846-7635

Fax: (650) 621-7817

Email: Pforeman@genencor.com

Seq primer: LT-F1 primer.

Location/Qualifiers

1..789

/organism="Hypocrea jecorina"

/mol\_type="mRNA"

/strain="QM6a"

/db\_xref="taxon:51453"

/clone="tric010xa18"

/dev\_stage="mycelia"

/clone\_lib="T. reesei mycelial culture, Version 3 april"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial  
culture grown from 24 hrs to 6 days with varying Carbon  
and Nitrogen sources and concentrations."

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

RESULT 22

AY413964

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGGNNNNN 18

Db 67 TCCTGAGGNNNNN 54

## RESULT 21

CB900187/c

LOCUS

DEFINITION 809 bp mRNA linear EST 02-JUL-2003

CB900187/c tric021xe04 T. reesei mycelial culture, Version 3 april Hypocrea

jecorina cDNA clone tric021xe04, mRNA sequence.

ACCESSION CB900187

VERSION CB900187.1 GI:301114845

KEYWORDS EST.

SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)

ORGANISM

REFERENCE

AUTHORS

FOREMAN, P.K., BROWN, D.E., DANKMEYER, L., DEAN, R., DIENER, S.,  
DUNN-COLEMAN, N.S., GOEDEGEBUUR, F., HOUTEK, T.D., ENGLAND, G.J.,  
KELLEY, A.S., MEERMAN, H.J., MITCHELL, T., MITCHINSON, C.,  
OLIVARES, H.A., TEUNISSEN, P.J., YAO, J., and WARD, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Pamela K. Foreman

Genencor Intl.

925 Page Mill Road, Palo Alto, CA 94304, USA

Tel: (650) 846-7635

Fax: (650) 621-7817

Email: Pforeman@genencor.com

Seq primer: LT-F1 primer.

Location/Qualifiers

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/organism="Hypocrea jecorina"

/mol\_type="mRNA"

/strain="QM6a"

/db\_xref="taxon:51453"

/clone="tric021xe04"

/dev\_stage="mycelia"

/clone\_lib="T. reesei mycelial culture, Version 3 april"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial  
culture grown from 24 hrs to 6 days with varying Carbon  
and Nitrogen sources and concentrations."

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

RESULT 22

AY413964

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AY413964 1392 bp DNA linear GSS 17-DEC-2003

AY413964 Homo sapiens FMNL gene, VIRTUAL TRANSCRIPT, partial, sequence.

AY413964 genomic survey sequence.

AY413964 AY413964.1 GI:39769926

GSS. Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1392)

Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,



REFERENCE 1 (bases 1 to 1527)  
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 REFERENCE 14671302  
 2 (bases 1 to 1527)  
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment  
 FEATURES  
 SOURCE Location/Qualifiers  
 1..1527  
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 /db\_xref="taxon:9598"  
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 /locus\_tag="HCM4278"  
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 Query Match 77.8%; Score 14; DB 9; Length 1527;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 UCCUGAGAGNNNNN 18  
 :||:|||||||  
 Db 420 TCCTGAGAGNNNNN 407  
 RESULT 26  
 AY18641 2907 bp DNA linear GSS 17-DEC-2003  
 LOCUS Homo sapiens NFKB1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AY18641  
 VERSION AY18641.1 GI:39774601  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2907)  
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 REFERENCE 14671302  
 2 (bases 1 to 2907)  
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment  
 FEATURES  
 SOURCE Location/Qualifiers  
 1..2907  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"

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 /locus\_tag="HCM6625"  
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 Query Match 77.8%; Score 14; DB 9; Length 2907;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 UCCUGAGAGNNNNN 18  
 :||:|||||||  
 Db 2114 TCCTGAGAGNNNNN 2127  
 RESULT 27  
 AY109382 5308 bp mRNA linear HTC 17-OCT-2002  
 LOCUS Zea mays CL2032\_1 mRNA sequence.  
 DEFINITION  
 ACCESSION AY109382  
 VERSION AY109382.1 GI:21213087  
 KEYWORDS HTC.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 5308)  
 Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
 TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes  
 JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 5308)  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Malhot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.  
 FEATURES  
 SOURCE Location/Qualifiers  
 1..5308  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="maizedb:630758"  
 /db\_xref="taxon:4577"  
 /clone\_id="Maize Mapping Project/Dupont Consensus Library"  
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"  
 ORIGIN  
 Query Match 77.8%; Score 14; DB 3; Length 5308;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 UCCUGAGAGNNNNN 18  
 :||:|||||||  
 Db 4002 TCCTGAGAGNNNNN 3989  
 RESULT 28  
 CG976547/c 91 bp DNA linear GSS 15-DEC-2003  
 LOCUS CG976547

DEFINITION CH240.166D21.TV CHORI-240 Bos taurus genomic clone CH240.166D21.  
 genomic survey sequence.  
 ACCESSION CG976547  
 VERSION CG976547.1 GI:39902326  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 91)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other\_GSSs: CH240.166D21.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have Phred quality value equal to or higher than 20.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (<http://www.chori.org/bacpac/ordering/information.htm>).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 166 row: D column: 21  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 91.  
 Location/Qualifiers  
 1..91  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_166D21"  
 /sex="male"  
 /cell\_type="Blood"  
 /clone\_id="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN  
 Query Match 72.2%; Score 13; DB 9; Length 91;  
 Best Local Similarity 92.3%; Pred. No. 6.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 25 CCTGAGNNNNNN 13

RESULT 29 122 bp mRNA linear EST 03-OCT-2001  
 BE242665  
 LOCUS TCAAP1711 Pediatric acute myelogenous leukemia cell (FAB M1)  
 DEFINITION Baylor-HSC project-TCAA Homo sapiens CDNA clone TCAAP1711, mRNA  
 sequence.  
 BE242665  
 VERSION BE242665.1 GI:9094395  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 122)  
 Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R.,  
 Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
 Pediatric Leukemia cDNA Sequencing Project  
 Unpublished (2000)  
 TITLE  
 JOURNAL Contact: Dr. Judith F. Margolin  
 Texas Children's Cancer Center and Human Genome Sequencing Center  
 at Baylor College of Medicine  
 1102 Bates, MC3-3320 Houston, TX 77030, USA  
 Tel: 832-824-4536  
 Fax: 832-825-4038  
 Email: clones@ccc.org  
 Citation: Carninci, P. and Hayashizaki, Y. High efficiency  
 full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Seq primer: M13 primer.  
 Location/Qualifiers  
 1..122  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="TCAAP1711"  
 /sex="male"  
 /tissue\_type="leukocytes"  
 /cell\_type="myeloid cell"  
 /dev\_stage="pediatric 6 years"  
 /lab\_host="DH10B"  
 /clone\_id="Pediatric acute myelogenous leukemia cell (FAB  
 M1) Baylor-HSC project-TCAA"  
 /note="Vector: lambda PSB; Site 1: BamHI; Site 2: EcoRI;  
 first strand cDNA was primed with an anchored  
 XhoI-oligo(dT) primer [5'GGAGACTCGAGCGCGCGAGGAG(T)VN  
 3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand  
 was primed with a BamHI-dC primer  
 [5'AGAGCTCGATCGCGCGCCCAATATATAT(C) 3'].  
 Double-stranded cDNA was then digested with BamHI and XhoI  
 and directionally cloned into the BamHI and SalI sites of  
 lambda PSB vector. Library went through one round of  
 normalization. Library was constructed by Wei Yu at RIKEN  
 of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T.,  
 Itoh M., Nagaoaka S., Sasaki N., Okazaki Y., Muramatsu M.,  
 Schneider C., Hayashizaki Y., High efficiency selection of  
 full-length cDNA by improved biotinylated cap trapper.  
 DNA Res 4: 1, 61-6, Feb 28, 1997")

ORIGIN  
 Query Match 72.2%; Score 13; DB 2; Length 122;  
 Best Local Similarity 84.6%; Pred. No. 6.5e+03;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGUCCUGAGN 13  
 |||:|||||  
 93 GGGGTCTCGAGN 105

RESULT 30 166 bp DNA linear GSS 12-DEC-2003  
 CG918380  
 LOCUS CH240.144J23.TV CHORI-240 Bos taurus genomic clone CH240.144J23,  
 genomic survey sequence.  
 ACCESSION CG918380  
 VERSION CG918380.1 GI:39778063  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 166)  
 Costa, J.N., Mota, M. and Caetano, A.R.



**TITLE** Brazil's Contribution to End-Sequencing the Bovine BAC Library  
**JOURNAL** CHORI-240  
**COMMENT** Unpublished (2003)  
 Other\_GSSs: CH240\_144J23.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have Phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering\_information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 144 row: J column: 23  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 166.  
**FEATURES**  
**source**  
 1. 166  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_144J23"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site\_1: MboI; Site\_2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

**ORIGIN**  
 Query Match 72.2%; Score 13; DB 9; Length 166;  
 Best Local Similarity 92.3%; Pred. No. 6.3e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**QY**  
 6 CCUGAGNNNNNN 18  
 ||:|||||  
 Db 134 CCTGGAGNNNNNN 146

**RESULT 31**  
 CG979398/c 211 bp DNA linear GSS 15-DEC-2003  
**LOCUS** CH240\_171D16.TV CHORI-240 Bos taurus genomic clone CH240\_171D16,  
**DEFINITION** genomic survey sequence.  
**ACCESSION** CG979398  
**VERSION** CG979398.1 GI:39905177  
**KEYWORDS** GSS.  
**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus (cow)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 211)  
**REFERENCE** Costa,J.N., Mota,M. and Caetano,A.R.  
**AUTHORS** Brazil's Contribution to End-Sequencing the Bovine BAC Library  
**TITLE** CHORI-240  
**JOURNAL** Unpublished (2003)  
**COMMENT** Other GSSs: CH240\_171D16.TV  
 Contact: Caetano AR  
 Department of Biotechnology

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 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have Phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering\_information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 171 row: D column: 16  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 211.  
**FEATURES**  
**source**  
 1. 211  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_171D16"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site\_1: MboI; Site\_2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

**ORIGIN**  
 Query Match 72.2%; Score 13; DB 9; Length 211;  
 Best Local Similarity 92.3%; Pred. No. 6.2e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**QY**  
 6 CCUGAGNNNNNN 18  
 ||:|||||  
 Db 54 CCTGGAGNNNNNN 42

**RESULT 32**  
 CL609827/c 212 bp DNA linear GSS 17-JUN-2004  
**LOCUS** CH240\_177J19.TV CHORI-240 Bos taurus genomic clone CH240\_177J19,  
**DEFINITION** genomic survey sequence.  
**ACCESSION** CL609827  
**VERSION** CL609827.1 GI:4887859  
**KEYWORDS** GSS.  
**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus (cow)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 212)  
**REFERENCE** Costa,J.N., Mota,M. and Caetano,A.R.  
**AUTHORS** Brazil's Contribution to End-Sequencing the Bovine BAC Library  
**TITLE** CHORI-240  
**JOURNAL** Unpublished (2003)  
**COMMENT** Other GSSs: CH240\_177J19.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 177 row: J column: 19  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 212.  
 Location/Qualifiers  
 1..212  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_177J19"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull U1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 212;  
 Best Local Similarity 92.3%; Pred. No. 6.2e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 125 CCGGAGNNNNNN 113

RESULT 33  
 CG986238 231 bp DNA linear GSS 15-DEC-2003  
 DEFINITION CH240\_156L04.TV CHORI-240 Bos taurus genomic clone CH240\_156L04,  
 genomic survey sequence.  
 ACCESSION CG986238  
 VERSION CG986238.1 GI:39912008  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 231)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_156L04.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 156 row: L column: 04  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 231.  
 Location/Qualifiers  
 1..231  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_156L04"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull U1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 231;  
 Best Local Similarity 92.3%; Pred. No. 6.1e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 155 CCGGAGNNNNNN 167

RESULT 34  
 CL603268 234 bp DNA linear GSS 17-JUN-2004  
 DEFINITION CH240\_178I01.TV CHORI-240 Bos taurus genomic clone CH240\_178I01,  
 genomic survey sequence.  
 ACCESSION CL603268  
 VERSION CL603268.1 GI:48871300  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 234)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_178I01.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Plate: 178 row: 1 column: 01  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 234.  
Location/Qualifiers

FEATURES  
source

1..234  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_178101"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull LI Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 234;  
Best Local Similarity 92.3%; Pred. No. 6.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNN 18  
||:|||||||  
Db 60 CCTGGAGAGNNNNN 48

RESULT 35  
LOCUS

CC467061 236 bp DNA linear GSS 12-JUN-2003  
DEFINITION CH240\_136F14.TJ CHORI-240 Bos taurus genomic clone CH240\_136F14,  
genomic survey sequence.

ACCESSION CC467061  
VERSION CC467061.1 GI:31653293  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 236)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library

REFERENCE  
AUTHORS  
TITLE  
CHORI-240  
Unpublished (2003)

JOURNAL  
COMMENT  
Other GSSs: CH240\_136F14.TV  
Contact: Caetano AR  
Department of Biotechnology  
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Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred  
quality value equal to or higher than 20. Bases with quality value  
below 20 were masked with 'N'. For BAC library availability, please  
contact Pieter de Jong (pdejong@mail.cho.org). Clones may be  
purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia  
with financing from Conselho Nacional de Desenvolvimento Cientifico  
e Tecnologico (CNPq), Brazil.  
Plate: 136 row: F column: 14  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 236.  
Location/Qualifiers

FEATURES  
source

1..236  
/organism="Bos taurus"

/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_136F14"  
/sex="Male"  
/cell\_type="Blood"

/clone\_lib="CHORI-240"  
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull LI Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 236;  
Best Local Similarity 92.3%; Pred. No. 6.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNN 18  
||:|||||||  
Db 25 CCTGGAGAGNNNNN 37

RESULT 36  
LOCUS

CG989067 250 bp DNA linear GSS 15-DEC-2003  
DEFINITION CH240\_146O19.TJ CHORI-240 Bos taurus genomic clone CH240\_146O19,  
genomic survey sequence.

ACCESSION CG989067  
VERSION CG989067.1 GI:39914846  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 250)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library

REFERENCE  
AUTHORS  
TITLE  
CHORI-240  
Unpublished (2003)

JOURNAL  
COMMENT  
Other GSSs: CH240\_146O19.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred  
quality value equal to or higher than 20. Bases with quality value  
below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 146 row: O column: 19  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 250.  
Location/Qualifiers

FEATURES  
source

1..250  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_146O19"  
/sex="Male"  
/cell\_type="Blood"

## ORIGIN

/clone.lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

Query Match 72.2%; Score 13; DB 9; Length 250;  
Best Local Similarity 92.3%; Pred. No. 6.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## QY

6 CCUGAGNNNNNN 18  
||:|||||||  
83 CCTGAGNNNNNN 95

## Db

## RESULT 37

CG982763 266 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_164102.TJ CHORI-240 Bos taurus genomic clone CH240\_164102,  
DEFINITION genomic survey sequence.

## ACCESSION

CG982763.1 GI:39908542

## KEYWORDS

GSS.

## SOURCE

Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

## REFERENCE

1 (bases 1 to 266)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library

## TITLE

CHORI-240  
Unpublished (2003)

## JOURNAL

Other GSSs: CH240\_164102.TJ  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

## COMMENT

Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 164 row: I column: 02  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 266.  
Location/Qualifiers  
1..266  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_164102"  
/sex="Male"  
/cell\_type="Blood"  
/clone.lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## FEATURES

## source

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 266;  
Best Local Similarity 92.3%; Pred. No. 6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## QY

6 CCUGAGNNNNNN 18  
||:|||||||  
37 CCTGAGNNNNNN 25

## Db

## RESULT 38

CG983959 327 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_153005.TJ CHORI-240 Bos taurus genomic clone CH240\_153005,  
DEFINITION genomic survey sequence.

## ACCESSION

CG983959.1 GI:39909738

## KEYWORDS

GSS.

## SOURCE

Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

## REFERENCE

1 (bases 1 to 327)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library

## TITLE

CHORI-240  
Unpublished (2003)

## JOURNAL

Other GSSs: CH240\_153005.TJ  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

## COMMENT

Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 153 row: O column: 05  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 327.  
Location/Qualifiers  
1..327  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_153005"  
/sex="Male"  
/cell\_type="Blood"  
/clone.lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## FEATURES

## source

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 327;  
Best Local Similarity 92.3%; Pred. No. 5.9e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## QY

6 CCUGAGNNNNNN 18  
||:|||||||

Db 209 CCTGGAGNNNNNN 221

RESULT 39  
CC470613 332 bp DNA linear GSS 12-JUN-2003  
LOCUS CH240\_144J13.TJ CHORI-240 Bos taurus genomic clone CH240\_144J13,  
DEFINITION genomic survey sequence.  
ACCESSION CC470613  
VERSION CC470613.1 GI:31656845  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 332)  
AUTHORS Coستا,J.N., Mota,M. and Caetano,A.R.  
TITLE Brazil's Contribution to End-Sequencing the Bovine BAC library  
CHORI-240  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: CH240\_144J13.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372-70770-900 Brasilia  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred  
quality value equal to or higher than 20. Bases with quality value  
below 20 were masked with 'N'. For BAC library availability, please  
contact Pletier de Jong (pdejong@mail.cho.org). Clones may be  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBMC) by Embrapa Recursos Geneticos e Biotecnologia  
with financing from Conselho Nacional de Desenvolvimento Cientifico  
e Tecnol6gico (CNPq), Brazil.  
Plate: 144 row: J column: 13  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 332.  
Location/Qualifiers  
1..332  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_144J13"  
/sex="Male"  
/cell\_type="Blood"  
/note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pletier de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 332;  
Best Local Similarity 92.3%; Pred. No. 5.9e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
||:|||||||  
Db 144 CCTGGAGNNNNN 156

RESULT 40  
CL211616 377 bp mRNA linear GSS 30-JUN-2004  
LOCUS CL211616/c  
DEFINITION W173C04 GGTc Gene Trap Library GV04C04 Mus musculus cDNA clone

W173C04, mRNA sequence.  
CL211616  
CL211616.1 GI:40728517  
GSS.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 377)  
AUTHORS Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,  
Arnold,H.H., Schutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.  
A large-scale, gene-driven mutagenesis approach for the functional  
analysis of the mouse genome  
Proc Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
JOURNAL 22810117  
MEDLINE 12904583  
PUBMED 12904583  
COMMENT Contact: GGTC  
German Genetrap Consortium (GGTC)  
Email: info@genetrap.de  
Rosabeteago gene trap. Sequence tag generated by 5'RACE. Additional  
sequence information can be found at:  
'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=W173C04' ES cell line harboring insertion mutation of  
target gene is available at:  
'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'  
1' Inhouse Sequence Identifier: 10363  
Class: Gene Trap.  
Location/Qualifiers  
1..377  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Sv"  
/db\_xref="taxon:10090"  
/clone="W173C04"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/note="ES cells 129S2 (formerly 129/SvPas) "  
/clone\_lib="GGTC Gene Trap Library GV04C04"  
/note="Vector: ROSAbeteago"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 377;  
Best Local Similarity 92.3%; Pred. No. 5.9e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
||:|||||||  
Db 129 CCTGGAGNNNNN 117

RESULT 41  
CB774359 392 bp mRNA linear EST 16-MAY-2003  
LOCUS CB774359/c  
DEFINITION AMGNMNC:NRPI3-00052-D2-A W Rat pituitary (10477) Rattus norvegicus  
cDNA clone nrpl3-00052-d2 5', mRNA sequence.  
CB774359  
CB774359.1 GI:29862750  
EST.  
ACCESSION CB774359  
VERSION CB774359.1  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 392)  
AUTHORS Amgen EST Program.  
TITLE Amgen Rat EST Program  
JOURNAL Unpublished (2003)  
COMMENT Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00052 row: d column: 2.  
Location/Qualifiers

```

source
1. .392
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrp13-00052-d2"
/issue_type="pituitary"
/clone_lib="W Rat pituitary (10477)"
/notes="Vector: pSPORT1, Site_1: SalI, Site_2: NotI, W Rat
pituitary adult female Wistar rat avg insert size 2.1 kb"

ORIGIN

Query Match      72.2%; Score 13; DB 6; Length 392;
Best Local Similarity 92.3%; Pred. No. 5.9e+03;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY
6 CCUGAGANNNNN 18
||:|||||
60 CCTGAGANNNNN 48

RESULT 42
CG989457      393 bp   DNA      linear   GSS 15-DEC-2003
LOCUS      CH240_146P24.TV CHORI-240 Bos taurus genomic clone CH240_146P24,
DEFINITION      genomic survey sequence.
ACCESSION      CG989457
VERSION      CG989457.1 GI:39915236
KEYWORDS      GSS.
SOURCE      Bos taurus (cow)
ORGANISM      Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 393)
Costa,J.N., Mota,M. and Caetano,A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished (2003)
Other_GSSs: CH240_146P24.TV
Contact: Caetano AR
Department of Biotechnology
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Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acetano@cenargen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have phred quality value equal to or higher than 20.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 146 row: P column: 24
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 393.
Location/Qualifiers
1. .393
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_146P24"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"

JOURNAL
COMMENT
Other_GSSs: CH240_146P24.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acetano@cenargen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have phred quality value equal to or higher than 20.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 161 row: C column: 05
Seq primer: T7
Class: BAC ends
High quality sequence stop: 412.
Location/Qualifiers
1. .412
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_161C05"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pPARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match      72.2%; Score 13; DB 9; Length 412;
Best Local Similarity 92.3%; Pred. No. 5.9e+03;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY
6 CCUGAGANNNNN 18
||:|||||
12 CCTGAGANNNNN 24

RESULT 43
CG980948      412 bp   DNA      linear   GSS 15-DEC-2003
LOCUS      CH240_161C05.TV CHORI-240 Bos taurus genomic clone CH240_161C05,
DEFINITION      genomic survey sequence.
ACCESSION      CG980948
VERSION      CG980948.1 GI:39906727
KEYWORDS      GSS.
SOURCE      Bos taurus (cow)
ORGANISM      Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 412)
Costa,J.N., Mota,M. and Caetano,A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished (2003)
Other_GSSs: CH240_161C05.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
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02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acetano@cenargen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have phred quality value equal to or higher than 20.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 161 row: C column: 05
Seq primer: T7
Class: BAC ends
High quality sequence stop: 412.
Location/Qualifiers
1. .412
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_161C05"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pPARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

```

Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
Matches 12: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNN 18  
Db 402 CCTGGAGNNNNN 390

## RESULT 44

CG984052/c

LOCUS CH240\_153A12.TV CHORI-240 Bos taurus genomic clone CH240\_153A12,  
DEFINITION genomic survey sequence.

ACCESSION

CG984052

VERSION

CG984052.1

KEYWORDS

GSS.

SOURCE

Bos taurus (cow)

ORGANISM

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE

1 (bases 1 to 424)

AUTHORS

Coستا, J.N., Mota, M. and Caetano, A.R.

TITLE

Brazil's Contribution to End-Sequencing the Bovine BAC Library

CHORI-240

COMMENT

Unpublished (2003)

Other\_GSSs: CH240\_153A12.TV

Contact: Caetano AR

Department of Biotechnology

Embrapa Recursos Geneticos e Biotecnologia

Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.

02372 70770-900 Brasil

Tel: 55 61 448 4778

Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm).

Bases shown have phred quality value equal to or higher than 20.

Bases with quality value below 20 were masked with 'N'.

For BAC library availability, please contact Pieter de Jong

(pjejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering/information.htm).

This work was undertaken as part of the International Bovine BAC

Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e

Biotecnologia with financing from Conselho Nacional de

Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil

Plate: 153 row: A column: 12

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 424.

Location/Qualifiers

1. .424

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="bred: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_153A12"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: pTRABAC1.3; Site\_1: MboI; Site\_2: MboI;

Hereford bull LI Domino 99375; CHORI-240 Bovine BAC

library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 424;

Best Local Similarity 92.3%; Pred. No. 5.8e+03;

Matches 12: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNN 18  
Db 35 CCTGGAGNNNNN 23

## RESULT 45

CL604436

LOCUS

DEFINITION

CH240\_180K02.TV CHORI-240 Bos taurus genomic clone CH240\_180K02,

genomic survey sequence.

CL604436

VERSION

CL604436.1

KEYWORDS

GSS.

SOURCE

Bos taurus (cow)

ORGANISM

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE

1 (bases 1 to 424)

AUTHORS

Coستا, J.N., Mota, M. and Caetano, A.R.

TITLE

Brazil's Contribution to End-Sequencing the Bovine BAC Library

CHORI-240

COMMENT

Unpublished (2003)

Other\_GSSs: CH240\_180K02.TV

Contact: Caetano AR

Department of Biotechnology

Embrapa Recursos Geneticos e Biotecnologia

Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.

02372 70770-900 Brasil

Tel: 55 61 448 4778

Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm).

Bases shown have phred quality value equal to or higher than 20.

Bases with quality value below 20 were masked with 'N'.

For BAC library availability, please contact Pieter de Jong

(pjejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering/information.htm).

This work was undertaken as part of the International Bovine BAC

Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e

Biotecnologia with financing from Conselho Nacional de

Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil

Plate: 180 row: K column: 02

Seq primer: T7

Class: BAC ends

High quality sequence stop: 424.

Location/Qualifiers

1. .424

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="bred: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_180K02"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: pTRABAC1.3; Site\_1: MboI; Site\_2: MboI;

Hereford bull LI Domino 99375; CHORI-240 Bovine BAC

library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 424;

Best Local Similarity 92.3%; Pred. No. 5.8e+03;

Matches 12: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNN 18  
Db 384 CCTGGAGNNNNN 396

## RESULT 46

B2759976/c

LOCUS

DEFINITION

622\_314\_E10\_BAC\_081 RPT-86 Male Feline BAC Fells catus genomic,

431 bp DNA linear GSS 12-MAR-2003

genomic survey sequence.

ACCESSION BZ759976  
 VERSION BZ759976.1 GI:28929399  
 KEYWORDS GSS.  
 SOURCE Felis catus (cat)  
 ORGANISM Felis catus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 1 (bases 1 to 431)  
 Banerji,N., Lilienel,M., Li,X., Zhang,Q., Dwan,C., Retzel,E., Yukhi,N., O'Brien,S., Kapur,V. and Kanjilal,S.  
 Felis catus BAC-end sequencing project  
 Unpublished (2002)  
 Contact: Kanjilal, S.  
 Comparative Cancer Genomics  
 University of Minnesota  
 1971 Commonwealth Ave. St. Paul, MN 55108, USA  
 Tel: 612-624-3248  
 Fax: 612-625-5203  
 Email: kanjilal@umn.edu

FEATURES  
 source  
 Location/Qualifiers  
 1..431  
 /organism="Felis catus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9685"  
 /clone\_lib="RPCI-86 Male Feline BAC"  
 /note="Vector: PTARBAC2; Site\_1: EcoRI"

ORIGIN  
 Query Match 72.2%; Score 13; DB 8; Length 431;  
 Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
 ||:|||||||  
 Db 200 CCTGAGANNNNN 188

RESULT 47  
 BZ759980  
 LOCUS 433 bp DNA linear GSS 12-MAR-2003  
 DEFINITION 622 J14 F02 BAC 025 RPCI-86 Male Feline BAC Felis catus genomic.  
 ACCESSION BZ759980  
 VERSION BZ759980.1 GI:28929403  
 KEYWORDS GSS.  
 SOURCE Felis catus (cat)  
 ORGANISM Felis catus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 1 (bases 1 to 433)  
 Banerji,N., Lilienel,M., Li,X., Zhang,Q., Dwan,C., Retzel,E., Yukhi,N., O'Brien,S., Kapur,V. and Kanjilal,S.  
 Felis catus BAC-end sequencing project  
 Unpublished (2002)  
 Contact: Kanjilal, S.  
 Comparative Cancer Genomics

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 1971 Commonwealth Ave. St. Paul, MN 55108, USA  
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 Email: kanjilal@umn.edu

FEATURES  
 source  
 Location/Qualifiers  
 1..433  
 /organism="Felis catus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9685"  
 /clone\_lib="RPCI-86 Male Feline BAC"  
 /note="Vector: PTARBAC2; Site\_1: EcoRI"

ORIGIN  
 Query Match 72.2%; Score 13; DB 8; Length 433;  
 Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
 ||:|||||||  
 Db 243 CCTGAGANNNNN 255

RESULT 48  
 CL604951/c  
 LOCUS 466 bp DNA linear GSS 17-JUN-2004  
 DEFINITION CH240\_181A02\_TV CHORI-240 Bos taurus genomic clone CH240\_181A02.  
 ACCESSION CL604951  
 VERSION CL604951.1 GI:48872983  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 466)  
 Costa,J.N., Mota,M. and Caetano,A.R.  
 Brazil's Contribution to End-sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other\_GSSes: CH240\_181A02\_TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estraco Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasilia  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources



(http://www.chori.org/bacpac/ordering information.htm).

This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brazil

Plate: 181 row: A column: 02  
Seq primer: T7  
Class: BAC ends

High quality sequence stop: 466.  
Location/Qualifiers

1. 466

/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_181A02"  
/sex="Male"  
/cell\_type="Blood"

/clone\_1b="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

#### ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 466;  
Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCUGAGNNNNNN 18  
||:|||||||  
46 CCTGGAGNNNNNN 34

#### RESULT 49

BM492637 484 bp mRNA linear EST 07-MAY-2003  
LOCUS NXRV\_027\_F08\_F NXRV (Nef Xylem Root wood Vertical) Pinus taeda cDNA  
DEFINITION clone NXRV\_027\_F08 5', mRNA sequence.  
BM492637  
BM492637.1 GI:18613568

EST.  
Pinus taeda (loblolly pine)  
Pinus taeda

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
REFERENCE 1 (bases 1 to 484)

AUTHORS Sederoff, R.  
TITLE Molecular Basis of Wood Formation in the Pine Megagenome  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron\_sederoff@ncsu.edu, jerri\_johnson@ncsu.edu  
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further  
information.  
Seq primer: T3.

FEATURES  
source Location/Qualifiers

1. 484  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NXRV\_027\_F08"  
/issue\_type="Xylem"  
/cell\_type="Root (primary)"  
/dev\_stage="Transitional"  
/lab\_host="XL1-Blue"  
/clone\_1b="NXRV (Nef Xylem Root wood Vertical)"  
/note="Vector: pBluescript SK-, Site\_1: Eco RI; Site\_2:

#### ORIGIN

Query Match 72.2%; Score 13; DB 4; Length 484;  
Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCUGAGNNNNNN 18  
||:|||||||  
442 CCTGGAGNNNNNN 454

#### RESULT 50

CG982237 494 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_163C16.TV CHORI-240 Bos taurus genomic clone CH240\_163C16,  
DEFINITION genomic survey sequence.  
CG982237  
CG982237.1 GI:3908016

KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 494)  
Costa, J.N., Mota, M. and Caetano, A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240

JOURNAL Unpublished (2003)  
COMMENT Other GSSs: CH240\_163C16.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Genéticos e Biotecnologia  
Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

Email: acaetano@embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have Phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cno.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
Plate: 163 row: C column: 16  
Seq primer: T7  
Class: BAC ends

High quality sequence stop: 494.  
Location/Qualifiers

1. 494  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_163C16"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_1b="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 494;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||  
 Db 207 CCTGAGNNNNNN 195

RESULT 51  
 CC467322/c 497 bp DNA linear GSS 12-JUN-2003  
 LOCUS CH240\_137M17.TV CHORI-240 Bos taurus genomic clone CH240\_137M17,  
 DEFINITION genomic survey sequence.

ACCESSION CC467322  
 VERSION CC467322.1 GI:31653554  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 497)  
 AUTHOR Costa, J.N., Mota, M. and Caetano, A.R.  
 TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 JOURNAL CHORI-240  
 COMMENT Unpublished (2003)

Other\_GSSs: CH240\_137M17.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Parque Recusos Geneticos e Biotecnologia  
 Estrada Recusos Geneticos, Final Av. W/S Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasilia  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658

Email: acetao@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred  
 quality value equal to or higher than 20. Bases with quality value  
 below 20 were masked with 'N'. For BAC library availability, please  
 contact Pieter de Jong (pdejong@mail.cho.org). Clones may be  
 purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm). This work  
 was undertaken as part of the International Bovine BAC Mapping  
 Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia  
 with financing from Conselho Nacional de Desenvolvimento Cientifico  
 e Tecnol6gico (CNPq), Brazil.  
 Plate: 137 row: M column: 17  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 497.

FEATURES  
 source  
 location/Qualifiers  
 1..497

/organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="Breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_137M17"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 497;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18

Db 119 CCTGAGNNNNNN 107  
 ||:|||||

RESULT 52  
 A0597630/c 503 bp DNA linear GSS 08-JUN-1999  
 LOCUS HS\_2065\_B2\_H08\_MR\_CIT Approved Human Genomic Sperm Library D Homo  
 DEFINITION sapiens genomic clone Plate=2065 Col=16 Row=F, genomic survey  
 sequence.

ACCESSION A0597630  
 VERSION A0597630.1 GI:5028842  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 503)  
 AUTHOR Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
 Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 JOURNAL MEDLINE  
 PUBMED 99380589  
 CONTACT: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887

Email: jwallace@u.washington.edu  
 Clones may be purchased from Research Genetics (info@resgen.com).  
 BAC end Web Server: http://www.htcc.washington.edu  
 Plate: 2065 row: P column: 16  
 Seq primer: M13 Reverse  
 Class: BAC ends  
 High quality sequence stop: 503.

FEATURES  
 source  
 location/Qualifiers  
 1..503

/organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9605"  
 /clone="Plate=2065 Col=16 Row=P"  
 /sex="male"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in  
 E-Coli DH10B"

## ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 503;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||  
 Db 62 CCTGAGNNNNNN 50

RESULT 53  
 CG986681/c 504 bp DNA linear GSS 15-DEC-2003  
 LOCUS CH240\_157H05.TV CHORI-240 Bos taurus genomic clone CH240\_157H05,  
 DEFINITION genomic survey sequence.

ACCESSION CG986681  
 VERSION CG986681.1 GI:39912460  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 504)  
 AUTHORS Costa,J.N., Mota,M. and Caetano,A.R.  
 TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 JOURNAL CHORI-240  
 COMMENT Unpublished (2003)  
 Other GSSs: CH240\_157H05.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acaetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering\_information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 157 row: H column: 05  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 504.  
 Location/Qualifiers  
 1..504  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_157H05"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 504;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGANNNNN 18  
 ||:|||||||  
 Db 41 CCTGGAGNNNNN 29

RESULT 54  
 LOCUS CL608092 506 bp DNA linear GSS 17-JUN-2004  
 DEFINITION CH240\_174M24.TV CHORI-240 Bos taurus genomic clone CH240\_174M24,  
 genomic survey sequence.  
 ACCESSION CL608092  
 VERSION CL608092.1 GI:48876124  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 506)  
 Costa,J.N., Mota,M. and Caetano,A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other\_GSSs: CH240\_174M24.TV

Contact: Caetano AR  
 Department of Biotechnology  
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 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acaetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering\_information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 174 row: M column: 24  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 506.  
 Location/Qualifiers  
 1..506  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_174M24"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 506;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGANNNNN 18  
 ||:|||||||  
 Db 14 CCTGGAGNNNNN 26

RESULT 55  
 LOCUS CG983697 509 bp DNA linear GSS 15-DEC-2003  
 DEFINITION CH240\_165H06.TV CHORI-240 Bos taurus genomic clone CH240\_165H06,  
 genomic survey sequence.  
 ACCESSION CG983697  
 VERSION CG983697.1 GI:39909476  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 509)  
 Costa,J.N., Mota,M. and Caetano,A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other\_GSSs: CH240\_165H06.TV  
 Contact: Caetano AR  
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 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778

Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.cho.org](mailto:pdjong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 165 row: H column: 06  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 509.  
 Location/Qualifiers  
 1..509  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_165H06"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 509;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTGGAGNNNNNN 18  
 ||:|||||||  
 Db 432 CCTGGAGNNNNNN 444

RESULT 56  
 CL608426 526 bp DNA linear GSS 17-JUN-2004  
 LOCUS CH240\_175007.TJ CHORI-240 Bos taurus genomic clone CH240\_175007,  
 DEFINITION genomic survey sequence.  
 ACCESSION CL608426  
 VERSION CL608426.1 GI:48976458  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 526)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: CH240\_175007.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.

For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.cho.org](mailto:pdjong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 175 row: O column: 07  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 526.  
 Location/Qualifiers  
 1..526  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_175007"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 526;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTGGAGNNNNNN 18  
 ||:|||||||  
 Db 15 CCTGGAGNNNNNN 27

RESULT 57  
 CG986353 536 bp DNA linear GSS 15-DEC-2003  
 LOCUS CH240\_157E15.TV CHORI-240 Bos taurus genomic clone CH240\_157E15,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG986353  
 VERSION CG986353.1 GI:39912132  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 536)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: CH240\_157E15.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.cho.org](mailto:pdjong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e

Biotechnology with financing from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 157 Row: E Column: 15  
 Seq primer: T7  
 Class: BAC ends

High quality sequence stop: 536.

FEATURES  
 SOURCE  
 Location/Qualifiers

1. 536  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_157B15"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_id="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 536;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGGNNNNN 18  
 ||:|||||||  
 Db 533 CCTGGAGNNNNN 521

## RESULT 58

LOCUS CG985260 573 bp DNA linear GSS 15-DEC-2003  
 DEFINITION CH240\_155K17\_TV CHORI-240 Bos taurus genomic clone CH240\_155K17,  
 genomic survey sequence.  
 ACCESSION CG985260  
 VERSION CG985260.1 GI:39911039  
 KEYWORDS GSS.

SOURCE  
 ORGANISM Bos taurus (cow)

Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.

REFERENCE  
 AUTHORS Costa,J.N., Mota,M. and Caetano,A.R.  
 TITLE Brazil's Contribution to End-Sequencing the Bovine BAC library  
 JOURNAL CHORI-240

COMMENT  
 Unpublished (2003)  
 Other GSSes: CH240\_155K17\_TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acaetano@embrapa.br

Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.choi.org).

Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm).

This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 155 Row: K Column: 17  
 Seq primer: T7  
 Class: BAC ends

High quality sequence stop: 573.

FEATURES  
 SOURCE  
 Location/Qualifiers

1. 573  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_155K17"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_id="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 573;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGGNNNNN 18  
 ||:|||||||  
 Db 14 CCTGGAGNNNNN 26

## RESULT 59

LOCUS BG713519 593 bp mRNA linear EST 08-MAY-2001  
 DEFINITION pgl1n.pk007.024 Normalized Liver Library Gallus gallus cDNA clone  
 pgl1n.pk007.024 5' similar to p1r|S57631|S57631 translation  
 elongation factor eEF-1 delta-2 chain - African clawed frog  
 p1r|S55483 translation elongation factor eEF-1 delta chain (version  
 2) - African clawed frog emb|CA59420.1| (X85096) elongation  
 factor-1 delta [X, mRNA sequence.  
 BG713519  
 BG713519.1 GI:14007469  
 EST.

ACCESSION BG713519  
 VERSION BG713519.1 GI:14007469  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE  
 AUTHORS Burnside,J., Morgan,R.W. and Cogburn,L.A.  
 TITLE Chicken ESTs from a normalized liver library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Joan Burnside  
 Molecular Endocrinology  
 University of Delaware  
 40 Townsend Hall, Newark, DE 19717, USA  
 Tel: 302 831-1345  
 Fax: 302 831-3411  
 Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES  
 SOURCE  
 Location/Qualifiers

1. 593  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="pgl1n.pk007.024"  
 /sex="Male and Female"  
 /tissue\_type="liver"  
 /lab\_host="E.coli EMDH10B"  
 /clone\_id="Normalized Liver Library"  
 /note="Vector: pCMVSPORT 6"

## ORIGIN

Query Match 72.2%; Score 13; DB 4; Length 593;  
 Best Local Similarity 84.6%; Pred. No. 5.7e+03;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGGNNNNN 17  
 ||:|||||||  
 Db 485 TCCTGGAGNNNNN 497

RESULT 60  
CG989575  
LOCUS  
DEFINITION CH240\_147M19.TU CHORI-240 Bos taurus genomic clone CH240\_147M19,  
genomic survey sequence.  
CG989575  
ACCESSION  
VERSION CG989575.1 GI:39915354  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 601)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
JOURNAL  
COMMENT Unpublished (2003)  
Other GSSs: CH240\_147M19.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetanoc@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have Phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 147 row: M column: 19  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 601.  
Location/Qualifiers  
1..601  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_147M19"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pPARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 601;  
Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCTGGAGNNNNNN 18.  
DB 525 CCTGGAGNNNNNN 537

RESULT 61  
CG978763  
LOCUS  
DEFINITION CH240\_170G16.TU CHORI-240 Bos taurus genomic clone CH240\_170G16,  
genomic survey sequence.  
CG978763  
ACCESSION  
VERSION CG978763.1 GI:39915354  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 604)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
JOURNAL  
COMMENT Unpublished (2003)  
Other GSSs: CH240\_170G16.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetanoc@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have Phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 170 row: G column: 16  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 604.  
Location/Qualifiers  
1..604  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_170G16"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pPARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 604;  
Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCTGGAGNNNNNN 18  
DB 93 CCTGGAGNNNNNN 105

RESULT 62  
CG992853  
LOCUS  
DEFINITION CH240\_152H24.TU CHORI-240 Bos taurus genomic clone CH240\_152H24,  
genomic survey sequence.  
CG992853  
ACCESSION  
VERSION CG992853.1 GI:39918632  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ACCESSION CG978763  
VERSION CG978763.1 GI:39904542  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 604)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
JOURNAL  
COMMENT Unpublished (2003)  
Other GSSs: CH240\_170G16.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetanoc@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have Phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 170 row: G column: 16  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 604.  
Location/Qualifiers  
1..604  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_170G16"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pPARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 604;  
Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCTGGAGNNNNNN 18  
DB 93 CCTGGAGNNNNNN 105

RESULT 62  
CG992853  
LOCUS  
DEFINITION CH240\_152H24.TU CHORI-240 Bos taurus genomic clone CH240\_152H24,  
genomic survey sequence.  
CG992853  
ACCESSION  
VERSION CG992853.1 GI:39918632  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 606)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_152H24.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P. 02372, 70770-900 Brasilia  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pletier de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 152 row: H column: 24  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 606.

FEATURES  
source  
Location/Qualifiers  
1..606  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_152H24"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pletier de Jong"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 606;  
Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNN 18  
||:|||||||  
40 CCTGGAGNNNNN 52

Db 40 CCTGGAGNNNNN 52

RESULT 63  
CA754085/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

CA754085 614 bp mRNA linear EST 27-NOV-2002  
BR040010000 PLATE D07\_52\_060.ab1 OA Oryza sativa (japonica cultivar-group) cDNA clone BR040010000\_PLATE\_D07\_52\_060.ab1 similar to No protein alignment, mRNA sequence.  
CA754085 GI:25798188  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 614)  
Bohner,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,H., Kawasaki,S., McCallough,A., Michalowski,C.B.,

Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.  
Functional Genomics of Plant Stress Tolerance  
Unpublished (2000)  
Contact: Mark Fredricksen  
Department of Plant Biology  
University of Illinois  
1201 W. Gregory Dr., Urbana, IL 61801, USA  
Tel: 2172655473  
Email: bohnerlab@life.uiuc.edu.

FEATURES  
source  
Location/Qualifiers  
1..614  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiivar="Nipponbare"  
/db\_xref="taxon:39947"  
/clone="BR040010000\_PLATE\_D07\_52\_060.ab1"  
/tissue\_type="roots"  
/dev\_stage="3-4 weeks"  
/clone\_lib="OA"  
/note="19 h 200mM NaCl"

ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 614;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNN 18  
||:|||||||  
424 CCTGGAGNNNNN 412

Db 424 CCTGGAGNNNNN 412

RESULT 64  
CG985739  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CG985739 615 bp DNA linear GSS 15-DEC-2003  
CH240\_155N02.TV CHORI-240 Bos taurus genomic clone CH240\_155N02, genomic survey sequence.  
CG985739  
CG985739.1 GI:39911518  
GSS.  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 615)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_155N02.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P. 02372, 70770-900 Brasilia  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pletier de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 155 row: N column: 02  
Seq primer: T7  
Class: BAC ends

High quality sequence strop: 615.  
Location/Qualifiers  
1. 615  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_155N02"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI; Hereford bull l1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 615;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
||:|||||||  
45 CCTGAGANNNNN 57

Db 46 CCTGAGANNNNN 58

RESULT 65  
AY417454 618 bp DNA linear GSS 12-DEC-2003  
LOCUS AY417454  
DEFINITION Pan troglodytes HCM6229 gene, VIRUTAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY417454  
VERSION AY417454.1 GI:39773414  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE 1 (bases 1 to 618)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J., Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 618)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment.  
Location/Qualifiers  
1. 618  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1.>618  
/locus\_tag="HCM6229"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 618;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
||:|||||||  
45 CCTGAGANNNNN 57

Db 45 CCTGAGANNNNN 57

RESULT 66  
B2922485 619 bp DNA linear GSS 12-JUN-2003  
LOCUS B2922485  
DEFINITION CH240\_121E17.TV CHORI-240 Bos taurus genomic clone CH240\_121E17, genomic survey sequence.  
ACCESSION B2922485  
VERSION B2922485.1 GI:31647871  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 619)  
Larkin,D.M., Everts-van der Wind,A., Rebelz,M., Schweitzer,P., Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L., Womack,J.E., de Jong,P.J. and Lewin,H.A.  
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human Genome Sequence  
Unpublished (2003)  
Other GSSs: CH240\_121E17.TV  
Contact: Harris Lewin  
Department of Animal Sciences  
University of Illinois at Urbana Champaign  
1201 W. Gregory Dr., Urbana, IL 61801, USA  
Tel: 217 353 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@uiuc.edu).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by the University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CRRES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative)  
Plate: 121 row: E column: 17  
Seq primer: 17  
Class: BAC ends.  
Location/Qualifiers  
1. 619  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_121E17"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI; Hereford bull l1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 619;  
Best Local Similarity 84.6%; Pred. No. 5.6e+03;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNN 17  
||:|||||||  
Db 551 TCCTGAGANNNN 563

RESULT 67  
BH760082 625 bp DNA linear GSS 14-MAR-2002  
LOCUS BH760082/c  
DEFINITION Mt\_H2M02\_021J13 r McH2 Medicago truncatula BAC library Medicago  
truncatula genomic clone Mt\_H2M02\_021J13, genomic survey sequence.  
ACCESSION BH760082  
VERSION BH760082.1 GI:19425219



**KEYWORDS**  
**SOURCE** GSS.  
**ORGANISM** Medicago truncatula (barrel medic)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

**REFERENCE**  
 1 (bases 1 to 625)  
 Larsen, D., Mudge, J., Denny, R., Yan, H. and Young, N.D.  
 BAC end sequencing of Medicago truncatula (UMN)  
 Unpublished (2002)  
**AUTHORS** Department of Plant Pathology  
**TITLE** University of Minnesota  
**JOURNAL** 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA  
**COMMENT** Tel: 612 625 2225  
 Fax: 612 625 9728  
 Email: nevin@tc.umn.edu  
 For more information, see the Center for Computational Genomics and Bioinformatics biodata web site at:  
<http://web.ahc.umn.edu/biodata/medicagoYoung/>  
 Seq primer: M13R  
 Class: BAC ends

**FEATURES**  
 source  
 Location/Qualifiers  
 1..625  
 /organism="Medicago truncatula"  
 /mol\_type="genomic DNA"  
 /cultivar="genotype A17"  
 /db\_xref="taxon:3880"  
 /clone\_lib="Mc H2M02\_021J13"  
 /note="Vector: pBelobAC1; Site\_1: HindIII; Site\_2: HindIII; Cook et al, in preparation"

**ORIGIN**  
 Query Match 72.2%; Score 13; DB 8; Length 625;  
 Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**QY** 6 CCUGAGAGNNNNN 18  
 ||:|||||  
 Db 614 CCTGAGAGNNNNN 602

**RESULT 68**  
**LOCUS** CG976913 638 bp DNA linear GSS 15-DEC-2003  
**DEFINITION** CH240\_167A15.TV CHORI-240 Bos taurus genomic clone CH240\_167A15, genomic survey sequence.  
**ACCESSION** CG976913  
**VERSION** CG976913.1 GI:39902692  
**KEYWORDS** GSS.  
**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 638)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
**AUTHORS** Other\_GSSs: CH240\_167A15.TV  
**TITLE** Contact: Caetano AR  
**JOURNAL** Department of Biotechnology  
**COMMENT** Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P. 02372-70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).

Bases shown have Phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'. For BAC library availability, please contact Pieter de Jong ([pdejong@mail.cfo.org](mailto:pdejong@mail.cfo.org)). Clones may be purchased from BACPAC Resources ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnol6gico (CNPq), Brazil Plate: 167 row: A column: 15  
 Seg primer: T7  
 Class: BAC ends  
 High quality sequence stop: 638.

**FEATURES**  
 source  
 Location/Qualifiers  
 1..638  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_167A15"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull Lt Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

**ORIGIN**  
 Query Match 72.2%; Score 13; DB 9; Length 638;  
 Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**QY** 6 CCUGAGAGNNNNN 18  
 ||:|||||  
 Db 604 CCTGAGAGNNNNN 616

**RESULT 69**  
**LOCUS** CG978073 655 bp DNA linear GSS 15-DEC-2003  
**DEFINITION** CH240\_169C17.TV CHORI-240 Bos taurus genomic clone CH240\_169C17, genomic survey sequence.  
**ACCESSION** CG978073  
**VERSION** CG978073.1 GI:39903852  
**KEYWORDS** GSS.  
**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 655)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
**AUTHORS** Other\_GSSs: CH240\_169C17.TV  
**TITLE** Contact: Caetano AR  
**JOURNAL** Department of Biotechnology  
**COMMENT** Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P. 02372-70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>). Bases shown have Phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'. For BAC library availability, please contact Pieter de Jong ([pdejong@mail.cfo.org](mailto:pdejong@mail.cfo.org)). Clones may be purchased from BACPAC Resources ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).

This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by Embrapa Recursos Genéticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brazil

Seq primer: 17  
Class: BAC ends

High quality sequence stop: 655.

FEATURES  
source  
Location/Qualifiers

1..655

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="bred: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_169C17"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

# ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 655;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNN 18  
||:|||||||

Db 46 CCTGGAGNNNNN 58

RESULT 70  
AY111821/c 674 bp mRNA linear HTC 17-OCT-2002  
LOCUS  
DEFINITION  
Zea mays CL16119.1 mRNA sequence.  
ACCESSION  
AY111821  
VERSION  
AY111821.1 GI:21216411  
KEYWORDS  
HTC.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes  
Unpublished (2002)  
2 (bases 1 to 674)  
Coe, E.H.  
Direct Submission  
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT  
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES  
source  
Location/Qualifiers

1..674

/organism="Zea mays"

/mol\_type="mRNA"

/db\_xref="maizedb:630459"

/db\_xref="taxon:4577"

/clone\_lib="Maize Mapping Project/Dupont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was

assembled by Dupont as part of a collaboration for the Overgo addressing of BACs in conjunction with the Maize Mapping Project"

# ORIGIN

Query Match 72.2%; Score 13; DB 3; Length 674;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNN 18  
||:|||||||

Db 515 CCTGGAGNNNNN 503

RESULT 71  
B2912643/c 675 bp DNA linear GSS 12-JUN-2003  
LOCUS  
DEFINITION  
CH240\_111E20.T1 CHORI-240 Bos taurus genomic clone CH240\_111E20, genomic survey sequence.  
ACCESSION  
B2912643  
VERSION  
B2912643.1 GI:31638029  
KEYWORDS  
GSS.  
SOURCE  
Bos taurus (cow)  
Bos taurus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 679)  
Larkin, D.M., Evers-van der Wind, A., Rebelz, M., Schweitzer, P., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A.  
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human Genome Sequence  
Unpublished (2003)  
Other GSSs: CH240\_111E20.TV  
Contact: Harris Lewin  
Department of Animal Sciences  
University of Illinois at Urbana Champaign  
1201 W. Gregory Dr., Urbana, IL 61801, USA  
Tel: 217 333 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu  
Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong ([pejong@mail.cho.org](mailto:pejong@mail.cho.org)). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering/information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11028 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative)  
Plate: 111 row: E column: 20  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source  
Location/Qualifiers

1..679

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="bred: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_111E20"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

# ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 679;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNN 18  
 ||:|||||  
 DB 597 CCTGGAGNNNNN 585

RESULT 72  
 LOCUS BM251975/c  
 DEFINITION BMT010100013\_F04 Normalized Bovine Total Leukocyte cDNA Library (BOLT) Bos taurus cDNA 3', mRNA sequence.

ACCESSION BM251975  
 VERSION BM251975.1 GI:17887603  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE  
 AUTHORS Yao, J., Burton, J.L., Sipkovsky, S. and Coussens, P.M.  
 TITLE Generation of EST and cDNA microarray resources for the study of bovine immunobiology  
 JOURNAL Acta Vet. Scand. 42 (3), 391-406 (2001)  
 MEDLINE 21885187  
 PUBMED 11887399

COMMENT  
 Contact: Jianbo Yao  
 Division of Animal and Veterinary Sciences  
 West Virginia University  
 Morgantown, WV 26506-6108, USA  
 Tel: 303-293-2631  
 Fax: 304-293-2322  
 Email: jianbo.yao@mail.wvu.edu  
 Seq primer: M13 Reverse  
 Location/Qualifiers  
 1..684  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /sex="female"  
 /tissue\_type="Blood"  
 /cell\_type="peripheral blood leukocytes"  
 /dev\_stage="mid-lactation"  
 /lab\_host="DH10B"  
 /clone\_lib="Normalized Bovine Total Leukocyte cDNA Library (BOLT)"  
 /note="vector: pSPORT1; Site\_1: NotI; Site\_2: SalI"

ORIGIN  
 Query Match 72.2%; Score 13; DB 4; Length 684;  
 Best Local Similarity 84.6%; Pred. No. 5.6e+03;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAGN 13  
 ||:|||||  
 DB 609 GGGGTCTGGAGN 597

RESULT 73  
 LOCUS CG992790  
 DEFINITION CH240\_152H03\_TV CHORI-240 Bos taurus genomic clone CH240\_152H03, genomic survey sequence.

ACCESSION CG992790  
 VERSION CG992790.1 GI:39918569  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE  
 AUTHORS 1 (bases 1 to 701)  
 Costa, J.N., Mota, M. and Caetano, A.R.

TITLE  
 CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other\_GSSs: CH240\_152H03.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estraco Biologica, Final Av. W/S Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have Phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pjejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering\_information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 152 row: H column: 03  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 701.  
 Location/Qualifiers  
 1..701  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="Breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_152H03"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="vector: pTARAPAC1.3; Site\_1: MboI; Site\_2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN  
 Query Match 72.2%; Score 13; DB 9; Length 701;  
 Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNN 18  
 ||:|||||  
 DB 675 CCTGGAGNNNNN 687

RESULT 74  
 LOCUS CN035898/c  
 DEFINITION nm\_11\_g12\_t3\_Mach Ambystoma mexicanum cDNA, mRNA sequence.

ACCESSION CN035898  
 VERSION CN035898.1 GI:45806269  
 KEYWORDS EST.  
 SOURCE Ambystoma mexicanum (axolotl)  
 ORGANISM Ambystoma mexicanum  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandridae; Ambystomatidae; Ambystoma.

REFERENCE  
 1 (bases 1 to 716)  
 Putta, S., Smith, J.J., Walker, J.A., Rondet, M., Weisrock, D.,  
 Monaghan, J., Samuels, A.K., Kump, K., King, D.C., Maness, N.J.,  
 Haberman, B., Tanaka, E., Bryant, S.V., Gardiner, D.M., Parichy, D.M.  
 and Voss, S.R.  
 From biomedicine to natural history research: EST resources for  
 ambystomid salamanders  
 BMC Genomics 5 (1), 54 (2004)  
 Contact: SR Voss

TITLE  
 JOURNAL  
 COMMENT

Department of Biology  
University of Kentucky  
TH Morgan Building, Lexington, KY 40506, USA  
Tel: 859 257 9888  
Fax: 859 257 1717  
Email: syros@uky.edu  
The EST is quality trimmed at the ends with a 20 base window and  
quality threshold of 15 (phred quality score). Please visit  
http://salamander.uky.edu for any information (trace, quality files  
etc) regarding this EST.

## FEATURES

source

Location/Qualifiers  
1..716  
/organism="Ambystoma mexicanum"  
/mol\_type="mRNA"  
/db\_xref="taxon:8296"  
/tissue\_type="Limb Blastema and Proximal Limb Tissue  
collected from larvae on days 1-6 of regeneration"  
/clone\_lib="Match"

## ORIGIN

Query Match 72.2%; Score 13; DB 7; Length 716;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
|||  
695 CCTGAGNNNNNN 683

RESULT 75 756 bp mRNA linear EST 29-NOV-2002  
BU438636 604145436P1 CSEQRBN11 Gallus gallus CDNA clone CHEST984h9 5', mRNA  
LOCUS  
DEFINITION  
SEQUENCE  
ACCESSION BU438636  
VERSION BU438636.1 GI:25927947  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 756)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
22335534  
12445392

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

Location/Qualifiers  
1..756  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST984h9"  
/sex="Male and female"  
/tissue\_type="muscle"  
/dev stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQRBN11"  
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;  
Site 2: NotI; This normalized library was constructed from  
1 million independent clones. cDNA synthesis was initiated  
using an oligo(dt) primer, using methylated C in the first

strand synthesis reaction. Following this first strand  
reaction, double-stranded cDNA was blunt-ended, ligated to  
NotI adapters, digested with EcoRI, size-selected, and  
cloned into the NotI and EcoRI compatible sites of a  
custom modified MCS of the pBluescript (KS+) vector. The  
library was normalized in 2 rounds using conditions  
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and  
Bonaldo et al., Genome Research 6 (1996): 791, except that  
a significantly longer reannealing hybridization was  
used."

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 756;  
Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
|||  
474 CCTGAGNNNNNN 486

RESULT 76 758 bp DNA linear GSS 16-JUL-1999  
AQ745042 HS\_3506\_A1 B06 SP6 RPCT-11 Human Male BAC Library Homo sapiens  
LOCUS genomic clone Plate=1082 Col=11 Row=C, genomic survey sequence.  
DEFINITION  
ACCESSION AQ745042  
VERSION AQ745042.1 GI:5522487  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 758)  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holman, T.,  
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
Hood, L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
MEDLINE  
JOURNAL  
TITLE  
AUTHORS  
REFERENCE  
COMMENT  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCT-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
or from Research Genetics (info@resgen.com). BAC end Web Server:  
http://www.htsc.washington.edu  
Plate: 1082 row: C column: 11  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 758.

## FEATURES

source

Location/Qualifiers  
1..758  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=1082 Col=11 Row=C"  
/sex="male"  
/clone\_lib="RPCT-11 Human Male BAC Library"  
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBAC3.6 vector at EcoRI sites"

## ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 758;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
 ||:|||||  
 Db 640 CCTGAGAGNNNNNN 652

RESULT 77  
 LOCUS CN042530  
 DEFINITION vtl\_p42\_o19\_c3\_010\_ab1 Match Ambystoma mexicanum cDNA, mRNA  
 ACCESSION CN042530  
 VERSION CN042530.1 GI:45812901  
 KEYWORDS EST.  
 SOURCE Ambystoma mexicanum (axolotl)  
 ORGANISM Ambystoma mexicanum  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Caudata; Salamandridae; Ambystomatidae;  
 Ambystoma.  
 1 (bases 1 to 783)  
 Putta, S., Smith, J.J., Walker, J.A., Rondet, M., Weisrock, D.,  
 Monaghan, J., Samuels, A.K., Kump, K., King, D.C., Maness, N.J.,  
 Habermann, B., Tanaka, E., Bryant, S.V., Gardiner, D.M., Patchy, D.M.  
 and Voss, S.R.  
 From biomedicine to natural history research: EST resources for  
 ambystomatid salamanders  
 BMC Genomics 5 (1), 54 (2004)  
 Contact: SR Voss  
 Department of Biology  
 University of Kentucky  
 TR Morgan Building, Lexington, KY 40506, USA  
 Tel: 859 257 9888  
 Fax: 859 257 1717  
 Email: svoss@uky.edu  
 The EST is quality trimmed at the ends with a 20 base window and  
 quality threshold of 15 (phred quality score). Please visit  
 http://salamander.uky.edu for any information (trace, quality files  
 etc) regarding this EST.  
 Location/Qualifiers  
 1..783  
 /organism="Ambystoma mexicanum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8296"  
 /tissue\_type="Limb Blastema and Proximal Limb Tissue"  
 collected from larvae on days 1-6 of regeneration"  
 /clone\_lib="Match"

ORIGIN  
 Query Match 72.2%; Score 13; DB 7; Length 783;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
 ||:|||||  
 Db 3 CCTGAGAGNNNNNN 15

RESULT 78  
 LOCUS AY111174  
 DEFINITION Zee may5 CL27726\_1 mRNA sequence.  
 ACCESSION AY111174  
 VERSION AY111174.1 GI:21215764  
 KEYWORDS HTC.  
 SOURCE Zee may5  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 802)  
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,  
 Arthur, L.M., Hanafe, M., Morgante, M. and Tingey, S.V.  
 TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of  
 Overgo Probes  
 JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 802)  
 AUTHORS Coe, E.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
 maize cDNA sequences is either Virginia Malbec, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
 www.zmdb.iastate.edu.  
 Location/Qualifiers  
 1..802  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="MaizeDB:631151"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/Dupont Consensus  
 Library"  
 /note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 contigs to seed Dupont contigs; this resource was  
 assembled by Dupont as part of a collaboration for the  
 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project"

ORIGIN  
 Query Match 72.2%; Score 13; DB 3; Length 802;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
 ||:|||||  
 Db 565 CCTGAGAGNNNNNN 577

RESULT 79  
 LOCUS AY405397  
 DEFINITION Pan troglodytes HCM2210 gene, VIRTUAL TRANSCRIPT, partial sequence.  
 ACCESSION AY405397  
 VERSION AY405397.1 GI:39761371  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 1 (bases 1 to 825)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 825)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission.  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering

FEATURES chem based on alignment.  
 Location/Qualifiers  
 source 1..825  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 <1..>825  
 /locus\_tag="HCM2210"

Query Match 72.2%; Score 13; DB 9; Length 825;  
 Best Local Similarity 84.6%; Pred. No. 5.5e+03;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUCUGAGANN 15  
 ||:|||||  
 Db 506 GGTCCTGGAGANN 518

RESULT 80  
 BQ948660 845 bp mRNA linear EST 21-AUG-2002  
 LOCUS AGENCOURT\_8784237 NIH\_MGC\_43 Homo sapiens CDNA clone IMAGE:6376418  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BQ948660  
 VERSION BQ948660.1 GI:22364138  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 845)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: L1CM2558 row: j column: 03  
 High quality sequence stop: 534.  
 Location/Qualifiers  
 1..845  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6376418"  
 /tissue\_type="normal pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_43"  
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; CDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-CDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library. |"

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 845;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
 ||:|||||  
 Db 725 CCTGGAGANNNNN 713

RESULT 81  
 CC921276/c 858 bp DNA linear GSS 08-AUG-2003  
 LOCUS t047002ba.f1 TAMBT Bos taurus genomic clone t047002ba, genomic  
 DEFINITION survey sequence.  
 ACCESSION CC921276  
 VERSION CC921276.1 GI:33554634  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 858)  
 Lin.S., Najjar, F.Z., Adelson, D., Gill, C.A. and Roe, B.A.  
 Bovine BAC End Sequences from Library TAMBT  
 Unpublished (2003)  
 Contact: Bruce A. Roe  
 Advanced Center for Genome Technology  
 University of Oklahoma Department of Chemistry and Biochemistry  
 620 Parrington Oval, Room 208, Norman, OK 73019, USA  
 Tel: 405 325 4912  
 Fax: 405 325 7762  
 Email: broeou.edu  
 Class: BAC ends  
 High quality sequence start: 119  
 High quality sequence stop: 441.  
 Location/Qualifiers  
 1..858  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="Angus bull T A M U Shoshone Y6 11519666"  
 /db\_xref="taxon:9913"  
 /clone="t047002ba"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="TAMBT"  
 /note="Vector: pBelBAC11; Site 1: HindIII; Site 2:  
 HindIII; TAMBT Bovine BAC library (Male) produced by Texas  
 A&M University, Department of Animal Science."

## FEATURES

source  
 Location/Qualifiers  
 1..858

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 858;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
 ||:|||||  
 Db 104 CCTGGAGANNNNN 92

RESULT 82  
 BU957217/c 873 bp mRNA linear EST 21-OCT-2002  
 LOCUS AGENCOURT\_10621575 NIH\_MGC\_107 Homo sapiens CDNA clone  
 DEFINITION IMAGE:6731210 5', mRNA sequence.  
 ACCESSION BU957217  
 VERSION BU957217.1 GI:24186789  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 873)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Query Match 72.2%; Score 13; DB 5; Length 845;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM3057 row: e column: 01  
 High quality sequence stop: 695.

## FEATURES

## SOURCE

1. 873  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6731210"  
 /issue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_107"  
 /note="Organ: breast; Vector: pOTB7; Site: 1: EcoRI;  
 Site 2: XhoI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 873;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 766 CCTGAGNNNNNN 754

RESULT 83  
 BUI96728/c  
 LOCUS BUI96728 895 bp mRNA linear EST 04-SEP-2002  
 DEFINITION AGNCOURT\_7974315 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6082172  
 5', mRNA sequence.  
 ACCESSION BUI96728  
 VERSION BUI96728.1 GI:22710712  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 895)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM2310 row: e column: 21  
 High quality sequence stop: 655.

## FEATURES

## SOURCE

1. 895  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6082172"  
 /issue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 895;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 840 CCTGAGNNNNNN 828

RESULT 84  
 AY110949  
 LOCUS AY110949 903 bp mRNA linear HTC 17-OCT-2002  
 DEFINITION Zea mays CL12681\_1 mRNA sequence.  
 ACCESSION AY110949  
 VERSION AY110949.1 GI:21215539  
 KEYWORDS HTC.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 903)  
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitstitt, M.S.,  
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
 Maize Mapping Project/Dupont Consensus Sequences for Design of  
 Overgo Probes  
 Unpublished (2002)  
 TITLE 2 (bases 1 to 903)  
 REFERENCE Coe, E.H.  
 DIRECT SUBMISSION  
 Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSL, [maizemap.org](http://maizemap.org); ZmDB, [www.zmdb.iastate.edu](http://www.zmdb.iastate.edu); TIGR,  
[www.tigr.org](http://www.tigr.org); or NCBI, [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
[www.zmdb.iastate.edu](http://www.zmdb.iastate.edu).

## FEATURES

## SOURCE

1. 903  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/Dupont Consensus  
 Library"  
 /note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 contigs to seed Dupont contigs; this resource was  
 assembled by Dupont as part of a collaboration for the  
 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project"

## ORIGIN

Query Match 72.2%; Score 13; DB 3; Length 903;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 514 CCTGAGNNNNNN 526

RESULT 85  
 AY110206/c

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LOCUS       AY110206               928 bp      mRNA      linear      HTC 17-OCT-2002
DEFINITION   Zea mays Cl25252_1 mRNA sequence.
ACCESSION    AY110206
VERSION      AY110206.1   GI:21214366
KEYWORDS     HTC.
SOURCE       Zea mays
ORGANISM     Zea mays
REFERENCE    1 (bases 1 to 928)
AUTHORS      Hailey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
              Arthur, L.W., Hanfey, M., Morgante, M. and Tingey, S.V.
TITLE        Maize Mapping Project/Dupont Consensus Sequences for Design of
              Overgo Probes
JOURNAL      Unpublished (2002)
REFERENCE    2 (bases 1 to 928)
AUTHORS      Coe, E.H.
TITLE        Direct Submission
JOURNAL      Submitted (25-APR-2002) Maize Mapping Project, University of
              Missouri, Columbia, MO 65211, USA
COMMENT      If you are interested in getting corresponding physical clones,
              these are publicly available from ZmDB and may be found by BLAST
              searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
              www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
              maize cDNA sequences is either Virginia Walbot, Stanford or Pat
              Schnable, Iowa State, then clones may be requested from ZmDB:
              www.zmdb.iastate.edu.

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     library"
     /note="this sequence is part of a project of EST
     assemblies resulting from the application of public
     configs to seed Dupont configs; this resource was
     assembled by Dupont as part of a collaboration for the
     overgo addressing of BACs in conjunction with the Maize
     Mapping Project"

ORIGIN
Query Match      72.2%; Score 13; DB 3; Length 928;
Best Local Similarity 92.3%; Pred. No. 5.5e+03;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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       library"
       /note="this sequence is part of a project of EST
       assemblies resulting from the application of public
       configs to seed Dupont configs; this resource was
       assembled by Dupont as part of a collaboration for the
       overgo addressing of BACs in conjunction with the Maize
       Mapping Project"

Db      312 CCTGAGANNNNNN 300

RESULT 86
LOCUS       BO927240               990 bp      mRNA      linear      EST 20-AUG-2002
DEFINITION   AGENCOURT 8774505 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6370157
ACCESSION    BO927240
VERSION      BO927240.1   GI:22342271
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 990)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Tissue Procurement: DCTD/DRP/Gazdar
              cDNA Library Preparation: Rubin Laboratory

FEATURES             source
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     1..1000
     /organism="Homo sapiens"
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     /db_xref="taxon:9606"
     /clone_lib="IMAGE:6651052"
     /tissue_type="adenocarcinoma, cell line"
     /lab_host="DH10B (phage-resistant)"
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     /note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2542 row: e column: 06
High quality sequence start: 42
High quality sequence stop: 744.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match      72.2%; Score 13; DB 5; Length 990;
Best Local Similarity 92.3%; Pred. No. 5.4e+03;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCUGAGANNNNNN 18
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       /clone_lib="IMAGE:6651052"
       /tissue_type="adenocarcinoma, cell line"
       /lab_host="DH10B (phage-resistant)"
       /clone_lib="NIH_MGC_107"
       /note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;

RESULT 87
LOCUS       BU860039               1000 bp      mRNA      linear      EST 16-OCT-2002
DEFINITION   AGENCOURT 10435318 NIH_MGC_107 Homo sapiens cDNA clone
ACCESSION    BU860039
VERSION      BU860039.1   GI:24045031
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 1000)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Plate: LNCM2697 row: e column: 04
              High quality sequence stop: 751.
              Location/Qualifiers
              1..1000
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
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              /tissue_type="adenocarcinoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_107"
              /note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;

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gene trios  
Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302

REFERENCE 2 (bases 1 to 1170)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..1170  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>1170  
/gene="SLC14A1"  
/locus\_tag="HCM3931"

ORIGIN  
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Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||||  
657 CCTGAGNNNNNN 669

RESULT 91  
LOCUS AY410560 1170 bp DNA linear GSS 16-DEC-2003  
DEFINITION Pan troglodytes SLC14A1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY410560  
VERSION AY410560.1 GI:39766528  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 1170)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
REFERENCE 14671302  
2 (bases 1 to 1170)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..1170  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
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/gene="SLC14A1"  
/locus\_tag="HCM3931"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 1170;  
Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||||  
Db 657 CCTGAGNNNNNN 669

RESULT 92  
LOCUS AY410561 1170 bp DNA linear GSS 16-DEC-2003  
DEFINITION Mus musculus SLC14A1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY410561  
VERSION AY410561.1 GI:39766529  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1170)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
REFERENCE 14671302  
2 (bases 1 to 1170)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..1170  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
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/locus\_tag="HCM3931"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 1170;  
Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||||  
Db 657 CCTGAGNNNNNN 669

RESULT 93  
LOCUS AY409438 1247 bp DNA linear GSS 12-DEC-2003  
DEFINITION Pan troglodytes HCM3557 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY409438  
VERSION AY409438.1 GI:39765406  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 1247)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Infering nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL  
Science 302 (5652), 1960-1963 (2003)

REFERENCE  
PUBMED  
14671302

AUTHORS  
2 (bases 1 to 1247)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Direct Submission

JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
Source  
Location/Qualifiers  
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/locus\_tag="HCM3557"

ORIGIN  
gene

Query Match 72.2%; Score 13; DB 9; Length 1247;  
Best Local Similarity 92.3%; Pred. No. 5.3e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||||  
Db 667 CCTGGAGNNNNNN 655

RESULT 94  
AY409437/c 1271 bp DNA linear GSS 12-DEC-2003

LOCUS  
Homo sapiens HCM3557 gene, VIRTUAL TRANSCRIPT, partial sequence,  
Genomic survey sequence.

ACCESSION  
AY409437

VERSION  
AY409437.1 GI:39765405

KEYWORDS  
GSS.

ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1271)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Infering nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL  
Science 302 (5652), 1960-1963 (2003)

REFERENCE  
PUBMED  
14671302

AUTHORS  
2 (bases 1 to 1271)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Direct Submission

JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
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Location/Qualifiers  
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Best Local Similarity 92.3%; Pred. No. 5.3e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||||  
Db 667 CCTGGAGNNNNNN 655

RESULT 95  
AY421522 1613 bp DNA linear GSS 17-DEC-2003

LOCUS  
Pan troglodytes EYA2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION  
AY421522

VERSION  
AY421522.1 GI:39748381

KEYWORDS  
GSS.

ORGANISM  
Pan troglodytes (chimpanzee)

REFERENCE  
AUTHORS  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 1613)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Infering nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL  
Science 302 (5652), 1960-1963 (2003)

REFERENCE  
PUBMED  
14671302

AUTHORS  
2 (bases 1 to 1613)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Direct Submission

JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
Source  
Location/Qualifiers  
1..1613  
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/locus\_tag="HCM7585"

ORIGIN  
gene

Query Match 72.2%; Score 13; DB 9; Length 1613;  
Best Local Similarity 92.3%; Pred. No. 5.2e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||||  
Db 968 CCTGGAGNNNNNN 980

RESULT 96  
AY409605 1920 bp DNA linear GSS 16-DEC-2003

LOCUS  
Homo sapiens EYA4 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION  
AY409605

VERSION  
AY409605.1 GI:39765573

KEYWORDS  
GSS.

ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1920)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
FERRIERA,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
2 (bases 1 to 1920)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment  
FEATURES  
source  
1..1920  
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ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 1920;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGAGNNNNN 18  
||:|||||  
Db 1101 CCTGAGAGNNNNN 1113

RESULT 97  
AY409606 1920 bp DNA linear GSS 16-DEC-2003  
LOCUS  
DEFINITION  
Pan troglodytes EYA4 gene, VIRUTAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION  
AY409606  
VERSION  
AY409606.1 GI:39765574  
KEYWORDS  
GSS.  
SOURCE  
Pan troglodytes (chimpanzee)  
ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 1920)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
2 (bases 1 to 1920)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment  
FEATURES  
source  
1..1920  
/organism="Pan troglodytes"  
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/db\_xref="taxon:9598"  
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ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 1920;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGAGNNNNN 18  
||:|||||  
Db 1101 CCTGAGAGNNNNN 1113

RESULT 98  
AY402163/c 2001 bp DNA linear GSS 15-DEC-2003  
LOCUS  
DEFINITION  
Pan troglodytes FZD3 gene, VIRUTAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION  
AY402163  
VERSION  
AY402163.1 GI:39758149  
KEYWORDS  
GSS.  
SOURCE  
Pan troglodytes (chimpanzee)  
ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 2001)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
2 (bases 1 to 2001)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment  
FEATURES  
source  
1..2001  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>2001  
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Best Local Similarity 84.6%; Pred. No. 5.1e+03;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGAGNNNN 17  
||:|||||  
Db 1586 TCCTGAGAGNNNN 1574

RESULT 99  
AY405709 2036 bp DNA linear GSS 15-DEC-2003  
LOCUS  
DEFINITION  
Pan troglodytes CYLN2 gene, VIRUTAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION  
AY405709  
VERSION  
AY405709.1 GI:39761683  
KEYWORDS  
GSS.  
SOURCE  
Pan troglodytes (chimpanzee)  
ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 2036)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2036)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source Location/Qualifiers  
1..2036  
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/db\_xref="taxon:9598"  
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ORIGIN  
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Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
Db 694 CCTGGAGNNNNNN 706

RESULT 100  
AY417388  
LOCUS 2073 bp DNA linear GSS 17-DEC-2003  
DEFINITION Pan troglodytes TGM3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417388  
VERSION AY417388.1 GI:39773348  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE 1 (bases 1 to 2073)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2073)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source Location/Qualifiers  
1..2073  
/organism="Pan troglodytes"

/mol\_type="genomic DNA"  
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<1..>2073  
/gene="TGM3"  
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ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 2073;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
Db 1787 CCTGGAGNNNNNN 1797

RESULT 101  
AY417387  
LOCUS 2075 bp DNA linear GSS 17-DEC-2003  
DEFINITION Homo sapiens TGM3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417387  
VERSION AY417387.1 GI:39773347  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2075)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2075)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source Location/Qualifiers  
1..2075  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>2075  
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/locus\_tag="HCM6207"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 2075;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
Db 1787 CCTGGAGNNNNNN 1797

RESULT 102  
AY417389  
LOCUS 2075 bp DNA linear GSS 17-DEC-2003  
DEFINITION Mus musculus TGM3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417389  
VERSION AY417389.1 GI:39773349

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 2075)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 2075)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source  
1..2075  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1..>2075  
/gene="TFM3"  
/locus\_tag="HCM6207"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 2075;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
||:|||||  
11:|||||  
Db 1787 CCTGAGNNNNNN 1799

RESULT 103  
AY413512/c  
LOCUS 2257 bp DNA linear GSS 17-DEC-2003  
DEFINITION Pan troglodytes RFX1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY413512  
VERSION AY413512.1 GI:39769474  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE 1 (bases 1 to 2257)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 2257)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering

them based on alignment.  
FEATURES  
source  
1..2257  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
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/locus\_tag="HCM4915"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 2257;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
||:|||||  
11:|||||  
Db 180 CCTGAGNNNNNN 192

RESULT 104  
AY410786  
LOCUS 2772 bp DNA linear GSS 12-DEC-2003  
DEFINITION Mus musculus HCM4006 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY410786  
VERSION AY410786.1 GI:3976754  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 2772)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 2772)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source  
1..2772  
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ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 2772;  
Best Local Similarity 92.3%; Pred. No. 5e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
||:|||||  
11:|||||  
Db 180 CCTGAGNNNNNN 192

RESULT 105  
AY405708  
LOCUS 3129 bp DNA linear GSS 15-DEC-2003  
DEFINITION Homo sapiens CYLN2 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION AY405708  
 VERSION AY405708.1 GI:39761682  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3129)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

TITLE  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 3129)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Direct Submision  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
 Location/Qualifiers  
 1..3129  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
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ORIGIN  
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 Best Local Similarity 92.3%; Pred. No. 4.9e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 1374 CCTGAGNNNNNN 1386

RESULT 106  
 AY420125 3878 bp DNA linear GSS 17-DEC-2003  
 LOCUS Mus musculus LAMC1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 AY420125  
 VERSION AY420125.1 GI:39776082  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 3878)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

TITLE  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 3878)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
 Location/Qualifiers  
 1..3878  
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ORIGIN  
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 Best Local Similarity 92.3%; Pred. No. 4.8e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 2891 CCTGAGNNNNNN 2903

RESULT 107  
 CG918361 69 bp DNA linear GSS 12-DEC-2003  
 LOCUS CH240\_143P18.TV CHORI-240 Bos taurus genomic clone CH240\_143P18,  
 CG918361  
 DEFINITION genomic survey sequence.  
 ACCESSION CG918361  
 VERSION CG918361.1 GI:39778044  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 69)  
 Costa,J.N., Mota,M. and Caetano,A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GS86: CH240\_143P18.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetanoc@embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 143 row: P column: 18  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 69.

FEATURES  
 Location/Qualifiers  
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 /strain="Bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_143P18"

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/sex="Male"
/cell_type="Blood"
/clone_id="CHORI-240"
/note="Vector: PTARBA1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match      66.7%; Score 12; DB 9; Length 69;
Best Local Similarity 91.7%; Pred. No. 2.4e+04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY
7 CUGGAGNNNNNN 18
11:|||||
15 CTGAGNNNNNN 26

RESULT 108
AF219075      73 bp  DNA      linear  GSS 17-APR-2000
LOCUS         AF219075 Human Homo sapiens genomic clone Nf1, genomic survey
DEFINITION    AF219075 Human Homo sapiens genomic clone Nf1, genomic survey
ACCESSION     AF219075.1 GI:7581521
KEYWORDS      GSS.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 73)
AUTHORS       Hamshire, M., Cross, S., Daniels, M., Lennon, G. and Brook, J.D.
TITLE         A transcript map of a 10-Mb region of chromosome 19: A source of
              genes for human disorders, including candidates for genes involved
              in asthma, heart defects, and eye disorders
JOURNAL       Genomics 63 (3), 425-429 (2000)
MEDLINE       20171383
PUBMED        10704290
COMMENT        Contact: Hamshire M
              Institute of Genetics
              University of Nottingham
              Queen's Medical Center, Nottingham, NG7 2LT, United Kingdom
              Class: exon-trapped.
              Location/Qualifiers
                1..73
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Nf1"
                /clone_id="Human"

ORIGIN
Query Match      66.7%; Score 12; DB 8; Length 73;
Best Local Similarity 83.3%; Pred. No. 2.4e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 GGGGUCCTCGAG 12
|||||
20 GGGGCTCTCGAG 31

RESULT 109
AA929340      94 bp  mRNA      linear  EST 23-APR-1998
LOCUS         AA929340 r1 Soares_thymus_2NDMT Mus musculus cDNA clone
DEFINITION    IMAGE:1329018 5' similar to TR.035449 O35449 HYPOTHETICAL 31.4 KD
              PROTEIN.; mRNA sequence.
ACCESSION     AA929340
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

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REFERENCE
AUTHORS      1 (bases 1 to 94)
              Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
              Getsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
              Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
              Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
              Waterston, R.
TITLE         The WashU-HMT Mouse EST Project
JOURNAL       Unpublished (1996)
COMMENT        Contact: Marra M/Mouse EST Project
              WashU-HMT Mouse EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watson.wustl.edu
              This clone is available royalty-free through LML; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:688562
              Possible reversed clone: similarity on wrong strand
              Seq primer: -28ml3 rev2 ET from Amersham
              High quality sequence stop: 78.
              Location/Qualifiers
                1..94
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:1329018"
                /sex="male"
                /tissue_type="thymus"
                /dev_stage="4 weeks"
                /lab_host="DH10B"
                /clone_id="Soares_thymus_2NDMT"
                /note="Vector: pT73D-pac (Pharmacia) with a modified
                polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer (5',
                TGTTCCATCTGAGTCGAGCGCGCGCTTTTCTTTTCTTTTCTTTTCTTTT
                3'); double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT73 vector. RNA
                provided by Dr. Bertrand Jordan. Library went through two
                rounds of normalization, and was constructed by Bento
                Soares and M. Fatima Bonaldo."

ORIGIN
Query Match      66.7%; Score 12; DB 1; Length 94;
Best Local Similarity 83.3%; Pred. No. 2.3e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 GGGGUCCTCGAG 12
|||||
58 GGGGCTCTCGAG 47

RESULT 110
BF374161      100 bp  mRNA      linear  EST 24-NOV-2000
LOCUS         BF374161 MRO-SN0040-250500-004-b07 SN0040 Homo sapiens cDNA, mRNA sequence.
DEFINITION    BF374161
ACCESSION     BF374161.1 GI:11336095
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 100)
AUTHORS       Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
              Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
              Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
              O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
              Simpson, A.J.
TITLE         Shotgun sequencing of the human transcriptome with ORF expressed

```



JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Sequence tags  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR0&ct2=MR0-SN0040-  
250500-004-b07&ct3=2000-05-25&ct4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 15  
High quality sequence stop: 100.

FEATURES  
source

1..100  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="SN0040"  
/note="Organ: stomach normal; Vector: puc18; Site\_1: Sma1;  
Site\_2: Sma1; A mini-library was made by cloning products  
derived from ORSTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 100;  
Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:||||  
45 GGGGTCCTGAG 56

RESULT 111  
CF537121/c 101 bp mRNA linear EST 12-SEP-2003  
LOCUS  
DEFINITION  
IMAGE:30535932 5', mRNA sequence.  
CF537121  
CF537121.1 GI:34589101  
EST.  
MUS musculus (house mouse)  
MUS musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 101)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strusberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
http://genome.uiowa.edu/distribution/mouse1.html  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP).  
Seq primer: pYX-5.  
Location/Qualifiers  
1..101

FEATURES  
source

1..101

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 101;  
Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:||||  
82 GGGGTCCTGAG 71

RESULT 112  
CK387998/c 102 bp mRNA linear EST 29-DEC-2003  
LOCUS  
DEFINITION  
IMAGE:30002288 5', mRNA sequence.  
CK387998  
CK387998.1 GI:40377001  
EST.  
MUS musculus (house mouse)  
MUS musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 102)  
Piao Y., Ko N.T., Lim M.K. and Ko M.S.H.  
Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
Genome Res. 11 (9), 1553-1558 (2001)  
21429098  
11544199  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@gsun-grc.nia.nih.gov  
Plate: L0923 row: G column: 09  
Seq primer: M13 Reverse  
High quality sequence stop: 102  
POLYA=No.  
Location/Qualifiers  
1..102  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:30535932"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"  
/lab\_host="MDH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP F10"  
/note="Organ: Brain; Vector: pYX-Asc; Site\_1: EcoR I;  
Site\_2: Not I; The library was constructed according  
Bonaldi, Lemmon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is AGCGAGCAG. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

FEATURES  
source

1..102  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:30002288"  
/tissue\_type="Newborn Kidney"

/dev stage="Newborn"  
 /lab host="DH10B"  
 /clone lib="NIA Mouse Newborn Kidney cDNA Library (long)"  
 /note=Torgan: kidney; vector: pSPORT1 (Invitrogen);  
 Site\_1: Sall; Site\_2: NotI; Mouse cDNA project by the  
 Laboratory of Genetics, National Institute on Aging (NIA)  
 Intramural Research Program, NIH  
 (<http://lgsun.grc.nia.nih.gov/cDNA/>). This is a  
 long-transcript enriched cDNA library (Ref. Genome Res.  
 11:1553-1558 (2001). [PMID:11544199]). In  
 brief double-stranded cDNAs were synthesized with an  
 oligo(dT) primer [Invitrogen: 5'-  
 pGACATAGTTCTTAGATCGGAGGCGCCGCTTTTTTTTTT-3'] from 26  
 microgram of total RNA, treated with T4 DNA polymerase,  
 and purified by ethanol-precipitation. The cDNAs were  
 ligated to lone-linker IL-Sal4, purified by  
 phenol/chloroform, and separated from free linkers by  
 Centricon 100. Then, the cDNAs were amplified by  
 long-range high fidelity PCR using Ex Taq polymerase  
 (Takara) with a primer Sal4-S. The products were purified  
 by phenol/chloroform and Centricon 100. The cDNAs were  
 digested with Sall and NotI enzymes, and cloned into  
 Sall/NotI site of pSPORT1 plasmid vector. The DH10 E.  
 coli host was transformed with ligation mixture by the  
 standard chemical method. The average insert size is about  
 3.0 kb. The library was constructed by Yulan Piao (NIA)."

Query Match	66.7%	Score 12;	DB 7;	Length 102;
Best Local Similarity	83.3%	Pred. NO.	2.3e+04;	
Matches	10;	Conservative	2;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	1	GGGGUCCUGAG	12	
		:		
db	59	GGGGUCCUGAG	48	

RESULT 113					
BQ809065/c					
LOCUS	BQ809065	105 bp	mRNA	linear	EST 01-AUG-2002
DEFINITION	1303008H12.x2 C. reinhardtii CC-1690, Deflagellation (normalized),				
	lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.				
ACCESSION	BQ809065				
VERSION	BQ809065.1	GI:22050095			
KEYWORDS	EST.				
SOURCE	Chlamydomonas reinhardtii				
ORGANISM	Chlamydomonas reinhardtii				
	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;				
	Chlamydomonadaceae; Chlamydomonas.				
REFERENCE	1 (bases 1 to 105)				

JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Charles Hauser

```
FEATURES      Location/Qualifiers
source        1. .105
```

```

/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Deflagellation
(normalized), lambda zap II"
/notes="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; Deflagellation library, constructed by John Davies

```

and Jeffrey McDermott, combines cDNAs from CC-1690 cells which had been re-synthesizing flagella for 15, 30 and 60 min after being deflagellated by pH shock. Poly(A) mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II Sk- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

Query Match	66.7%	Score 12	DB 5	Length 105
Best Local Similarity	83.3%	Pred. No. 2	3e+04	
Matches 10	Conservative	2	Mismatches 0	Indels 0
			Gaps 0	
Qy	1	GGGGUCCUGGAG	12	
Db	42	GGGGUCCUGGAG	31	

RESULT	114
AA915600	
LOCUS	107 bp mRNA linear EST 14-APR-1998
DEFINITION	v332f08.r1 Soares thymus.2NMT Mus musculus cDNA clone
IMAGE:	1338199_5', mRNA sequence.
ACCESSION	AA915600
VERSION	AA915600.1 GI:3054992
KEYWORDS	EST
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 107)	Marx, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kuchba, T., Lacey, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepec, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lemon, S., Soares, B., Wilson, R. and Waterston, R.	The MASHU-HMM Mouse EST Project	Unpublished (1996)	Contact: Maria W/Mouse EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:687743  
Seq primer: -28m3 rev2 ET from Amerham  
High quality sequence stop: 94.  
Location/Qualifiers  
1..107

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1328139"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DHL0B"
/clone_lib="Soares thymus 2NbMT"
/note="Vector: pRT3d-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5,
TGTAAACAACGTGAAGTGGAGACGCCGCGCTTTTTCCTTTTTCCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTV73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two

```

ORIGIN

rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 66.7%; Score 12; DB 1; Length 107;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 DB 88 GGGGTCCTGGAG 99

## RESULT 115

AZ557012 110 bp DNA linear GSS 20-NOV-2000  
 DEFINITION RPI-23-179N14.TV RPI-23 Mus musculus genomic clone  
 RPI-23-179N14, genomic survey sequence.

ACCESSION AZ557012  
 VERSION AZ557012.1 GI:11236832  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

## REFERENCE

AUTHORS Zhao,S., Nieman,W., Feldblum,T., Malek,J., Shatsman,S., Akiner,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Frazer,C.M.  
 Mouse BAC End Sequences from Library RPI-23  
 Unpublished (1999)  
 COMMENT Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@igf.org

Clones are derived from the mouse BAC library RPI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Reseach Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac/ends/mouse/bac\_end\_intro.html  
 Plate: 179 row: N column: 14  
 Seq primer: 17  
 Class: BAC ends.

## FEATURES

source 1..110  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPI-23-179N14"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /clone\_lib="RPI-23"  
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Site selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

## ORIGIN

Query Match 66.7%; Score 12; DB 8; Length 110;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 DB 5 GGGGTCCTGGAG 16

## RESULT 116

AM326734 116 bp mRNA linear EST 25-APR-2001  
 LOCUS 19665 MARC 280V Bos taurus cDNA 5', mRNA sequence.  
 DEFINITION AM326734  
 ACCESSION AM326734  
 VERSION AM326734.1 GI:6762655

KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

## REFERENCE

AUTHORS Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Caeas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perte,G., Holt,I., Karayancheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
 Genome Res. 11 (4), 626-630 (2001)

## COMMENT

CONTACT: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@meat.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 20 and -mismatch 12 options.  
 PCR primers  
 FORWARD: AGGAACAGCATGACCAT  
 BACKWARD: GTTTCAGTCAGCAGC  
 Plate: 10 row: O column: 13  
 Seq primer: ATTAGTGACACTAATG.

## FEATURES

source 1..116  
 Location/Qualifiers  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 280V"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

## ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 116;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 DB 83 GGGGTCCTGGAG 94

## RESULT 117

COS49288 121 bp mRNA linear EST 01-SEP-2004  
 LOCUS LYEST6835 Sea lamprey LyEST Petromyzon marinus cDNA, mRNA sequence.  
 DEFINITION COS49288  
 ACCESSION COS49288  
 VERSION COS49288.1 GI:51797604

KEYWORDS EST.  
 SOURCE Petromyzon marinus (sea lamprey)  
 ORGANISM Petromyzon marinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; Petromyzontiformes; Petromyzontidae; Petromyzon.

REFERENCE 1 (bases 1 to 121)  
 AUTHORS Pancer, Z., Mayer, W.E., Klein, J. and Cooper, M.D.  
 TITLE Prototypic T-cell receptor and CD4-like coreceptor expressed in lymphocytes of the agnathan sea lamprey  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 101, 13273-13278 (2004)  
 COMMENT Contact: Pancer, Zeev  
 Division of Developmental and Clinical Immunology  
 The University of Alabama at Birmingham  
 378 Wallace Tumor Institute, 1530 Third Avenue, South, Birmingham, AL 35294-3300  
 Tel: 205-975-5812  
 Fax: 205-975-7218  
 Email: zpancer@uab.edu.

FEATURES  
 source Location/Qualifiers  
 1..121  
 /organism="Petromyzon marinus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7757"  
 /cell\_type="lymphocyte"  
 /dev\_stage="unstimulated larvae"  
 /clone\_lib="Sea lamprey LyEST"  
 /note="Vector: Lambda ZAP Express; lymphocyte mRNA ESTs from unstimulated larvae. All are from arrayed colonies from a directionally cloned cDNA library in Lambda ZAP Express (Stratagene). All are single pass 5' sequences."

ORIGIN  
 Query Match 66.7%; Score 12; DB 7; Length 121;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|||||  
 Db 107 GGGGTCTGTGAG 118

RESULT 118  
 LOCUS CD286354  
 DEFINITION 11 K23.abd POE14 (Day\_14\_pregnant\_ovine\_endometrium) Ovis aries cDNA, mRNA sequence.  
 ACCESSION CD286354  
 VERSION CD286354.1 GI:31084397  
 KEYWORDS EST.  
 SOURCE Ovis aries (sheep)  
 ORGANISM Ovis aries  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.  
 1 (bases 1 to 123)  
 Gray, C.A., Adelson, D.L. and Spencer, T.E.  
 Ovine ESTs  
 Unpublished (2003)  
 Contact: Thomas E. Spencer  
 Center for Animal Biotechnology and Genomics  
 Texas A&M University  
 Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA  
 Tel: 9798454896  
 Fax: 9798622662  
 Email: tspancer@tamuc.tamu.edu.

FEATURES  
 source Location/Qualifiers  
 1..123  
 /organism="Ovis aries"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9940"  
 /sex="Female"  
 /tissue\_type="endometrium"  
 /dev\_stage="Day 14 pregnant"  
 /clone\_lib="POE14 (Day 14 pregnant ovine endometrium)"  
 /note="Organ: uterus; Vector: Triplex2; Site 1: EcoRI; Site 2: XhoI; Non-normalized library, sequenced 5' with Triplex2 primer (CTCCGAGATCTGACGAGC). Library constructed

ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 123;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|||||  
 Db 49 GGGGTCTGTGAG 38

RESULT 119  
 LOCUS AM480318  
 DEFINITION 30824 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.  
 ACCESSION AM480318  
 VERSION AM480318.1 GI:7050424  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 128)  
 Vallet, J., Wise, T., Rohrer, G.A., Perrea, G., Sultana, R., Quackenbush, J. and Keefe, J.W.  
 Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly  
 Mamm. Genome 13 (8), 475-478 (2002)  
 22213789  
 MEDLINE 12226715  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@mail.marc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 20 and -mismatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCATGACCAT  
 BACKWARD: GTTTCACATGACGACG  
 Place: 17 row: K column: 1  
 Seq primer: ATTGAGTGACATATAG.  
 Location/Qualifiers  
 1..128  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 2P1G"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 128;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|||||  
 Db 52 GGGGTCTGTGAG 63

RESULT 120  
 LOCUS AM385180  
 DEFINITION PM1-HT0452-291299-001-C01 HT0452 Homo sapiens cDNA, mRNA sequence.

ACCESSION AM385180  
 VERSION AM385180.1 GI:6889839  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 133)  
 AUTHORS HCCP <http://www.ludwig.org.br/ORESTES>.  
 TITLE The FAPESP/LICR Human Cancer Genome Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&v2=PM1-HT0452-291299-001-c01&t3=1999-12-29&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 133.

FEATURES  
 source  
 1..133  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /def\_stage="Adult"  
 /clone\_lib="HT0452"  
 /note="Organ: head\_neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 133;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCCCGAG 12  
 ||||:||||  
 2 GGGGTCTCTGGAG 13

RESULT 121  
 AI280744 134 bp mRNA linear EST 21-DEC-1998  
 LOCUS GW07C10.X1 NCI\_CGAP\_uc3 Homo sapiens cDNA clone IMAGE:1990386 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AI280744  
 VERSION AI280744.1 GI:3918977  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 134)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the [www.a.g.e.consortium/LNW.ac](http://www.a.g.e.consortium/LNW.ac):  
[www-bio.llnl.gov/bdrrp/image/image.html](http://www-bio.llnl.gov/bdrrp/image/image.html)  
 Insert Length: 1474 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 119.

FEATURES  
 source  
 1..134  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1990386"  
 /tissue\_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP uc3"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NciI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"

ORIGIN  
 Query Match 66.7%; Score 12; DB 1; Length 134;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCCCGAG 12  
 ||||:||||  
 109 GGGGTCTCTGGAG 120

RESULT 122  
 AM358302 134 bp mRNA linear EST 25-APR-2001  
 LOCUS 42366 MABC 3BOV Bos taurus cDNA 5', mRNA sequence.  
 DEFINITION AM358302  
 ACCESSION AM358302  
 VERSION AM358302.1 GI:6862308  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 134)  
 AUTHORS Smith,T.P.L., Grosee,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pettes,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.  
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
 JOURNAL Genome Res. 11 (4), 626-630 (2001)  
 MEDLINE 21180013  
 PUBMED 11282878

COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: [smitht@mail.marc.usda.gov](mailto:smitht@mail.marc.usda.gov)  
 Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 20 and -mismatch 12 options.  
 PCR primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCACAGTCACGACG  
 Plate: 22 row: N column: 9  
 Seq primer: ATTGAGTGACACTATG.  
 Location/Qualifiers  
 1..134  
 /organism="Bos taurus"  
 /mol\_type="mRNA"

/db\_xref="taxon:9913"  
 /issue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 3BOV"  
 /note="Vector: PCMV SPOR6; Site 1: NotI; Site 2: SalI;  
 library made from pooled tissue from marrow, alveolar  
 macrophage, ovary, fetal semitendinosus muscle, and fetal  
 longissimus muscle."

## ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 134;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||:|:|:|:|  
 Db 73 GGGGCTCTGGAG 84

## RESULT 123

CA378150 135 bp mRNA linear EST 06-NOV-2002  
 LOCUS 65698 NCCWA IRT Oncorhynchus mykiss cDNA clone IRT42H16\_D\_D08 5',  
 mRNA sequence.  
 CA378150  
 ACCESSION CA378150.1 GI:24697751  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oncorhynchus mykiss (rainbow trout)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 1 (bases 1 to 135)  
 Rexroad, C.E., 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,  
 Koop, B., Gah, S.A., Palti, Y., and Quackenbush, J.  
 Sequence analysis of a rainbow trout cDNA library and creation of a  
 gene index

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)  
 Contact: Rexroad CE  
 USA, ARS, National Center for Cool and Cold Water Aquaculture  
 11876 Leetown Road, Kearneysville, WV 25430, USA  
 Tel: 304 724 8340 x2129  
 Fax: 304 725 0351  
 Email: crexroad@nccwa.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_al option. Vector identified by  
 cross match v0.990329.  
 Seq primer: AGCGATACATTTTCACACAGA.

## FEATURES

## SOURCE

1..135  
 Location/Qualifiers  
 /organism="Oncorhynchus mykiss"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8022"  
 /clone\_lib="IRT42H16\_D\_D08"  
 /issue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="NCCWA IRT"  
 /note="Vector: PCMV SPOR6; Site 1: NotI; Site 2: SalI;  
 library made from pooled tissue from brain, gill, liver,  
 spleen, muscle, and kidney."

## ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 135;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||:|:|:|:|  
 Db 22 GGGGCTCTGGAG 33

RESULT 124  
 CL965510

LOCUS CL965510 141 bp DNA linear GSS 21-SEP-2004  
 DEFINITION OsIFCC03107 Oryza sativa indica cultivar-group)  
 cultivar-group) genomic, genomic survey sequence.  
 ACCESSION CL965510  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Oryza sativa (indica cultivar-group)  
 Oryza sativa (indica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriophytidae; Oryzoideae; Oryza.  
 1 (bases 1 to 141)

## REFERENCE

## AUTHORS

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,  
 Wang, G.K.S., Deng, X.W., and Wang, J.  
 An analysis of transcriptional regulation of the rice genome and  
 its comparison to Arabidopsis  
 unpublished (2004)

## JOURNAL

## COMMENT

Contact: Chen Chen  
 Department of Bioinformatics  
 Beijing Institute of Genomics  
 Chinese Academy of Sciences, Beijing 101300, China  
 Tel: 86-10-80481559  
 Fax: 86-10-80488676  
 Email: chenchen@genomics.org.cn  
 Rice genomic sequence.  
 Class: exon-trapped.  
 Location/Qualifiers

## FEATURES

## SOURCE

1..141  
 /organism="Oryza sativa (indica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:39946"  
 /clone\_lib="Oryza sativa Expressed library"  
 /note="Oryza sativa exon trapped genomic sequences"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 141;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||:|:|:|:|  
 Db 50 GGGGCTCTGGAG 61

## RESULT 125

BB606528 143 bp mRNA linear EST 06-DEC-2000  
 LOCUS BB606528 RIKEN full-length enriched, 0 day neonate eyeball Mus  
 musculus cDNA clone E130102K01 5', mRNA sequence.  
 ACCESSION BB606528  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus (house mouse)  
 Mus musculus

## REFERENCE

## AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 143)  
 Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T.,  
 Carninci, P., Hanagaki, T., Hayatsu, N., Hirooka, T., Hirozane, T.,  
 Hodojima, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J.,  
 Kojima, Y., Kono, H., Kusakabe, M., Matsuyama, T., Miyazaki, A.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y.,  
 Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K.,  
 Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,  
 Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T.,  
 Watabiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A.,  
 Muramatsu, M., and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Aizawa, K. et al. 2000)  
 Unpublished (2000)

## TITLE

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute

Lymphocytes of the agnathan sea lamprey

Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 142 row: 5 column: 06

Class: BAC ends  
High quality sequence stop: 147.  
Location/Qualifiers  
1. 147

FEATURES  
source  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_14206"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: PTARBA1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN  
Query Match 66.7%; Score 12; DB 9; Length 147;  
Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGNNNNNN 18  
Db 72 CTGAGNNNNNN 61

RESULT 128  
CG918034/c 150 bp DNA linear GSS 12-DEC-2003  
LOCUS CH240\_136J13.TJ CHORI-240 Bos taurus genomic clone CH240\_136J13,  
DEFINITION genomic survey sequence.  
ACCESSION CG918034  
VERSION CG918034.1 GI:39777717  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 150)  
Costa, J.N., Mota, M. and Caetano, A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other\_GSS: CH240\_136J13.TJ  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/S Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetan@cena.gen.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 136 row: J column: 13  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 150.  
Location/Qualifiers  
1. 150  
/organism="Bos taurus"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 66.7%; Score 12; DB 9; Length 150;  
Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGNNNNNN 18  
Db 132 CTGAGNNNNNN 121

RESULT 129  
BZ280016/c 151 bp DNA linear GSS 15-OCT-2002  
LOCUS CH230\_480K1.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone  
DEFINITION CH230\_480K1, genomic survey sequence.  
ACCESSION BZ280016  
VERSION BZ280016.1 GI:24006179  
KEYWORDS GSS.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 151)  
Zhao, S., Shetty, U., Shatsman, S., Tsegaye, G., Geer, K.,  
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,  
Riggs, F., de Jong, P. and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 MboI segment  
Unpublished (1999)  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@igr.org  
Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). BAC end  
page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 480 row: K column: 1  
Seq primer: SP6  
Class: BAC ends  
Location/Qualifiers  
1. 151  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SnHsd/MCW"  
/db\_xref="taxon:10116"  
/clone="CH230\_480K1"  
/sex="Female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 2"  
/note="Vector: PTARBA1.3; Site 1: MboI; Site 2: MboI;  
CHORI-230 Rat (BN/SnHsd/MCW) BAC library produced by  
Pieter de Jong"

## FEATURES

source

1. 150  
/organism="Bos taurus"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 151;  
Best Local Similarity 93.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



QY 1 GGGGUCUGAG 12  
 |||||  
 Db 98 GGGGTCTCGAG 87

RESULT 130  
 CE594318/c  
 LOCUS CE594318  
 DEFINITION tigr-gss-dog-17000366530020 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

ACCESSION CE594318  
 VERSION CE594318.1 GI:36911099  
 KEYWORDS GSS  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris

REFERENCE  
 AUTHORS Kirkenes, R.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Ruch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M., and  
 Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627  
 COMMENT Contact: Kirkenes EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirkenes@tigr.org  
 Class: Shotgun.

FEATURES  
 source Location/Qualifiers  
 1..151

/organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

Query Match 66.7%; Score 12; DB 9; Length 151;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
 |||||  
 Db 89 GGGGTCTCGAG 78

RESULT 131  
 CB482046/c  
 LOCUS CB482046  
 DEFINITION jn86.C03.f jns Sue scrofa cDNA 5', mRNA sequence.  
 ACCESSION CB482046  
 VERSION CB482046.1 GI:29288432  
 KEYWORDS EST  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 152)  
 AUTHORS Neilan, J.G., Kurish, G.F., Lu, Z., Zsak, A., and Rock, D.L.  
 TITLE Sequence analysis of African swine fever virus infected and  
 non-infected porcine macrophage cDNA libraries  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Neilan JG  
 Plum Island Animal Disease Center  
 US Department of Agriculture, Agricultural Research Service

PO Box 848, Greenport, NY 11944-848, USA  
 Tel: 631 323 3133  
 Fax: 631 323 3044  
 Email: jneilan@iadc.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim alt option. Vector identified by  
 cross-match v0.990329 and Lucy v1.17p.  
 Seq primer: M13 Forward.

FEATURES  
 source Location/Qualifiers  
 1..152

/organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9623"  
 /issue\_type="lymphoid"  
 /cell\_type="macrophage"  
 /lab\_host="DH10B"  
 /clone\_lib="jns"  
 /note="Vector: pSPOR1; Site 1: NotI; Site 2: SalI;  
 Library made from pools of polyA selected RNA. Macrophages  
 were derived from peripheral blood mononuclear cells  
 cultured for 48 hrs on plastic in the presence of 30% L929  
 supernatant."

Query Match 66.7%; Score 12; DB 6; Length 152;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
 |||||  
 Db 141 GGGGTCTCGAG 130

RESULT 132  
 CG677253/c  
 LOCUS CG677253  
 DEFINITION tmf1008 tmf Aegilops tauschii genomic clone tmf17L06, genomic  
 survey sequence.

ACCESSION CG677253  
 VERSION CG677253.1 GI:37506320  
 KEYWORDS GSS  
 SOURCE Aegilops tauschii  
 ORGANISM Aegilops tauschii

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Aegilops.  
 1 (bases 1 to 155)

REFERENCE Li, W., Zhang, P., Fellars, J., Friebe, B. and Gill, B.S.  
 TITLE Sequence composition, organization and evolution of a basic  
 Triticeae genome of the grass family  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Li, W  
 Dr. Bikram S. Gill's Lab  
 Wheat Genetics Resource Center, Kansas State University  
 4024 Throckmorton, Manhattan, KS 66506-5502, USA  
 Tel: 785-532-1108  
 Fax: 785-532-5692  
 Email: wli@ksu.edu  
 Seq primer: T7  
 Class: sheared ends.

FEATURES  
 source Location/Qualifiers  
 1..155

/organism="Aegilops tauschii"  
 /mol\_type="genomic DNA"  
 /strain="AL 8/78"  
 /db\_xref="taxon:37682"  
 /clone="tmf17L06"  
 /issue\_type="leaves"  
 /dev\_stage="shoot"  
 /lab\_host="E. coli strain DH5alpha"  
 /clone\_lib="tmf"  
 /note="Vector: PCR 4Blunt-TOP; 0.8-1.2 kb methylation  
 filtered genomic DNA library"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 155;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
 |||||:  
 78 GGGGCTCTGGAG 67

RESULT 133  
 CL303190/c 155 bp mRNA linear GSS 30-JUN-2004  
 LOCUS P005612, mRNA sequence.  
 DEFINITION CL303190.1 GI:42744019  
 ACCESSION GSS.  
 VERSION CL303190.1  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 155)  
 Hansen, J., Floss, T., van Sloun, P., Fuchsbauer, E.M., Vauti, F., Arnold, H.H., Schultgen, F., Murest, W., Von Melchner, H., Ruiz, P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome  
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
 JOURNAL 22810117  
 MEDLINE 12904583  
 PUBMED  
 COMMENT Contact: GGTC  
 German Genetrap Consortium (GGTC)  
 Email: info@genetrap.de  
 FlpRosaBetageo gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at: 'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=P005612' ES cell line harboring insertion mutation of target gene is available at: 'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm' 1' Inhouse Sequence Identifier: 13210  
 Class: Gene Trap

FEATURES  
 source  
 location/Qualifiers  
 1..155  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"  
 /clone="P005612"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
 /clone\_id="GGTC Gene Trap library GV08C05"  
 /note="Vector: FlpRosaBetageo"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 155;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
 |||||:  
 60 GGGGCTCTGGAG 49

RESULT 134  
 CL607849 158 bp DNA linear GSS 17-JUN-2004  
 LOCUS CH240.174109.TJ CHORI-240 Bos taurus genomic clone CH240.174109,  
 DEFINITION genomic survey sequence.  
 ACCESSION CL607849  
 VERSION CL607849.1 GI:48875881  
 KEYWORDS GSS.

SOURCE  
 ORGANISM Bos taurus (cow)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 158)  
 Costa, J.N., Mota, M., and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: CH240.174109.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P. 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acaetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have Phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong (pdejong@mail.cno.org).  
 Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnolico (CNPq), Brazil  
 Plate: 174 row: 1 column: 09  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 158.

FEATURES  
 source  
 location/Qualifiers  
 1..158  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240.174109"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTRBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull l1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 158;  
 Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18  
 |||||:  
 149 CTGAGNNNNNN 138

RESULT 135  
 CR081247 160 bp DNA linear GSS 05-JUL-2004  
 LOCUS Reverse strand read from insert in 3'HPRT insertion targeting and  
 DEFINITION chromosome engineering clone MHP68114, genomic survey sequence.  
 ACCESSION CR081247.1 GI:49814836  
 VERSION X081247  
 KEYWORDS GSS; genome survey sequence; MICE.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 160)  
 Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,

Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,  
Rogers, J. and Bradley, A.

TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

FEATURES  
SOURCE Location/Qualifiers  
1..160  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPP68114"  
/clone\_lib="MHPP"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 160;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
||||:|||||  
DB 42 GGGGTCTGGAG 53

RESULT 136  
BP651925/c 161 bp mRNA linear EST 25-APR-2001  
LOCUS  
DEFINITION 275345 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BP651925  
VERSION BP651925.1 GI:11917055  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 161)  
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
Cavaa, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,  
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,  
Chitko-McKown, C.G., Perteau, G., Holt, I., Karaycheva, S., Liang, F.,  
Quackenbush, J. and Keefe, J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)

## REFERENCE

## AUTHORS

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: [smitht@mail.marc.usda.gov](mailto:smitht@mail.marc.usda.gov)  
Single pass sequencing. Bases called and alt trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.  
PCR primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCACGACG  
Plate: 64 row: D column: 4  
Seq primer: ATTAGGTGACATCTAG.

## FEATURES

## SOURCE

1..161  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH108"  
/clone\_lib="MARC 3BOV"  
/note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinous muscle, and fetal  
longissimus muscle."

## ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 161;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
||||:|||||  
DB 86 GGGGTCTGGAG 75

RESULT 137  
AW848479/c 163 bp mRNA linear EST 19-MAY-2000  
LOCUS  
DEFINITION IL3-CT0214-170200-006-D08 CT0214 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW848479  
VERSION AW848479.1 GI:7943996  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 163)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## TITLE

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the PAPSP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=st2=IL3-CT0214-170>  
200-006-D08&t3=2000-02-17&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 163.

## FEATURES

## SOURCE

1..163  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="CT0214"  
/note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 163;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
||||:|||||  
DB 160 GGGGTCTGGAG 149

## RESULT 138

BBS69306 168 bp mRNA linear EST 29-NOV-2000  
BBS69306 RIKEN full-length enriched, 10 days embryo Mus musculus  
cDNA clone 3426406E15 5', mRNA sequence.  
BBS69306 BBS69306.1 GI:11460214  
EST.

Mus musculus (house mouse)  
Mus musculus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scurionathii; Muridae; Murinae; Mus.  
1 (bases 1 to 168)

Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T.,  
Carninci,P., Nishiyama,T., Hayatsu,N., Hirooka,T., Hirozane,T.,  
Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J.,  
Kojima,Y., Konno,H., Kusabe,M., Matsuyama,T., Miyazaki,A.,  
Nakamura,M., Nihi,K., Nomura,K., Numasaki,R., Okazaki,Y.,  
Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Seto,K.,  
Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y.,  
Suzuki,H., Tagawa,A., Takanashi,F., Tanaka,T., Toya,T.,  
Watanuki,A., Yamawara,T., Yasunishi,A., Yoshida,K., Yoshihiki,A.,  
Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Aizawa,K. et al. 2000)  
Unpublished (2000)  
Contact: Yoshinide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
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Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-gsc@riken.jp, URL:<http://genome.gsc.riken.jp/>  
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S.,  
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermosensitization and thermoactivation of thermolabile enzymes by  
retroalose and its application for the synthesis of full length  
cDNA. Proc.Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Kitsuuti,T., Akiyama,Y., Shibata,K., Izawa,M., Kawai,J.,  
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,  
Okazaki,Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

Location/Qualifiers  
1. .168

*Organism*=*"Mus musculus"*  
*mol\_type*=*"cDNA"*  
*strain*=*"C57BL/6J"*  
*db\_xref*=*"taxon:10090"*  
*clone*=*"3426406E15"*  
*/sex*=*"mixed"*  
*/dev\_stage*=*"10 days embryo"*  
*/lab\_host*=*"DH10B"*  
*/clone\_lib*=*"Riken full-length enriched, 10 days embryo"*  
*/note*=*"Site 1: Salt; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'*  
GAGGAGAGAGAGATCCAAAGCTCTTTTTTTTTTTTTN 3']". cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trisepher. Second strand cDNA was prepared with the  
primer adapter of sequence [5'  
GAGGAGAGAGATTTCGGATTATAAATTAATNACC(CCCCCCCC 3')". cDNA  
was cloned into the XhoI and BamHI sites. Vector: a  
modified pluescript KS(+) after bulk excision from Lambda

RESULT	139
LOCUS	CA850537/c
DEFINITION	CA850537 171 bp mRNA linear EST 01-AUG-2003
ACCESSION	D03A06.seq CDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone.
VERSION	D03A06.5, mRNA sequence.
KEYWORDS	CA850537 CA850537.1 GI:33387330
SOURCE	EST.
ORGANISM	Glycine max (soybean)
	Glycine max

USDA  
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350.  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharon@da.ars.usda.gov.

### Source

```

/organism="Glycine max"
/mol_type="mRNA".
/cultivar="Peking"
/db_xref="taxon:3647"
/clone="D03A06"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pluscript SK-+ cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

```

Query Match	66.7%;	Score 12;	DB 6;	Length 171;
Best Local Similarity	83.3%;	Pred. No. 2.2e+04;		
Matches 10;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	GGG	UCC	UGAG	12
		:			
Db	57	GGG	TCCTG	GAG	46

RESULT 140  
CE350113

LOCUS	171 bp	DNA	linear	GSS 26-SEP-200
DEFINITION	tigr-gss-dog-17000334168375	Dog	Library	Canis familiaris genomic,
	genomic survey sequence.			

ACCESSION	CE350113
VERSION	CE350113.1
	GI:36184115

KEYWORDS	GSS.
SOURCE	Canis familiaris (dog)
ORGANISM	Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 171)  
 AUTHORS Kirkness E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Ruesch, D.B., Deitcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirkness@tigr.org  
 Class: Shotgun.  
 FEATURES  
 source 1..171  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"  
 ORIGIN  
 Query Match 66.7%; Score 12; DB 9; Length 171;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 Db 110 GGGGTCCTGGAG 121  
 ||||:||||  
 RESULT 141  
 LOCUS CD557019 172 bp mRNA linear EST 11-JUN-2003  
 DEFINITION AGNCOURT\_14400763 NIH\_MGC\_179 Homo sapiens cDNA clone  
 IMAGE:30392397 5', mRNA sequence.  
 ACCESSION CD557019  
 VERSION CD557019.1 GI:31583087  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 172)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Daniela S. Gerhard, Ph.D.  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein  
 CDNA Library Preparation: Invitrogen Corp  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 Plate: NDAM467 row: j column: 22  
 High quality sequence start: 4  
 High quality sequence stop: 172.  
 FEATURES  
 source 1..172  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"

/clone="IMAGE:30392397"  
 /tissue\_type="pituitary"  
 /lab\_host="DH10B-Ton A ( T1 and T5 phage resistances) "  
 /clone\_lib="NIH\_MGC\_179"  
 /note="Organ: brain; Vector: pCMV-Sport6.1; Site 1: EcoRV  
 (destroyed); Site 2: NotI; Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.1 kb. Library was  
 constructed by (Invitrogen). Note: this is a NIH\_MGC  
 Library."  
 ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 172;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 Db 44 GGGGTCCTGGAG 55  
 ||||:||||  
 RESULT 142  
 LOCUS CD519554 173 bp mRNA linear EST 06-JUN-2003  
 DEFINITION AGNCOURT\_14369178 NIH\_MGC\_181 Homo sapiens cDNA clone  
 IMAGE:30356597 5', mRNA sequence.  
 ACCESSION CD519554  
 VERSION CD519554.1 GI:31451296  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 173)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Daniela S. Gerhard, Ph.D.  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein  
 CDNA Library Preparation: Invitrogen Corp  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 Plate: NDAM478 row: j column: 22  
 High quality sequence start: 4  
 High quality sequence stop: 173.  
 FEATURES  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30396597"  
 /tissue\_type="White Matter"  
 /dev\_stage="Unknown"  
 /lab\_host="DH10B-Ton A ( T1 and T5 phage resistances) "  
 /clone\_lib="NIH\_MGC\_181"  
 /note="Vector: pCMV-Sport6.1; Site 1: NotI; Site 2: EcoRV  
 (destroyed); Library is oligo-dT primed and directionally  
 cloned (EcoRV site is destroyed upon cloning). Average  
 insert size 1.42 kb. Library was constructed by  
 (Invitrogen). Note: this is a NIH\_MGC Library."  
 ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 173;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 Db 44 GGGGTCCTGGAG 55

RESULT 143  
 AV275702 174 bp mRNA linear EST 05-NOV-1999  
 AV275702 RIKEN full-length enriched, adult male testis (DH10B) Mus  
 musculus cDNA clone 4932430B17 3', mRNA sequence.

ACCESSION  
 AV275702  
 AV275702.1 GI:6263739

VERSION  
 EST

KEYWORDS  
 Mus musculus (house mouse)

SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 174)  
 Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,  
 Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,  
 Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadoya, K., Kagawa, I.,  
 Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,  
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
 Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,  
 Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
 Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomihaga, N.,  
 Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,  
 Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Kono, H., et al. 1999)  
 Unpublished (1999)

TITLE  
 JOURNAL  
 COMMENT  
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 1-7-22 Shinto-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: http://genome-gsc.riken.jp/  
 Sasaki, N., Izawa, M., Watabiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,  
 Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y., and  
 Hayashizaki, Y.  
 Transcriptional sequencing: A method for DNA sequencing using RNA  
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
 Okazaki, Y., and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (http://genome-rtc.riken.go.jp) for  
 further details.

FEATURES  
 source  
 Location/Qualifiers  
 1..174  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
 /clone="4932430B17"  
 /sex="male"  
 /tissue\_type="testis"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_1lb="RIKEN full-length enriched, adult male testis  
 (DH10B)"  
 /note="Site 1: Sali, Site 2: BamHI, cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'

QY 1 GGGGUCCTGGAG 12  
 Db 88 GGGGTCCTGGAG 99

RESULT 144  
 B0326528 174 bp mRNA linear EST 17-MAY-2002  
 LOCUS  
 B0326528  
 DEFINITION  
 B0326528  
 B0326528.1 GI:20942307  
 VERSION  
 EST  
 KEYWORDS  
 Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 174)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1et2=PM1-CN0151-  
 190301-004-g12et3=2001-03-19et4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 20  
 High quality sequence stop: 43.

FEATURES  
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 Location/Qualifiers  
 1..174  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_1lb="CN0151"  
 /note="Organ: colon, normal, Vector: puc18, Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORS215 PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

ORIGIN

Query Match 66.7%; Score 12; DB 5; Length 174;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
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 Db 130 GGGGCTCTGGAG 141

RESULT 145  
 CL303253 174 bp mRNA linear GSS 30-JUN-2004  
 LOCUS CL303253/c  
 DEFINITION P005A07 GGTC Gene Trap Library GV08C05 Mus musculus cDNA clone  
 ACCESSION CL303253  
 VERSION CL303253.1 GI:42744082  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Hansen, J., Flores, T., van Sloun, P., Fuchsbauer, E.M., Vauti, F.,  
 Arnold, H.H., Schnitgen, F., Murst, W., Von Melchner, H. and Ruiz, P.  
 A large-scale, gene-driven mutagenesis approach for the functional  
 analysis of the mouse genome  
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)

JOURNAL MEDLINE 12904583  
 PUBMED 12904583

COMMENT Contact: GGTC  
 German Genetrapp Consortium (GGTC)  
 Email: info@genetrapp.de  
 FliProSAbetaGeo gene trap. Sequence tag generated by 5'RACE.  
 Additional sequence information can be found at:  
 'http://genetrapp.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=P005A07'. ES cell line harboring insertion mutation of target gene is available at:  
 'http://genetrapp.gsf.de/project/web\_new/order\_clones/howtoorder.htm'. Inhouse Sequence Identifier: 13255  
 Class: Gene Trap.

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 /clone="P005A07"  
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 /cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
 /clone\_lib="GGTC Gene Trap Library GV08C05"  
 /note="Vector: FliProSAbetaGeo"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 174;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
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 Db 79 GGGGCTCTGGAG 68

RESULT 146  
 BE926972 175 bp mRNA linear EST 02-OCT-2000  
 LOCUS BE926972/c  
 DEFINITION RC0-CN0026-300800-012-e10 CN0026 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BE926972  
 VERSION BE926972.1 GI:10453152  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 175)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matukuma, A., Bala, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000).

JOURNAL MEDLINE 20202663  
 PUBMED 10737800

COMMENT Contact: Simpson A.J.J.  
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 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the PAPSP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2-RC0-CN0026-300  
 800-012-e10&t3=2000-08-30&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 16  
 High quality sequence stop: 175.

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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="CN0026"  
 /note="Organ: colon normal; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 175;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 90 GGGGCTCTGGAG 79

RESULT 147  
 T20038 175 bp mRNA linear EST 28-NOV-1994  
 LOCUS T20038  
 DEFINITION B300R Heart Homo sapiens cDNA clone B300, mRNA sequence.  
 ACCESSION T20038  
 VERSION T20038.1 GI:597783  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 175)  
 Liew, C.C., Hwang, D.M., Fung, Y.W., Laurensen, C., Cukerman, E.,  
 Tsui, S. and Lee, C.Y.  
 A catalogue of genes in the cardiovascular system as identified by  
 expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 91, 10645-10649 (1994)

JOURNAL MEDLINE 95024171  
 PUBMED 7938007

COMMENT Other ESTs: B300F  
Contact: Liew CC  
Brigham and Women's Hospital  
Harvard Medical School  
75 Francis St., Boston, MA 02115, USA  
Tel: 6173328915  
Fax: 6179750995  
Email: cliew@rics.bwh.harvard.edu  
Seq primer: GACACCGACCACTGGTATG.

FEATURES  
source  
1..175  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/clone\_1lb="Heart"  
/note="Vector: Lambda gtl1; Site\_1: EcoRI; Site\_2: EcoRI"

ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 175;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTCGAG 12  
||||:|||||  
50 GGGGTCCTCGAG 61

Db

RESULT 148  
LOCUS B0348169 176 bp mRNA linear EST 20-MAY-2002  
DEFINITION RC0-HT0295-141199-011-e06 HT0295 Homo sapiens cDNA, mRNA sequence.  
ACCESSION B0348169  
VERSION B0348169.1 GI:21012225  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 176)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matukuma, A., Bata, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
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Ludwig Institute for Cancer Research  
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Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC0&t2=RC0-HT0295-  
141199-011-e06&t3=1999-11-14&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 86  
High quality sequence stop: 121.  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"

FEATURES  
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COMMENT /clone\_1lb="HT0295"  
/note="Organ: head neck; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No.196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

ORIGIN

Query Match 66.7%; Score 12; DB 5; Length 176;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTCGAG 12  
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78 GGGGTCCTCGAG 67

Db

RESULT 149  
LOCUS CE745681 176 bp DNA linear GSS 30-SEP-2003  
DEFINITION tigr-gss-dog-17000369548879 Dog Library Canis familiaris genomic.  
ACCESSION CE745681  
VERSION CE745681.1 GI:37086028  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 176)  
Kirkness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
22875432  
14512627  
Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: Shotgun.  
Location/Qualifiers  
1..179  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_1lb="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 179;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTCGAG 12  
||||:|||||  
66 GGGGTCCTCGAG 77

Db

RESULT 150  
LOCUS AJ463066 180 bp mRNA linear EST 24-MAY-2002  
DEFINITION AJ463066 S00002 Hordeum vulgare subsp. vulgare cDNA clone  
S0000200024F08F1, mRNA sequence.  
ACCESSION AJ463066



VERSION AJ43066.1 GI:21061986  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 180)  
AUTHORS Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H.  
TITLE Barley EST<sup>8</sup>  
JOURNAL Unpublished (2002)  
COMMENT Contact: Schulman AH  
Institute of Biotechnology  
University of Helsinki  
P.O.Box 56 (Valkinkaaari 6A), University of Helsinki FIN-00014,  
Finland.  
FEATURES  
source Location/Qualifiers  
1..180  
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/mol\_type="mRNA"  
/cultivar="Saana"  
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ORIGIN  
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Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
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63 GGGGCTCTGGAG 52  
RESULT 151  
BG062863 182 bp mRNA linear EST 10-JUN-2003  
LOCUS L0958H12-5 NIA Mouse Newborn Kidney cDNA Library2 (Short) Mus  
DEFINITION musculus cDNA clone L0958H12 5', mRNA sequence.  
ACCESSION BG062863  
VERSION BG062863.2 GI:31577341  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 182)  
AUTHORS Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.  
TITLE Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)  
MEDLINE 21429098  
PUBMED 11544199  
COMMENT On Jan 25, 2001 this sequence version replaced gi:12533767.  
Other ESTs: L0958H12-3  
Contact: George J. Kargul  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
niEST (http://igsun.grc.nia.nih.gov/cdna/cdna.html)  
Plate: L0958 row: H column: 12  
Seq primer: -21M3 Reverse  
High quality sequence stop: 182  
POLYA=NO.  
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1..182  
/organism="Mus musculus"

/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
/clone="L0958H12"  
/issue\_type="Newborn kidney"  
/dev\_stage="Newborn"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Newborn Kidney cDNA Library2  
(Short)"  
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://igsun.grc.nia.nih.gov/cdna). This is  
a short-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). [PMID: 11544199]). In brief,  
double-stranded cDNAs were synthesized with an Oligo (dT)  
primer (Invitrogen: 5'-  
pgactagcttcagatccgagccgccctttttttttttt-3') from 26  
ug of total RNA, created with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to lone-linker Lr-Sal4, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-L. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 1.5 kb. The library was constructed  
by Yulan Piao(NIA)."

ORIGIN  
Query Match 66.7%; Score 12; DB 4; Length 182;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
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141 GGGGCTCTGGAG 152  
RESULT 152  
BM183955 182 bp mRNA linear EST 05-NOV-2002  
LOCUS BM183955  
DEFINITION BM183955 Nori Satoh unpublished cDNA library, heart Ciona  
intestinalis cDNA clone rc1hc001m03 3', mRNA sequence.  
ACCESSION BM183955  
VERSION BM183955.1 GI:24574216  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.  
REFERENCE 1 (bases 1 to 182)  
AUTHORS Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.  
TITLE Expressed genes in Ciona intestinalis (2002c)  
JOURNAL Unpublished (2002)  
COMMENT Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.  
FEATURES  
source Location/Qualifiers  
1..182  
/organism="Ciona intestinalis"  
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/db\_xref="taxon:7719"  
/clone="rc1hc001m03"  
/issue\_type="heart"

QY 1 GGGUCCUGAG 12  
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REFERENCE  
1 (bases 1 to 165)  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Zusatzinformation: 1 (bases 1 to 165)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, P., Trivaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

## TITLE

The Mashu-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Insert Size: 1066

High quality sequence stops: 118

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 1066 Std Error: 0.00

Seq primer: M13Rpl

High quality sequence stop: 118.

## FEATURES

## source

Location/Qualifiers

1..185

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3830487"

/db\_xref="taxon:9606"

/clone="IMAGE:192271"

/sex="Male"

/dev\_stage="55-year old"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares adult brain N294HB55"

/note="Organ: brain; Vector: pT713D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTCGAGCGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

## ORIGIN

## Query Match

Best Local Similarity 66.7%; Score 12; DB 7; Length 185;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12

||||:|||||

Db 38 GGGGTCTCGAG 27

## RESULT 156

## BB281821

## LOCUS

## DEFINITION

BB281821 RIKEN full-length enriched, adult retina Mus musculus cDNA

## ACCESSION

BB281821

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

BB281821 186 bp mRNA linear EST 01-AUG-2000  
Clone A930033K16 3', mRNA sequence.  
BB281821.1 GI:8982270  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 186)

Komno, H., Akawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kodama, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saico, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toyota, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamane, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermostabilization and thermoactivation of thermostable enzymes by trehalose and its application for the syntheses of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kikuchi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

## FEATURES

## source

Location/Qualifiers

1..186

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="A930033K16"

/tissue\_type="retina"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="RIKEN full-length enriched, adult retina"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTTCAGATTAATTAATTCCTCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I. -Retina RNA was provided by Stefano Giarinich, Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA, whose assistance we gratefully acknowledge."

## ORIGIN

## Query Match

Best Local Similarity 66.7%; Score 12; DB 2; Length 186;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
 |||||:|||||  
 Db 102 GGGGTCCTGAG 113

RESULT 157  
 CE739078 188 bp DNA linear GSS 30-SEP-2003  
 LOCUS tigr-gss-dog-17000330307476 Dog library Canis familiaris genomic,  
 DEFINITION genomic survey sequence.  
 ACCESSION CE739078  
 VERSION CE739078.1 GI:37079340  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Canis familiaris (dog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 188)  
 Kirchner, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Ruch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 22875432  
 14512627  
 CONTACT: Kirchner EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirchner@tigr.org  
 Class: shotgun.

FEATURES  
 source location/Qualifiers  
 1..188  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

ORIGIN  
 Query Match 66.7%; Score 12; DB 9; Length 188;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
 |||||:|||||  
 Db 1 GGGGTCCTGAG 12

RESULT 158  
 CD016191 189 bp mRNA linear EST 07-MAY-2003  
 LOCUS NC01 029 C01 F NC01 (Nsf Xylem Compression wood Inclined) Pinus  
 DEFINITION taeda cDNA clone NC01\_029\_C01 5', mRNA sequence.  
 ACCESSION CD016191  
 VERSION CD016191.1 GI:30354841  
 KEYWORDS EST.  
 SOURCE Pinus taeda (loblolly pine)  
 ORGANISM Pinus taeda (loblolly pine)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
 1 (bases 1 to 189)  
 Sederoff, R.  
 Molecular Basis of Wood Formation in the Pine Megagenome  
 Unpublished (2000)  
 Contact: Sederoff, Ron  
 Forest Biotechnology

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

North Carolina State University  
 840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
 NC 27695, USA  
 Tel: 919 515 7800  
 Fax: 919 515 7801  
 Email: ron\_sederoff@ncsu.edu, jerry\_johnson@ncsu.edu  
 Please see http://web.ahc.unm.edu/biodata/nsfpine/ for further  
 information.  
 Seq primer: T3.

FEATURES  
 source location/Qualifiers  
 1..189  
 /organism="Pinus taeda"  
 /mol\_type="mRNA"  
 /strain="Coastal plain loblolly pine from North Carolina"  
 /db\_xref="taxon:3352"  
 /clone\_lib="NC01 029 C01"  
 /tissue\_type="Xylem"  
 /cell\_type="Compression"  
 /dev\_stage="Juvenile"  
 /lab\_host="X11-Blue"  
 /clone\_lib="NC01 (Nsf Xylem Compression wood Inclined)"  
 /note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:  
 XhoI; The library is from early (spring) wood, taken from  
 three six-year old trees (three different genotypes), in  
 the juvenile phase. These trees were induced to form  
 compression wood by bending to a 45 degree angle and tying  
 them to the ground. Differentiating xylem was harvested  
 from the bottoms of the inclined stems, and a mixture of  
 all three genotypes was used for the library. oligo-dr  
 primed cDNA was directionally cloned into the EcoRI-XhoI  
 Bluescript SK vector arms. NOTE: The sequences contain a  
 'cDNA adapter' between the EcoRI site and the start of the  
 EST. The adapter sequence is 'AATTGACACGAG'."

ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 189;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
 |||||:|||||  
 Db 63 GGGGTCCTGAG 74

RESULT 159  
 CD612432/c 190 bp mRNA linear EST 12-JAN-2004  
 LOCUS 56086375H1 FLP Homo sapiens cDNA, mRNA sequence.  
 DEFINITION CD612432  
 ACCESSION CD612432  
 VERSION CD612432.1 GI:40260696  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 190)  
 Fu, G.K., Wang, J.T., Yang, J., Au-Yang, J. and Stuve, L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 CONTACT: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com.

FEATURES  
 source location/Qualifiers  
 1..190  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 190;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
 |||||:|||||  
 |||||:|||||  
 Db 21 GGGGCTCTGGAG 10

RESULT 160  
 CE683453 190 bp DNA linear GSS 29-SEP-2003  
 LOCUS tigr-gss-dog-17000314478830 Dog library Canis familiaris genomic,  
 DEFINITION genomic survey sequence.  
 CE683453  
 ACCESSION CE683453.1 GI:37002489  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Canis familiaris (dog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 190)  
 Kirchner, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)

TITLE  
 JOURNAL The dog genome: survey sequencing and comparative analysis  
 MEDLINE Science 301 (5641), 1898-1903 (2003)  
 PUBMED 14512627

COMMENT  
 Contact: Kirchner EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirchner@tigr.org  
 Class: shotgun.

FEATURES  
 source Location/Qualifiers  
 1..190  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

ORIGIN  
 Query Match 66.7%; Score 12; DB 9; Length 190;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
 |||||:|||||  
 |||||:|||||  
 Db 158 GGGGCTCTGGAG 169

RESULT 161  
 BF832234 191 bp mRNA linear EST 13-JAN-2001  
 LOCUS PM3-HT0925-181000-004-c12 HT0925 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION  
 BF832234  
 ACCESSION BF832234.1 GI:12180760  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE Homo sapiens (human)

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 191)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matukuma, A., Bata, G.S., Simpson, D.H.,

Brustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the PAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM862=PM3-HT0925-  
 181000-004-c12&t3=2000-10-18&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 3  
 High quality sequence stop: 191.

FEATURES  
 source Location/Qualifiers  
 1..191  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="HT0925"  
 /note="Organ: head neck; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORSTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 191;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
 |||||:|||||  
 |||||:|||||  
 Db 142 GGGGCTCTGGAG 153

RESULT 162  
 CD612433 191 bp mRNA linear EST 12-JAN-2004  
 LOCUS 5608637501 FLP Homo sapiens cDNA, mRNA sequence.  
 DEFINITION  
 CD612433  
 ACCESSION CD612433.1 GI:40260697  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE Homo sapiens (human)

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 191)  
 Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)

COMMENT  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com

FEATURES  
 source Location/Qualifiers  
 1..191  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

ORIGIN  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /note="Vector: pDrive Cloning Vector"

Query Match 66.7%; Score 12; DB 6; Length 191;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 170 GGGGTCCTGGAG 181

RESULT 163  
 LOCUS CV298789/c 191 bp mRNA linear EST 23-SEP-2004  
 DEFINITION EST887248 petunia floral post-pollination cDNA library Petunia x hybrida cDNA clone Petunia-PP-12-D03 5' end, mRNA sequence.  
 ACCESSION CV298789  
 VERSION CV298789.1 GI:52592435  
 KEYWORDS EST.  
 SOURCE Petunia x hybrida  
 ORGANISM Petunia x hybrida  
 BUKARYOTA; VIRIDIPHYTES; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Petunia.  
 1 (bases 1 to 191)  
 Shibusaki, K., Underwood, B., Loucas, H., Farmerie, W., Jones, M. and Clark, D.  
 Petunia x hybrida EST collection  
 Unpublished (2004)  
 Contact: David Clark  
 UF Horticulture Biotechnology Lab  
 University of Florida  
 Environmental Horticulture Department, 1545 Fifield Hall, Box 110670, Gainesville, FL 32611-0670, USA  
 Tel: 352-392-1831 x370  
 Fax: 352-392-3870  
 Email: dclark@mail.ifas.ufl.edu  
 Contact Dr. Clark (dclark@mail.ifas.ufl.edu) for clone information  
 Seq primer: T3 primer.  
 Location/Qualifiers  
 1..191

FEATURES  
 source  
 1..191  
 Location/Qualifiers  
 /organism="Petunia x hybrida"  
 /mol\_type="mRNA"  
 /cultivar="Mitchell Diploid (aka. Mitchell, aka W15 in Europe)"  
 /db\_xref="taxon:4102"  
 /clone="Petunia-PP-12-D03"  
 /tissue\_type="all floral organs"  
 /lab\_host="lambda ZAP11 unidirectional"  
 /clone\_lib="petunia floral post-pollination cDNA library"  
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; supplier: Petunia x hybrida cv. Mitchell Diploid plants were grown from seeds to a fully flowering stage under standard greenhouse conditions. Flowers at anthesis stage were self-pollinated and entire flowers were collected at 0, 5, 10, 24, 36 and 48 hours after pollination from plants grown in standard greenhouses. Total RNA was extracted from each sample, and 100 micrograms of each sample was combined for subsequent poly A+ mRNA selection and cDNA synthesis."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 191;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 43 GGGGTCCTGGAG 32

Db

RESULT 164  
 LOCUS CF613742 192 bp mRNA linear EST 01-OCT-2003  
 DEFINITION CES007966 Bos taurus fat cDNA library Bos taurus cDNA clone  
 CCL007966 5', mRNA sequence.  
 ACCESSION CF613742  
 VERSION CF613742.1 GI:37238840  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 192)  
 Wang, Y.H., Byrne, K., Vuocolo, T., Tan, S.H., McWilliam, S., Dierens, L. and Lehnert, S.  
 Transcription profiling of bovine skeletal muscle and subcutaneous fat

TITLE Unpublished (2003)  
 CONTACT: Dr Sigrid Lehnert  
 Functional Genomics Lab  
 CSIRO Livestock Industries  
 Level 5, Queensland Bioscience Precinct, University of Queensland,  
 306 Carmody Road St. Lucia QLD Australia  
 Tel: 07 3214 2445  
 Fax: 07 3214 2480  
 Email: Sigrid.lehnert@csiro.au  
 Plate: 02 row: H column: 02.  
 Location/Qualifiers  
 1..192

FEATURES  
 source

1..192  
 Location/Qualifiers  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /strain="Angus"  
 /db\_xref="taxon:9913"  
 /clone="CCL007966"  
 /sex="male"  
 /tissue\_type="subcutaneous fat tissue"  
 /dev\_stage="Young Adult"  
 /lab\_host="XL1-BlueMRF' strain"  
 /clone\_lib="Bos taurus fat cDNA library"  
 /note="Vector: Uni-ZAPXR; Site 1: EcoRI; Site 2: Xho I; library made from subcutaneous fat of a 14 month old Angus steer."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 192;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 27 GGGGTCCTGGAG 38

Db

RESULT 165  
 LOCUS CG987201/c 192 bp DNA linear GSS 15-DEC-2003  
 DEFINITION CH240\_158J01.TJ CHORI-240 Bos taurus genomic clone CH240\_158J01, genomic survey sequence.  
 ACCESSION CG987201  
 VERSION CG987201.1 GI:39912980  
 KEYWORDS GSS.

SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 192)  
 Costa, J.N., Mota, M. and Gaetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)

JOURNAL

## COMMENT

Other GSSs: CH240.158J01.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658

Email: acetanoc@embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/ordering/information.htm).  
 Bases shown have Phred quality value equal to or higher than 20.  
 For BAC library availability, please contact Pieter de Jong  
 (pje@ngemall.chi.cho.org).

Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 158 row: J column: 01  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 192.

## FEATURES

source Location/Qualifiers

1..192  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_158J01"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pPRABAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 192;

Best Local Similarity 91.7%; Pred. No. 2.2e+04;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNN 18

Db 39 CTGAGNNNNN 28

## RESULT 166

CE424526

LOCUS CE424526 193 bp DNA linear GSS 27-SEP-2003

DEFINITION tigr-gss-dog-17000362791914 Dog library Canis familiaris genomic,

genomic survey sequence.

ACCESSION CE424526 GI:36692430

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Canis familiaris (dog)  
 Canis familiaris  
 Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 193)  
 Kirksnes, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Kirksnes EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA

## FEATURES

source

Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

Location/Qualifiers  
 1..193  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 193;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12

Db 82 GGGGTCCTGGAG 93

## RESULT 167

BM238031

LOCUS

DEFINITION BM238031 194 bp mRNA linear EST 07-JUN-2003

CDNA Library (Long) Mus musculus cDNA clone NIA:K0511B01

IMAGE:30064908 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

JOURNAL

MEDLINE

PUBMED

COMMENT

COMMENT

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COMMENT

Program, NIH (<http://igsn.gsc.nia.nih.gov/cdna>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen: 5'-pGACTGATCTTTCATCGGAGCGCCGCTTTT-3') from 4.8 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker IL-Sal4, purified by phenol/chloroform, and separated from free linkers by centrifugation 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.7 kb. The library was constructed by Yulan Piao (NIA)."

## ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 194;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
DB 57 GGGGTCCTGGAG 68

RESULT 168  
B017291/c  
LOCUS B017291 195 bp mRNA linear EST 22-JUN-2000  
DEFINITION musculus cDNA clone 4930567J02 3', mRNA sequence.  
VERSION B017291  
KEYWORDS B017291.1 GI:8186607  
SOURCE EST.  
ORGANISM Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 195)

REFERENCE  
AUTHORS Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukumishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamuro, T., Yamana, K., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE  
JOURNAL  
COMMENT RIKEN Mouse ESTs (Komno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.jp, URL: <http://genome-gsc.riken.jp/>  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagakura, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Thermoequilization and thermoequilization of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

## FEATURES

## source

Itoh, M., Katsunari, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (<http://genome.rcc.riken.go.jp/>) for further details.

## Location/Qualifiers

1..195  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="4930567J02"  
/sex="male"  
/tissue\_type="testis"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_1ib="RIKEN full-length enriched, adult male testis (DH10B)"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATTCGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGCTCTTTTCTTTTCTTTTCTTTT 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda phage I. Cloning sites, 5' end: SalI, 3' end: BamHI."

## ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 195;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
DB 51 GGGGTCCTGGAG 40

RESULT 169  
B1047499  
LOCUS B1047499 195 bp mRNA linear EST 14-JUN-2001  
DEFINITION MR4-ST0240-080101-024-g07 ST0240 Homo sapiens cDNA, mRNA sequence.  
VERSION B1047499  
KEYWORDS B1047499.1 GI:14454121  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 195)

REFERENCE  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE  
JOURNAL  
MEDLINE  
PUBMED Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800



## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&cl2=MR4-ST0240-080101-024-g07&cl3=2001-01-08&cl4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 35  
High quality sequence stop: 195.

## FEATURES

Location/Qualifiers  
1..195

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="ST0240"  
/note="Organ: stomach; Vector: puc18; Site: 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORSRES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 195;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
||||:|||||

Db 184 GGGGTCTCGAG 195

## RESULT 170

LOCUS CVO25592 195 bp mRNA linear EST 20-AUG-2004  
DEFINITION 3333 Full length cDNA from the Mammalian Gene Collection Homo  
sapiens cDNA 5' similar to BC000262, mRNA sequence.

## ACCESSION

VERSION CVO25592  
KEYWORDS CVO25592.1 GI:51483533

## SOURCE

ORGANISM Homo sapiens (human)

Homosapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

## AUTHORS

Rui J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,  
1 (bases 1 to 195)  
Clingingemith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,  
Stamons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,  
Haudenaut, J., Cusick, M.E., Alcala, J.S., Hill, D.E. and Vidal, M.  
Human ORFeome Version 1.1: a platform for Reverse Proteomics  
Genome Res. (2004) In press  
Contact: Vidal M

## TITLE

## JOURNAL

## COMMENT

Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu  
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF  
results from a PCR reaction using an MGC full-length cDNA as  
template DNA and ORF specific primers  
PCR Primers  
FORWARD: ATGAGCTGAGAGAGATCGT  
BACKWARD: TATGCGTATCAGCATCATGTA

Insert Length: 195 Std Error: 130.00  
Plate: 11084 row: 06 column: A  
Seq primer: ACTGCGCTGCTTTACACATCTGACTGGAGAAC  
High quality sequence start: 99  
High quality sequence stop: 194  
POLYA=No.

## FEATURES

## source

Location/Qualifiers  
1..195  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="mixed"  
/clone\_lib="Full length cDNA from the Mammalian Gene  
Collection"  
/note="Vector: mixed; The ORFs were PCR amplified from the  
MGC (Mammalian Gene Collection) as of April 2004 and  
cloned by recombinational Gateway cloning into pDONR223  
Donor vector. Reference: MGC (Mammalian Gene Collection)  
Program Team, Generation and Initial Analysis of more than  
15,000 Full-length Human and Mouse cDNA Sequences. PNAS,  
2002, 99(26), 16899-16903"

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 195;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
||||:|||||

Db 109 GGGGTCTCGAG 120

## RESULT 171

LOCUS D45320 195 bp mRNA linear EST 30-DEC-1995  
DEFINITION HUMHG5144 Human cerebral cortex Homo sapiens cDNA, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Homosapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

Contact: Nobuaki Takahashi  
Institute of Medical Science  
University of Tokyo  
Shirokanedai 4-6-1, Minato-ku, Tokyo, Japan 108  
Tel: 03-5449-5625  
Fax: 03-5449-5445.

## FEATURES

## source

Location/Qualifiers  
1..195  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="Human cerebral cortex"  
/note="Adult male cerebral cortex tissue."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 195;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
||||:|||||

Db 9 GGGGTCTCGAG 20

RESULT 172  
 AM836385 196 bp mRNA linear EST 18-MAY-2000  
 DEFINITION PMO-LT0030-101299-001-h04 LT0030 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AM836385  
 VERSION AM836385.1 GI:7930359  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 196)  
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et2-PMO-LT0030-101299-001-h04&t3=1999-12-10&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 3  
 High quality sequence stop: 196.  
 Location/Qualifiers  
 1..196  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="LT0030"  
 /note="Organ: leiomyos; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 196;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCGCGAG 12  
 |||||:  
 Db 37 GGGGCTCTGGAG 48

RESULT 173  
 CF162671/c 197 bp mRNA linear EST 25-JUL-2003  
 DEFINITION B0715A10-5 NIA Mouse Embryonic Germ Cell cDNA Library (Long) Mus  
 ACCESSION musculus cDNA clone NIA:B0715A10 IMAGE:30459273 5', mRNA sequence.  
 VERSION CF162671  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 197)  
 Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.  
 Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method  
 Genome Res. 11 (9), 1553-1558 (2001)  
 JOURNAL MEDLINE 21429098  
 PUBMED 11544199  
 COMMENT Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@lgsun.grc.nia.nih.gov  
 Plate: B0715 row: A column: 10  
 Seq primer: M13 Reverse  
 High quality sequence stop: 197  
 POLYA=No.  
 Location/Qualifiers  
 1..197  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taeEST:B0715A10-5"  
 /db\_xref="taxon:10090"  
 /clone="NIA:B0715A10 IMAGE:30459273"  
 /sex="male"  
 /dev\_stage="embryonic day 8"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse Embryonic Germ Cell cDNA Library (Long)"  
 /note="Vector: pCMV-SPORT6 (Invitrogen); Site\_1: SalI; Site\_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Mark G. Carter (NIH/NIA-IRP). EG cells were cultured at 37. C, 5% CO2 in DMEM supplemented with 15% ES cell-qualified FBS, 0.1mM non-essential amino acids, 1 mM glutamine, penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 1000000 units of LIF per liter. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen):  
 5'-POACTAGTCTAGATCGGCGCGCCGCTTTT-3' from 2.5 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LR-Sa14, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 4.0 kb. The library was constructed by Yulan Piao."

ORIGIN  
 Query Match 66.7%; Score 12; DB 7; Length 197;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCGCGAG 12  
 |||||:  
 Db 102 GGGGCTCTGGAG 91

RESULT 174

AA337180 200 bp mRNA linear EST 21-APR-1997  
 LOCUS AA337180  
 DEFINITION Endometrial tumor Homo sapiens cDNA 5' end, mRNA sequence.  
 ACCESSION AA337180  
 VERSION 1 GI:1989417  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 200)  
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Clifton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Gladek,A., Ghehmi,C.B., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmasos,S.M., Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shiley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Fairfax,A., Fischer,C., Hastings,G.A., He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weisener,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,N.A., Fields,C., Fraser,C.M., and Venter,J.C.  
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
 MEDLINE 95026280  
 PUBMED 7566098  
 COMMENT Other\_ESTs: THC193172  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (inhost):138909"  
 /db\_xref="taxon:9606"  
 /sex="female"  
 /dev\_stage="adult"  
 /clone\_lib="Endometrial tumor"  
 /note="Organ: endometrium; Vector: pBluescript SK-"  
 Site\_1: EcoRI; Site\_2: XhoI

ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 200;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
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 Db 22 GGGGTCCTGGAG 33

RESULT 175  
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 LOCUS BE398334  
 DEFINITION WHE0010.E12P000701 ITTC WHE wheat Endospem Library Triticum aestivum cDNA clone WHE0010.E12, mRNA sequence.  
 ACCESSION BE398334

VERSION BE398334.1 GI:9357808  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poidea; Triticeae; Triticum.  
 REFERENCE 1 (bases 1 to 200)  
 AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrey,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioli,N., Qualset,C., Schuch,W., Selvaraj,G., Shrifton,M., Sorrells,M., Warburton,M., and Wenzel,G.  
 International Triticaceae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticaceae Unpublished (2000)  
 JOURNAL USDA ARS WRC  
 CONTACT: Anderson OA  
 800 Buchanan Street, Albany, CA 94710-1105 USA  
 Tel: 510 559 5773  
 Fax: 510 559 5818  
 Email: oanderson@wrc.usda.gov  
 International Triticaceae EST Cooperative (ITEC)  
<http://wheat.pw.usda.gov/genome>.  
 Location/Qualifiers  
 1..200  
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 /mol\_type="mRNA"  
 /cultivar="Cheyenne"  
 /db\_xref="taxon:4565"  
 /clone="WHE0010.E12"  
 /tissue="endospem"  
 /dev\_stage="5-30 days post anthesis"  
 /clone\_lib="ITEC WHE wheat Endospem Library"  
 /note="Vector: Lambda ZAPII; Wheat Endospem Library constructed in Lambda ZAPII with 8-mer adapter."

ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 200;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
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 Db 167 GGGGTCCTGGAG 156

RESULT 176  
 BE1047779 200 bp mRNA linear EST 14-JUN-2001  
 LOCUS BE1047779  
 DEFINITION MR4-ST0240-310101-029-e01 ST0240 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BE1047779  
 VERSION B1047779.1 GI:14454401  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 200)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Bioness,M.R., Negai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4&t2=MR4-ST0240-  
310101-029-e01&t3=2001-01-31&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 68  
High quality sequence stop: 200.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="ST0240"  
/note="Organ: stomach; Vector: puc18; Site\_1: Sma1;  
Site\_2: Sma1; A man1-library was made by cloning products  
derived from ORSITES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 200;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
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Db 161 GGGGTCCTGGAG 172

RESULT 177  
A2791991 201 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0043H07F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCG2M0043H07 F, genomic survey sequence.  
ACCESSION A2791991  
VERSION A2791991.1 GI:12935458  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 201)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Niederhauer, A., and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
UNIVERSITY OF UTAH  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0043 row: H column: 07  
Seq primer: CGTTGTAAACGACGCGCCACT  
Class: plasmid ends  
High quality sequence stop: 201.  
Location/Qualifiers  
1..201

## ORIGIN

Query Match 66.7%; Score 12; DB 8; Length 201;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
||||:|||||  
Db 62 GGGGTCCTGGAG 73

RESULT 178  
A1503108/c 203 bp mRNA linear EST 11-MAR-1999  
LOCUS vm92a11.x1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA  
DEFINITION clone IMAGE:1005692 3', mRNA sequence.  
ACCESSION A1503108  
VERSION A1503108.1 GI:4400959  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 203)  
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,  
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
CONTACT: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LINT; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:569908  
This clone was previously sequenced on the 5' end only, this new  
data is from the 3' end  
Seq primer: Primer name ambiguous.  
Location/Qualifiers  
1..203  
/organism="Mus musculus"

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/mol_type="mRNA"
/strain="CS7BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:1005692"
/libase_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
/clone_lib="Knowles Solter mouse blastocyst B1"
/note="Organ: embryo; Vector: pSPORT; Site_1: Nct1; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(dT): 5'-CGTCCGACCGTCGACCGCTTTTCTTTT-3'. cDNAs were cloned into the Nct1/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger inserts) and B3."

ORIGIN
Query Match      66.7%; Score 12; DB 1; Length 203;
Best Local Similarity 83.3%; Pred. No. 2.2e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 GGGGUCCTCGAG 12
||||:|||||
Db      167 GGGGTCTCTGAG 156

RESULT 179
AW204396/c 203 bp mRNA linear EST 02-DEC-1999
DEFINITION
U-H-B11-adv-d-04-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2718007 3', mRNA sequence.
ACCESSION
AW204396
VERSION
AW204396.1 GI:6503868
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 203)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/BLN at:
www.bio.lit.nih.gov/bdrip/image/image.html
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source
Location/Qualifiers
1..203
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2718007"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP_Sub3"
/note="Vector: pT7TD-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI-CGAP Sub3 library is a subcloned library derived from
the NCI CGAP Sub1 library, which is a subcloned library
normalized or subcloned NCI CGAP libraries:
NCI-CGAP_Co4, NCI-CGAP_P122, NCI-CGAP_P228, NCI-CGAP_Co10,
NCI-CGAP_Co16, NCI-CGAP_Kid5, NCI-CGAP_Kid12,
NCI-CGAP_Kid3, NCI-CGAP_Kid11, NCI-CGAP_Lym2,
NCI-CGAP_Br2, NCI-CGAP_Co8, NCI-CGAP_CLL1, NCI-CGAP_Le12,
NCI-CGAP_Brn3, NCI-CGAP_Lu5, NCI-CGAP_Lu24,
```

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NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6,
NCI CGAP Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI CGAP Kid3 pool 1 LAM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonides 1322376-1323911,
1456008-1456775, 1505552-1502855); NCI CGAP Kid5 pool 1
LAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonides
1333912-1325831, 1471368-1472903, 1492104-1493255);
NCI CGAP Lu5 pool 1 LAM 3575-3582, 3851-3854 (IMAGE
Clonides 1414920-1417991, 1520904-1522439); NCI CGAP GC4
pool 1 LAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
Clonides 1257096-1258631, 1458064-1470983, LAM 2457-2459,
1475592-1476743); NCI CGAP P122 pool 1 LAM 2758-2759,
3062-3068 (IMAGE Clonide 985608-986759,
1101192-1101959, 1217928-1220615); NCI CGAP Co10 pool 1
LAM 2644-2653, 2871-2872 (IMAGE Clonides 1057416-1061255,
114584-1145351). Subtraction was performed as previously
described [Bonaldo, Lennon & Soares (1996): Normalization
and Subtraction: Two Approaches to Facilitate Gene
Discovery, Genome Research 6, 791-806.
TAG TISSUE=kidney
TAG LIB=NCI CGAP_Kid3
TAG_SEQ=ATGCG"

ORIGIN
Query Match      66.7%; Score 12; DB 2; Length 203;
Best Local Similarity 83.3%; Pred. No. 2.2e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 GGGGUCCTCGAG 12
||||:|||||
Db      129 GGGGTCTCTGAG 118

RESULT 180
BB246707 203 bp mRNA linear EST 06-JUL-2000
DEFINITION
BB246707 RIKEN full-length enriched, 7 days neonate cerebellum Mus
musculus cDNA clone A730015K23 3', mRNA sequence.
ACCESSION
BB246707
VERSION
BB246707.1 GI:8939453
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 203)
Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadoya, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watanabe, A.,
Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A.,
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
Hayashizaki, Y.
RIKEN Mouse ESTs (Kono, H., et al.)
Unpublished (2000)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9216
Email: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,
```

Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Thermotransformation and thermotransformation of thermotransformable enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kikuchi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Okazaki, Y., and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P., and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

#### FEATURES

##### source

1. 203  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="A730015K23"  
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cerebellum"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5',  
GAGAGAGAGATTCGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
transcribed and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 20.0 and subtraction to Rot = 459.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGATTCGAGCTCTTTTCTTTTCTTTT 3']. cDNA was  
modified pluscript KS(+) after bulk excision from Lambda  
FLC I."

##### ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 203;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
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Db 119 GGGGTCCTCGAG 130

RESULT 181  
BB523008/c 204 bp mRNA linear EST 28-JUL-2000  
LOCUS BB523008 RIKEN full-length enriched, 15 days embryo head Mus  
DEFINITION musculus cDNA clone D930011G06 3', mRNA sequence.  
ACCESSION BB523008  
VERSION BB523008.1 GI:9574466  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

#### REFERENCE

##### AUTHORS

Komuro, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,  
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,  
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,  
Okazaki, Y., Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K.,

#### TITLE

##### JOURNAL

Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,  
Takahashi, F., Tomimura, N., Toya, T., Tsunoda, Y., Wachihi, A.,  
Watanabe, S., Yamamura, T., Yamanka, I., Yano, R., Yasunishi, A.,  
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and  
Hayashizaki, Y.  
RIKEN Mouse ESTs (Kono, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagao, S.,  
Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Thermotransformation and thermotransformation of thermotransformable enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kikuchi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Okazaki, Y., and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P., and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

#### FEATURES

##### source

1. 204  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
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/sex="mixed"  
/tissue\_type="head"  
/dev\_stage="15 days embryo"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 15 days embryo  
head"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5',  
GAGAGAGAGATTCGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
transcribed and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5',  
GAGAGAGATTCGAGCTCTTTTCTTTTCTTTT 3']. cDNA  
was cloned into the XhoI and BamHI sites. Vector: a  
modified pluscript KS(+) after bulk excision from Lambda  
FLC I."

##### ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 204;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
||||:|||||  
Db 78 GGGGTCCTCGAG 67

RESULT 182  
CB935713

LOCUS CB935713 205 bp mRNA linear EST 29-APR-2003  
 DEFINITION tab5a01.x1 Hydra EST -III Hydra magnipapillata cDNA 3' similar to  
 ACCESSION TR:000484 Q00484 MINI-COLLAGEN PRECURSOR.; mRNA sequence.  
 VERSION CB935713  
 KEYWORDS EST.  
 SOURCE GI:30221104  
 ORGANISM Hydra magnipapillata  
 Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;  
 Hydridae; Hydra.  
 1 (bases 1 to 205)  
 Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,O.,  
 Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,  
 Hillier,L., Martin,J., Wyllie,T., Dante,M., Theising,B., Bowers,Y.,  
 Gibbons,M., Ritter,E., Bennett,J., Konkoy,I., Teagarden,V.,  
 Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.  
 WASHU Hydra EST Project  
 Unpublished (2002)  
 TITLE WASHU Hydra EST Project  
 JOURNAL  
 COMMENT Contact: Hans Bode  
 WASHU Hydra EST Project  
 Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watsn.wustl.edu  
 Library was constructed by Bruce Blumberg & Jisong Pang, Univ. of  
 Calif. Irvine Library materials provided by Hans Bode & Lydia Gee,  
 Univ. of Calif., Irvine DNA sequencing by: Washington University  
 Genome Sequencing Center For information on obtaining a clone  
 please contact: Hans Bode (hrobde@uci.edu)  
 Trace considered overall poor quality  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..205  
 /organism="Hydra magnipapillata"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6085"  
 /lab\_host="DH10B"  
 /clone\_lib="Hydra EST -III"  
 /note="Vector: PCS22; Site 1: XhoI; Site 2: PstI; a) 1st  
 strand cDNA was primed with a XhoI oligo (dr) primer (5'  
 ACTAAGGGCTCGAG(T)18NN(3'; b) Double-stranded cDNA was  
 ligated to PstI linker, digested with PstI and XhoI and  
 cloned into the PstI and XhoI sites of a PCS22 vector,  
 which is a modified PCS2+ vector. c) The PCS22 vector  
 contains a T7 promoter site [standard from Bluescript] at  
 the 5' end of the cloning site, and a T3 promoter site  
 [standard from pBluescript] at the 3' end of the cloning  
 site. d) The ligation mix was transformed into TOP10P  
 cells (= DH10B cells). e) The cells were grown in SOC =  
 5% yeast, 20% tryptone, 0.5% NaCl, 10mM MgSO4, 10mM MgCl,  
 0.2% glucose/liter, (no antibiotic). f) The frequency of  
 vectors containing inserts is >90% [42 of 42]. g) The  
 average size of the 42 inserts is 1075 +/- 8501."

ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 205;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCCTCGAG 12  
 |||||:  
 Db 124 GGGGCTCTCGAG 135

RESULT 183  
 AM53129 206 bp mRNA linear EST 25-APR-2001  
 LOCUS AM53129  
 DEFINITION 34973 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION AM53129  
 VERSION AM53129.1 GI:6852119  
 KEYWORDS EST.

SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 206)  
 Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,  
 Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,  
 Chitko-McKown,C.G., Perte,G., Holt,I., Karaycheva,S., Liang,F.,  
 Quackenbush,J. and Keefe,J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle  
 Genome Res. 11 (4), 626-630 (2001)  
 21180013  
 11282978  
 TITLE JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 20  
 and -mismatch 12 options.  
 PCR primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCACACTCAGCAG  
 Plate: 16 row: H column: 13  
 Seq primer: ATTGAGTGACACTATAG.  
 Location/Qualifiers  
 1..206  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /cblseq\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 2BOV"  
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;  
 Library made from pooled tissue from testis, thymus,  
 semitendinosus muscle, longissimus muscle, pancreas,  
 adrenal, and endometrium."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 206;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCCTCGAG 12  
 |||||:  
 Db 40 GGGGCTCTCGAG 29

RESULT 184  
 N84369 207 bp mRNA linear EST 01-APR-1996  
 LOCUS N84369  
 DEFINITION KK8245F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA  
 clone KK8245 5' similar to EST(Y163C04.R1), mRNA sequence.  
 ACCESSION N84369  
 VERSION N84369.1 GI:1259994  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 207)  
 Liew C.C.  
 cDNAs from fetal heart (1996)  
 JOURNAL  
 COMMENT Unpublished (1996)  
 Contact: Liew CC  
 Brigham and Women's Hospital  
 Harvard Medical School  
 75 Francis St. Boston, MA 02115, USA

Tel: 6177328915  
Fax: 6179750995

Email: c1iewer@rics.bwh.harvard.edu  
Seq primer: GAAATTACCTCCTAAAGG.

## FEATURES

source

1..207  
Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="XK8245"

/lab\_host="E. coli XL1-Blue"

/clone\_lib="Human fetal heart, lambda ZAP Express"

/note="Vector: lambda ZAP Express; Site 1: EcoRI; Site 2: XhoI; mRNA was synthesized using a XhoI-011go cT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 207;  
Best Local Similarity 83.3%; Pred. NO. 2.2e+04;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
||||:|||||

Db 55 GGGGTCCTCGAG 66

## RESULT 185

AM353798/c

LOCUS 208 bp mRNA linear EST 09-JUL-2000  
DEFINITION 33497 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.  
ACCESSION AM353798  
VERSION AM353798.1 GI:6852725

KEYWORDS EST.

SOURCE Sus scrofa (pig)

## REFERENCE

AUTHORS

## TITLE

Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,  
Vallier, J., Wise, T., Rohrer, G.A., Perlee, G., Sultana, R.,  
Quackenbush, J., and Keele, J.W.  
Porcine gene discovery by normalized cDNA-library sequencing and  
EST cluster assembly

Mamm. Genome 13 (8), 475-478 (2002)

JOURNAL MEDLINE  
PUBMED 22213789

## COMMENT

12226715  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390

Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.960904.e. Vector identified by cross\_match with the -minscore 20  
and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGTATGACCAT  
BACKWARD: GTTTCCTCAGCAGCAGC

Plate: 19 Row: C Column: 20  
Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

1..208

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/tissue\_type="pooled"

/lab\_host="DH10B"

/clone\_lib="MARC 2P1G"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from testis, ovary,

Library made from pooled tissue from testis, ovary,

## ORIGIN

endometrium, hypothalamus, pituitary, and placenta."

Query Match 66.7%; Score 12; DB 2; Length 208;  
Best Local Similarity 83.3%; Pred. NO. 2.2e+04;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
||||:|||||

Db 164 GGGGTCCTCGAG 153

## RESULT 186

BI017022

LOCUS 208 bp mRNA linear EST 13-JUN-2001  
DEFINITION PM3-ET0207-300301-012-c03 ET0207 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BI017022

VERSION BI017022.1 GI:14421093

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 208)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE  
PUBMED 20202663

COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the RAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM3-ET0207-  
300301-012-c03&t3=2001-03-30&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 8  
High quality sequence stop: 183.

Location/Qualifiers

1..208

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev stage="Adult"

/clone\_lib="ET0207"

/note="Organ: lung\_tumor; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORST35 PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 208;  
Best Local Similarity 83.3%; Pred. NO. 2.2e+04;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
||||:|||||

Db 184 GGGGTCCTCGAG 195



RESULT 187  
CE614056/c  
LOCUS  
DEFINITION CE614056 208 bp mRNA linear EST 01-OCT-2003  
CE5013429 Bos taurus fat cDNA library Bos taurus cDNA clone  
CC011537 NULL, mRNA sequence.  
ACCESSION CE614056  
VERSION CE614056.1 GI:37239434  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 208)  
Wang,Y.H., Byrne,K., Vuocolo,T., Tan,S.H., McWilliam,S., Dierens,L.  
and Lehnert,S.  
Transcription profiling of bovine skeletal muscle and subcutaneous  
fat  
TITLE Unpublished (2003)  
JOURNAL Contact: Dr Sigrid Lehnert  
COMMENT Functional Genomics Lab  
CSIRO Livestock Industries  
Level 5, Queensland Bioscience Precinct, University of Queensland,  
306 Carmody Road St. Lucia QLD Australia  
Tel: 07 3214 2445  
Fax: 07 3214 2480  
Email: Sigrid.Lehnert@csiro.au  
Plate: 25 row: H column: 11.  
FEATURES  
SOURCE Location/Qualifiers  
1..208  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Angus"  
/db\_xref="taxon:9913"  
/clone="CCL011537"  
/sex="male"  
/tissue\_type="subcutaneous fat tissue"  
/dev\_stage="Young Adult"  
/lab\_host="XL1-BlueMRF'strain"  
/clone\_lib="Bos taurus fat cDNA library"  
/note="Vector: Uni-ZAPXR; Site 1: EcoRI; Site 2: Xho I;  
Library made from subcutaneous fat of a 14 month old Angus  
steer."  
ORIGIN  
Query Match 66.7%; Score 12; DB 7; Length 208;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGAG 12  
||||:||||  
Db 76 GGGGTCTCGAG 65  
RESULT 188  
CE743112  
LOCUS  
DEFINITION CE743112 208 bp DNA linear GSS 30-SEP-2003  
tigr-gss-dog-17000315835346 Dog library Canis familiaris genomic,  
genomic survey sequence.  
ACCESSION CE743112  
VERSION CE743112.1 GI:37083459  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 208)  
Kirkness,E.F., Balfour,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.  
FEATURES  
SOURCE Location/Qualifiers  
1..208  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BclXI; Libraries were prepared from  
peripheral blood"  
ORIGIN  
Query Match 66.7%; Score 12; DB 9; Length 208;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGAG 12  
||||:||||  
Db 165 GGGGTCTCGAG 176  
RESULT 189  
A1594283  
LOCUS 209 bp mRNA linear EST 21-APR-1999  
DEFINITION vm2a11.y1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA  
clone IMAGE:1005692 5', mRNA sequence.  
ACCESSION A1594283  
VERSION A1594283.1 GI:4603331  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 209)  
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Scepcoe,M., Theising,B., Allen,M., Bowers,Y.,  
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,  
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterston,R. and Wilson,R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LIND; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:569908  
This read is a RESSEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: -40RP.  
FEATURES  
SOURCE Location/Qualifiers  
1..209  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J x DBA/2J F1"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1005692"  
/tissue\_type="blastocyst"  
/dev\_stage="embryo (pre-implantation)"

/lab host="DH10B"  
 /clone\_lib="Knowles Solter mouse blastocyst B1"  
 /note="Organ: embryo; Vector: pSPORT; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally from mRNA prepared  
 from 800 blastocysts. Primer: SalI (dT):  
 5'-GGGTGACCGTCGACGGTCTTTTCTTT-3'. cDNAs were  
 cloned into the NotI/SalI sites of a pSPORT vector (Life  
 Technologies). Two different size selections: B1 (larger  
 inserts) and B3."

## ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 209;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
 |||||:  
 Db 47 GGGGTCTGTGAG 58

RESULT 190  
 LOCUS CV337093 209 bp mRNA linear EST 24-SEP-2004  
 DEFINITION IL5-HT0702-160600-098-907 HT0702 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CV337093  
 VERSION CV337093.1 GI:52660307  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

## AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bionesi, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsumura, A., Bata, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## JOURNAL

## MEDLINE

## PUBMED

10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. <http://www.ludwig.org.br>.

## FEATURES

## source

1. 209  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="HT0702"  
 /note="Organ: head, neck; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 209;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
 |||||:  
 Db 86 GGGGTCTGTGAG 75

## RESULT 191

LOCUS CL603743 209 bp DNA linear GSS 17-JUN-2004  
 DEFINITION CH240\_179103.TV CHORI-240 Bos taurus genomic clone CH240\_179103,  
 genomic survey sequence.  
 ACCESSION CL603743  
 VERSION CL603743.1 GI:48871775  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished (2003)  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final AV. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.choi.org).

Clones may be purchased from BACPAC Resources  
 (<http://www.chori.org/bacpac/ordering/information.htm>).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnológico (CNPq), Brazil  
 Place: 179 row: 1 column: 03  
 Seq primer: T7  
 Class: BAC ends

High quality sequence stop: 209.

## FEATURES

## source

1. 209  
 Location/Qualifiers  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_179103"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 209;  
 Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTGAGANNNNN 18  
 |||||:  
 Db 149 CTGAGANNNNN 160

## RESULT 192

LOCUS	BBO82813	210 bp	mRNA	linear	EST-28-JUN-2000
DEFINITION	BB082813 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone g930177G07.3 similar to D29763 mouse mRNA for seizure-related gene product 6, mRNA sequence.				
ACCESSION	BB082813				
VERSION	BB082813.1 GI:6647873				
KEYWORDS	EST.				
SOURCE	Mus musculus	(house mouse)			
ORGANISM	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	Mullaly, P., Endo, T., Fukuda, S., Fukuishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kuwabara, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watanaka, I., Watanabe, S., Yamamura, T., Yamagata, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.				
TITLE	RIKEN Mouse ESTs (Kono, H., et al.)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagasaki, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermostabilization and thermoinactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Katsunami, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, T., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site ( <a href="http://genome.rtc.riken.go.jp">http://genome.rtc.riken.go.jp</a> ) for further details.				
FEATURES	Location/Qualifiers				
SOURCE	1..210				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="Cs7BL/6J"				
	/db_xref="taxon:10090"				
	/clone="g930177G07"				
	/sex="male"				
	/tissue_type="dienecephalon"				
	/dev_stage="adult"				
	/lab_host="DH10B"				
	/clone_lib="RIKEN full-length enriched, adult male dienecephalon"				
	/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGGAGAGAGATCCAGAGCTCTTTTTCCTTTTTTTTNN 3'], cDNA was prepared by using retrovirus thermo-activated reverse				

ORIGIN	Query Match	66.7%;	Score 12;	DB 2;	Length 210;	
Best Local Similarity	83.3%;	Pred. No. 2.2e+04;				
Matches	10;	Conservative	2;	Mismatches	0;	Indels 0; Gaps 0;
Qy	1	GGGGUCCUGAG 12				
		:				
Db	86	GGGCTCTGGAG 75				
RESULT 193						
AL764056/c						
LOCUS						
DEFINITION	AL764056	210 bp	DNA	linear	GenSeq 01-APR-2004	
ACCESSION	Arabidopsis thaliana T-DNA flanking sequence GK-045H01-015475,					
VERSION	genomic survey sequence.					
KEYWORDS	AL764056					
SOURCE	AL764056.1	GI:21515877				
ORGANISM	GSS.					
	Arabidopsis thaliana (thale cress)					
	Arabidopsis thaliana					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
REFERENCE	1					
AUTHORS	Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.					
TITLE	GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana					
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)					
MEDLINE	22755829					
PUBMED	12874060					
REFERENCE	2					
AUTHORS	Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.					
TITLE	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics					
JOURNAL	Plant Mol. Biol. 53 (1-2), 247-259 (2003)					
MEDLINE	23117147					
PUBMED	14756321					
REFERENCE	3					
AUTHORS	Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.					
TITLE	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines					
JOURNAL	Biotechniques 35 (6), 1164-1168 (2003)					
MEDLINE	14682050					
PUBMED	4 (bases 1 to 210)					
REFERENCE	Strizhov, N., Li, Y., Rosso, M.G. and Weishaar, B.					
AUTHORS	Direct Submission					
TITLE	Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany					
JOURNAL	This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g23810.					
COMMENT	Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <a href="http://www.mpil-koeln.mpg.de/GABI-Kat/">http://www.mpil-koeln.mpg.de/GABI-Kat/</a> .					
	Location/Qualifiers					
FEATURES	1..210					
source	/organism="Arabidopsis thaliana"					
	/mol_type="genomic DNA"					

/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 210;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
DB 175 GGGGTCCTGGAG 164

RESULT 194  
CG988556/c 210 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_145E01.TV CHORI-240 Bos taurus genomic clone CH240\_145E01,  
DEFINITION genomic survey sequence.  
ACCESSION CG988556  
VERSION CG988556.1 GI:39914335  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
1 (bases 1 to 210)  
Costa, J.N., Mota, M. and Caetano, A.R.  
Brazill's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
JOURNAL Other GSSs: CH240\_145E01.TJ  
COMMENT Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acaetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cno.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnol6gico (CNPq), Brazil  
Plate: 145 row: E column: 01  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 210.  
Location/Qualifiers  
1..210

## FEATURES

source  
1..210  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="Breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_145E01"

/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull 13 Domingo 99373; CHORI-240 Bovine BAC  
Library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 210;  
Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTGAGNNNNN 18  
DB 164 CTGAGNNNNN 153

RESULT 195  
AA607115 211 bp mRNA linear EST 30-SEP-1997  
LOCUS VM92a11.r1 Knowles Solter mcuse blastocyst B1 Mus musculus cDNA  
DEFINITION clone IMAGE:1005692 5', mRNA sequence.  
AA607115  
ACCESSION AA607115.1 GI:2456008  
VERSION  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 211)  
Marrs, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubague, T.,  
Schellendberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterson, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
JOURNAL Contact: Marrs M/Mouse EST Project  
COMMENT WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watsn.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:569908  
putative full length read  
vector to vector length is 212.  
Location/Qualifiers  
1..211

## FEATURES

source  
1..211  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J x DBA/2J F1"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1005692"  
/tissue\_type="blastocyst"  
/dev\_stage="embryo (pre-implantation)"  
/lab\_host="DH10B"  
/clone\_lib="Knowles Solter mouse blastocyst B1"  
/note="Organ: embryo; Vector: pSPORT; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally from mRNA prepared  
from 800 blastocysts. Primer: SalI(dT):  
5'-CGGTCGACGCGACCGCTTTTCTTTT-3'. cDNAs were  
cloned into the NotI/SalI sites of a pSPORT vector (Life  
Technologies). Two different size selections: B1 (larger  
inserts) and B3."

## ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 211;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
 ||||:||||  
 Db 47 GGGGTCTCGAG 58

RESULT 196  
 LOCUS BM705448  
 DEFINITION UT-E-C11-afg-a-01-0-UI.r2 UI-E-C11 Homo sapiens cDNA clone  
 UT-E-C11-afg-a-01-0-UI 5', mRNA sequence.  
 BM705448 211 bp mRNA linear EST 28-FEB-2002

ACCESSION BM705448  
 VERSION BM705448  
 KEYWORDS  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 211)  
 Bernaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548

COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu

Tissue procurement: Dr. Gregg Hageman  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse

FEATURES  
 Source Location/Qualifiers

1..211  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UT-E-C11-afg-a-01-0-UI"  
 /tissue\_type="RPE and Choroid"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 UT-E-C11 is a normalized cDNA library containing the  
 following tissue(s): RPE and Choroid. The library was  
 constructed according to Bernaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is ACCGA.  
 This library was created for the program, Gene Discovery  
 in the Visual System, supported by National Eye Institute  
 (NEI)."

ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 211;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
 ||||:||||  
 Db 9 GGGGTCTCGAG 20

RESULT 197  
 LOCUS CV494873/C  
 DEFINITION 39970.1 Cold Sweetening B Solanum tuberosum cDNA clone 39970 5',  
 mRNA sequence.  
 CV494873 211 bp mRNA linear EST 04-OCT-2004

ACCESSION CV494873  
 VERSION CV494873.1  
 KEYWORDS  
 SOURCE Solanum tuberosum (potato)  
 ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 211)  
 Flinn, B., Rochwell, C., Sardana, R., Griffiths, R., Laque, M., De  
 Koeijer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.  
 Generation of ESTs from tubers following 3 months storage at 4  
 degrees Celsius, and 95% relative humidity  
 Unpublished (2004)

JOURNAL The Canadian Potato Genome Project - BioAtlantech  
 921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
 Email: bflinn@bioatlantech.nb.ca  
 Seq primer: T3

FEATURES  
 Source Location/Qualifiers

1..211  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Shepody"  
 /db\_xref="taxon:4113"  
 /clone="39970"  
 /tissue\_type="Tubers"  
 /lab\_host="X110-Gold"  
 /note="Vector: pBluescript II SK(+); XR; Site\_1: EcoRI;  
 Site\_2: XhoI; supplier: Developmental series. Plants from  
 pathogen-free Solanum tuberosum var. Shepody, clone 1756,  
 nuclear stock were grown in a greenhouse under natural  
 conditions. Mature, harvested tubers were stored in the  
 dark at 4C, 95% relative humidity for 3 months. RNA was  
 isolated for library construction. A normalized library  
 was constructed following a modified protocol of Bernaldo  
 et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 211;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
 ||||:||||  
 Db 101 GGGGTCTCGAG 90

RESULT 198  
 LOCUS AV152436/C  
 DEFINITION 212 bp mRNA linear EST 07-JUL-1999  
 AV152436 Mus musculus hippocampus C57BL/6J adult Mus musculus cDNA  
 clone 2900037B13, mRNA sequence.  
 AV152436 212 bp mRNA linear EST 07-JUL-1999

ACCESSION AV152436  
 VERSION AV152436.1  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 212)  
 Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,  
 Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,  
 Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,  
 Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsunuma, H., Oda, H.,

Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Yoshinaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
 RIKEN Mouse ESTs  
 Unpublished (1999)  
 Contact: Chie Owa  
 Genome Science Laboratory  
 RIKEN  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-9145  
 Fax: 81-298-36-9098  
 Email: genome-res@rtc.riken.go.jp

Thermotabilization and thermoinactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details

#### FEATURES

source  
 Location/Qualifiers  
 1..212  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="2900037B13"  
 /sex="male"  
 /tissue\_type="hippocampus"  
 /dev\_stage="adult"  
 /clone\_lib="Mus musculus hippocampus C57BL/6J adult"

#### ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 212;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
 |||||:  
 Db 109 GGGGTCCTGGAG 98

RESULT 199  
 BM756685  
 LOCUS K-EST0033393 S6SNU620 Homo sapiens cDNA clone S6SNU620-26-F01 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BM756685.1 GI:19086300  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 212)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.  
 21C Frontier Korean EST Project 2001  
 Unpublished (2002)  
 Contact: Kim YS

TITLE  
 JOURNAL  
 COMMENT  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4409  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 26 row: F column: 01  
 High quality sequence stop: 212.

FEATURES  
 source  
 1..212  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

#### ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 212;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
 |||||:  
 Db 200 GGGGTCCTGGAG 211

RESULT 200  
 CE204336  
 LOCUS tigr-gss-dog-17000372580913 Dog library Canis familiaris genomic,  
 DEFINITION genomic survey sequence.  
 ACCESSION CE204336  
 VERSION CE204336.1 GI:35359991  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Canis familiaris (dog)

REFERENCE  
 AUTHORS Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 212)  
 Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 14512627  
 Contact: Kirkness EF

TITLE  
 JOURNAL  
 COMMENT  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirkness@tigr.org  
 Class: shotgun.

FEATURES  
 source  
 1..212  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

#### ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 212;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCUCUGAG 12  
|||:|:|  
Db 177 GGGGTCCTCGAG 188

Search completed: April 25, 2005, 14:50:29  
Job time : 1794.32 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:45 ; Search time 68.6842 Seconds  
(without alignments)  
428.817 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18  
Sequence: 1 CGCGCCCGAGGNNNNN 18

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 8181359 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
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3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCBUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	72.2	59479	4	US-09-949-016-16910
C 2	12	66.7	12	4	US-09-647-344A-43
C 3	12	66.7	14	3	US-08-650-093C-97
C 4	12	66.7	16	3	US-08-954-210-39
C 5	12	66.7	16	3	US-09-431-419A-39
C 6	12	66.7	19	4	US-09-782-361-14
C 7	12	66.7	20	2	US-08-483-695-22
C 8	12	66.7	20	2	US-07-965-285-22
C 9	12	66.7	20	2	US-08-487-231-32
C 10	12	66.7	20	3	US-09-201-912-32
C 11	12	66.7	20	3	US-08-397-220B-38
C 12	12	66.7	20	3	US-08-397-220B-39
C 13	12	66.7	20	3	US-08-397-220B-40
C 14	12	66.7	20	3	US-08-397-220B-41
C 15	12	66.7	20	3	US-08-397-220B-44
C 16	12	66.7	20	3	US-08-650-093C-38
C 17	12	66.7	20	3	US-08-650-093C-39
C 18	12	66.7	20	3	US-08-650-093C-40
C 19	12	66.7	20	3	US-08-650-093C-41
C 20	12	66.7	20	3	US-08-650-093C-44
C 21	12	66.7	20	4	US-09-647-344A-49
C 22	12	66.7	22	4	US-09-647
C 23	12	66.7	24	2	US-08-639-080-22
C 24	12	66.7	25	4	US-09-647
C 25	12	66.7	25	4	US-09-647-344A-47
C 26	12	66.7	26	3	US-08-397-220B-98
C 27	12	66.7	26	3	US-08-650-093C-98

C 28	12	66.7	30	1	US-08-240-547-7	Sequence 7, Appl
C 29	12	66.7	39	1	US-08-530-492-66	Sequence 66, Appl
C 30	12	66.7	39	3	US-08-906-517-66	Sequence 66, Appl
C 31	12	66.7	46	4	US-09-647-344A-48	Sequence 48, Appl
C 32	12	66.7	47	4	US-09-422-978-2597	Sequence 2597, Ap
C 33	12	66.7	61	4	US-09-621-976-10142	Sequence 10142, A
C 34	12	66.7	155	3	US-08-474-700B-61	Sequence 41, Appl
C 35	12	66.7	177	2	US-08-256-568B-61	Sequence 61, Appl
C 36	12	66.7	177	2	US-08-256-568B-67	Sequence 67, Appl
C 37	12	66.7	177	2	US-08-256-568B-68	Sequence 68, Appl
C 38	12	66.7	177	2	US-08-256-568B-69	Sequence 69, Appl
C 39	12	66.7	177	2	US-08-256-568B-70	Sequence 70, Appl
C 40	12	66.7	177	2	US-08-256-568B-72	Sequence 72, Appl
C 41	12	66.7	177	2	US-08-256-568B-73	Sequence 73, Appl
C 42	12	66.7	177	2	US-08-256-568B-74	Sequence 74, Appl
C 43	12	66.7	177	2	US-08-256-568B-75	Sequence 75, Appl
C 44	12	66.7	177	2	US-08-256-568B-76	Sequence 76, Appl
C 45	12	66.7	177	2	US-08-256-568B-77	Sequence 77, Appl
C 46	12	66.7	177	2	US-08-256-568B-78	Sequence 78, Appl
C 47	12	66.7	177	2	US-08-256-568B-79	Sequence 79, Appl
C 48	12	66.7	177	2	US-08-256-568B-80	Sequence 80, Appl
C 49	12	66.7	177	3	US-09-038-369B-61	Sequence 61, Appl
C 50	12	66.7	177	3	US-09-038-369B-67	Sequence 67, Appl
C 51	12	66.7	177	3	US-09-038-369B-68	Sequence 68, Appl
C 52	12	66.7	177	3	US-09-038-369B-69	Sequence 69, Appl
C 53	12	66.7	177	3	US-09-038-369B-70	Sequence 70, Appl
C 54	12	66.7	177	3	US-09-038-369B-72	Sequence 72, Appl
C 55	12	66.7	177	3	US-09-038-369B-73	Sequence 73, Appl
C 56	12	66.7	177	3	US-09-038-369B-74	Sequence 74, Appl
C 57	12	66.7	177	3	US-09-038-369B-75	Sequence 75, Appl
C 58	12	66.7	177	3	US-09-038-369B-76	Sequence 76, Appl
C 59	12	66.7	177	3	US-09-038-369B-77	Sequence 77, Appl
C 60	12	66.7	177	3	US-09-038-369B-78	Sequence 78, Appl
C 61	12	66.7	177	3	US-09-038-369B-79	Sequence 79, Appl
C 62	12	66.7	177	3	US-09-038-369B-80	Sequence 80, Appl
C 63	12	66.7	177	4	US-09-378-900A-61	Sequence 61, Appl
C 64	12	66.7	177	4	US-09-378-900A-67	Sequence 67, Appl
C 65	12	66.7	177	4	US-09-378-900A-68	Sequence 68, Appl
C 66	12	66.7	177	4	US-09-378-900A-69	Sequence 69, Appl
C 67	12	66.7	177	4	US-09-378-900A-70	Sequence 70, Appl
C 68	12	66.7	177	4	US-09-378-900A-72	Sequence 72, Appl
C 69	12	66.7	177	4	US-09-378-900A-73	Sequence 73, Appl
C 70	12	66.7	177	4	US-09-378-900A-74	Sequence 74, Appl
C 71	12	66.7	177	4	US-09-378-900A-75	Sequence 75, Appl
C 72	12	66.7	177	4	US-09-378-900A-76	Sequence 76, Appl
C 73	12	66.7	177	4	US-09-378-900A-77	Sequence 77, Appl
C 74	12	66.7	177	4	US-09-378-900A-78	Sequence 78, Appl
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C 76	12	66.7	177	4	US-09-378-900A-80	Sequence 80, Appl
C 77	12	66.7	177	4	US-09-899-044-61	Sequence 61, Appl
C 78	12	66.7	177	4	US-09-899-044-67	Sequence 67, Appl
C 79	12	66.7	177	4	US-09-899-044-68	Sequence 68, Appl
C 80	12	66.7	177	4	US-09-899-044-69	Sequence 69, Appl
C 81	12	66.7	177	4	US-09-899-044-70	Sequence 70, Appl
C 82	12	66.7	177	4	US-09-899-044-72	Sequence 72, Appl
C 83	12	66.7	177	4	US-09-899-044-73	Sequence 73, Appl
C 84	12	66.7	177	4	US-09-899-044-74	Sequence 74, Appl
C 85	12	66.7	177	4	US-09-899-044-75	Sequence 75, Appl
C 86	12	66.7	177	4	US-09-899-044-76	Sequence 76, Appl
C 87	12	66.7	177	4	US-09-899-044-77	Sequence 77, Appl
C 88	12	66.7	177	4	US-09-899-044-78	Sequence 78, Appl
C 89	12	66.7	177	4	US-09-899-044-79	Sequence 79, Appl
C 90	12	66.7	177	4	US-09-899-044-80	Sequence 80, Appl
C 91	12	66.7	178	2	US-08-256-568B-59	Sequence 59, Appl
C 92	12	66.7	178	2	US-08-256-568B-71	Sequence 71, Appl
C 93	12	66.7	178	3	US-09-038-369B-59	Sequence 59, Appl
C 94	12	66.7	178	3	US-09-038-369B-71	Sequence 71, Appl
C 95	12	66.7	178	4	US-09-378-900A-59	Sequence 59, Appl
C 96	12	66.7	178	4	US-09-378-900A-71	Sequence 71, Appl
C 97	12	66.7	178	4	US-09-899-044-59	Sequence 59, Appl
C 98	12	66.7	178	4	US-09-899-044-71	Sequence 71, Appl
C 99	12	66.7	180	3	US-08-441-971-50	Sequence 50, Appl
C 100	12	66.7	180	3	US-08-441-971-51	Sequence 51, Appl















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C 977 11 61.1 601 4 US-09-949-016-21112 Sequence 21112, A
C 978 11 61.1 601 4 US-09-949-016-21113 Sequence 21113, A
C 979 11 61.1 601 4 US-09-949-016-21114 Sequence 21114, A
C 980 11 61.1 601 4 US-09-949-016-21194 Sequence 21194, A
C 981 11 61.1 601 4 US-09-949-016-21195 Sequence 21195, A
C 982 11 61.1 601 4 US-09-949-016-21196 Sequence 21196, A
C 983 11 61.1 601 4 US-09-949-016-21197 Sequence 21197, A
C 984 11 61.1 601 4 US-09-949-016-22265 Sequence 22265, A
C 985 11 61.1 601 4 US-09-949-016-22269 Sequence 22269, A
C 986 11 61.1 601 4 US-09-949-016-22920 Sequence 22920, A
C 987 11 61.1 601 4 US-09-949-016-22921 Sequence 22921, A
C 988 11 61.1 601 4 US-09-949-016-23001 Sequence 23001, A
C 989 11 61.1 601 4 US-09-949-016-23130 Sequence 23130, A
C 990 11 61.1 601 4 US-09-949-016-23131 Sequence 23131, A
C 991 11 61.1 601 4 US-09-949-016-23132 Sequence 23132, A
C 992 11 61.1 601 4 US-09-949-016-24638 Sequence 24638, A
C 993 11 61.1 601 4 US-09-949-016-26121 Sequence 26121, A
C 994 11 61.1 601 4 US-09-949-016-26267 Sequence 26267, A
C 995 11 61.1 601 4 US-09-949-016-27307 Sequence 27307, A
C 996 11 61.1 601 4 US-09-949-016-27476 Sequence 27476, A
C 997 11 61.1 601 4 US-09-949-016-27859 Sequence 27859, A
C 998 11 61.1 601 4 US-09-949-016-29148 Sequence 29148, A
C 999 11 61.1 601 4 US-09-949-016-29149 Sequence 29149, A
C 1000 11 61.1 601 4 US-09-949-016-32534 Sequence 32534, A

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## ALIGNMENTS

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RESULT 1
US-09-949-016-16910/c
; Sequence 16910, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16910
; LENGTH: 59479
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(59479)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16910

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Query Match 72.2%; Score 13; DB 4; Length 59479;
Best Local Similarity 92.3%; Pred. No. 1.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 6 CCUGAGNNNNNN 18
DB 11936 CCGAGNNNNNN 11924

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RESULT 2
US-09-647-344A-43/c
; Sequence 43, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.

```

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; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678 PCT US
; CURRENT APPLICATION NUMBER: US/09/647, 344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 43
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..6
; OTHER INFORMATION: A portion of an antisense library including a Bpm1 site.
US-09-647-344A-43

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Query Match 66.7%; Score 12; DB 4; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.6e+02;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 7 CCUGAGNNNNNN 18
DB 12 CCGAGNNNNNN 1

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RESULT 3
US-08-650-093C-97/c
; Sequence 97, Application US/08650093C
; Patent No. 6391342
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment Of
; Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LICATA & TYRELL, P.C.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650, 093C
; FILING DATE: 17-May-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/452, 841
; FILING DATE: May 30, 1995
; APPLICATION NUMBER: 08/397, 220
; FILING DATE: March 9, 1995
; APPLICATION NUMBER: 07/945, 289
; FILING DATE: September 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: 11PH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear

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; ANTI-SENSE: No
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-08-650-093C-97
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Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGUCCTGGAG 12
        |||:|||||
Db      14 GGGGCTCTGGAG 3

RESULT 4
US-08-954-210-39
; Sequence 39, Application US/08954210
; Patent No. 6043077
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack R.
; APPLICANT: Welch, Peter J.
; APPLICANT: Tritz, Richard
; APPLICANT: Yel, Soompin
; TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,210
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-954-210-39
Query Match      66.7%; Score 12; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGUCCTGGAG 12
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Db      3 GGGGUCCTGGAG 14

RESULT 5
US-09-431-419A-39
; Sequence 39, Application US/09431419A
; Patent No. 6458567
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack R.
; APPLICANT: Welch, Peter J.
; APPLICANT: Tritz, Richard
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; APPLICANT: Yel, Soompin
; APPLICANT: Yu, Mang
; TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
; FILE REFERENCE: 480124.403C3
; CURRENT APPLICATION NUMBER: US/09/431,419A
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Hepatitis C Virus
US-09-431-419A-39
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Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGUCCTGGAG 12
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Db      3 GGGGUCCTGGAG 14

RESULT 6
US-09-782-361-14
; Sequence 14, Application US/09782361
; Patent No. 6811974
; GENERAL INFORMATION:
; APPLICANT: Hu, Yu-Men
; TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GE
; FILE REFERENCE: 2883-4757US
; CURRENT APPLICATION NUMBER: US/09/782,361
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer for PSMEA
US-09-782-361-14
Query Match      66.7%; Score 12; DB 4; Length 19;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGUCCTGGAG 12
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Db      2 GGGGCTCTGGAG 13

RESULT 7
US-08-483-695-22/C
; Sequence 22, Application US/08483695
; Patent No. 5866139
; GENERAL INFORMATION:
; APPLICANT: Brecht, Christian
; APPLICANT: Kremendorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-08-483-695-22

Query Match: 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
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Db 19 GGGGTCTCGAG 8

RESULT 8  
US-07-965-285-22/c  
Sequence 22, Application US/07965285  
Patent No. 5879904  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-07-965-285-22

NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-07-965-285-22

Query Match: 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 19 GGGGTCTCGAG 8

RESULT 9  
US-08-487-231-22/c  
Sequence 22, Application US/08487231  
Patent No. 5919454  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,231  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-08-487-231-22

Query Match 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 19 GGGGTCTCGAG 8

## RESULT 10

US-09-201-912-22/c  
Sequence 22, Application US/09201912  
Patent No. 6210962  
GENERAL INFORMATION:  
APPLICANT: Brecht, Christian  
APPLICANT: Kremdorf, Dina  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,912  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,285  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-09-201-912-22

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 19 GGGGTCTCGAG 8

## RESULT 11

US-08-397-220B-38  
Sequence 38, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289  
FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-397-220B-38

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 1 GGGGTCTCGAG 12

RESULT 12  
US-08-397-220B-39  
Sequence 39, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002

## RESULT 12

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289  
FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-08-397-220B-39

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 3 GGGGCTCTGGAG 14

RESULT 13  
US-08-397-220B-40  
Sequence 40, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289

FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-08-397-220B-40

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 5 GGGGCTCTGGAG 16

RESULT 14  
US-08-397-220B-41  
Sequence 41, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289  
FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes

SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-08-397-220B-41

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
DB 7 GGGGCTCGAG 18

## RESULT 15

US-08-397-220B-44  
Sequence 44, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289  
FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-08-397-220B-44

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
DB 9 GGGGCTCGAG 20

RESULT 16  
US-08-650-093C-38  
Sequence 38, Application US/08650093C

Patent No. 6391542  
GENERAL INFORMATION:

APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:

ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053

## COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-650-093C-38

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
DB 1 GGGGCTCGAG 12

RESULT 17  
US-08-650-093C-39  
Sequence 39, Application US/08650093C  
Patent No. 6391542  
GENERAL INFORMATION:  
APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-08-650-093C-39

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 3 GGGGTCCTGGAG 14

RESULT 18  
US-08-650-093C-40  
Sequence 40, Application US/08650093C  
Patent No. 6391542  
GENERAL INFORMATION:  
APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-08-650-093C-40

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 5 GGGGTCCTGGAG 16

RESULT 19  
US-08-650-093C-41  
Sequence 41, Application US/08650093C  
Patent No. 6391542  
GENERAL INFORMATION:  
APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/550,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-08-650-093C-41

Query Match 66.7%; Score 12; DB 3; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
 |||||:  
 Db 7 GGGGCTCGAG 18

## RESULT 20

US-08-650-093C-44  
 ; Sequence 44; Application US/08650093C  
 ; Patent No. 6391542

GENERAL INFORMATION:

APPLICANT: Kevin P. Anderson et al.  
 TITLE OF INVENTION: Compositions And Methods For Treatment Of  
 Hepatitis C Virus-Associated Diseases

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESSES:

ADDRESSEE: LICATA & TYRRELL P.C.  
 STREET: 66 E. Main Street  
 CITY: Marlton  
 STATE: NJ

COUNTRY: USA

ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WORDPERFECT 6.1 for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/650,093C

FILING DATE: 17-May-1996

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/452,841

FILING DATE: May 30, 1995

APPLICATION NUMBER: 08/397,220

FILING DATE: March 9, 1995

APPLICATION NUMBER: 07/945,289

FILING DATE: September 10, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

SEQUENCE DESCRIPTION: SEQ ID NO: 44:

US-08-650-093C-44

Query Match 66.7%; Score 12; DB 3; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
 |||||:  
 Db 9 GGGGCTCGAG 20

## RESULT 21

US-09-647-344A-49/c  
 ; Sequence 49; Application US/09647344A  
 ; Patent No. 6586180

GENERAL INFORMATION:

APPLICANT: Ruffner, Duane E.

APPLICANT: Pierce, Michael L.

APPLICANT: Chen, Zhidong

TITLE OF INVENTION: Directed Antisense Libraries

FILE REFERENCE: T6678.PCT.US

CURRENT APPLICATION NUMBER: US/09/647,344A

CURRENT FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: PCT/US99/06742

PRIOR FILING DATE: 1999-03-28

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 49

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..14

OTHER INFORMATION: Deletion fragment in a deletion fragment library, including a pc

US-09-647-344A-49

Query Match 66.7%; Score 12; DB 4; Length 20;  
 Best Local Similarity 91.7%; Pred. No. 9.1e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGGAGNNNNN 18  
 |||||:  
 Db 20 CTGGAGNNNNN 9

## RESULT 22

US/09/647/c  
 ; Sequence 38; Application US/09647344A  
 ; Patent No. 6586180

GENERAL INFORMATION:

APPLICANT: Ruffner, Duane E.

APPLICANT: Pierce, Michael L.

APPLICANT: Chen, Zhidong

TITLE OF INVENTION: Directed Antisense Libraries

FILE REFERENCE: T6678.PCT.US

CURRENT APPLICATION NUMBER: US/09/647,344A

CURRENT FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: PCT/US99/06742

PRIOR FILING DATE: 1999-03-28

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 38

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..16

OTHER INFORMATION: Portion of an intermediate in the making of a deletion library,

US/09/647,344A-38

Query Match 66.7%; Score 12; DB 4; Length 22;  
 Best Local Similarity 91.7%; Pred. No. 9e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGGAGNNNNN 18  
 |||||:  
 Db 22 CTGGAGNNNNN 11

## RESULT 23

US-08-639-080-22  
 ; Sequence 22; Application US/08639080  
 ; Patent No. 5843661

GENERAL INFORMATION:

APPLICANT: Rothmund, Paul W.K.

TITLE OF INVENTION: METHOD FOR CONSTRUCTING UNIVERSAL DNA

TITLE OF INVENTION: BASED MOLECULAR TURNING MACHINE

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Ste 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/639,080  
FILING DATE: April 24, 1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Harris, Scott C.  
REGISTRATION NUMBER: 32,030  
REFERENCE/DOCKET NUMBER: 06618/129001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5095  
TELEX:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: oligonucleotide  
FEATURE:  
LOCATION: 7-24  
OTHER INFORMATION: where N at positions 6-13 can be adenine,  
OTHER INFORMATION: guanine, cytosine, thymine or uracil  
US-08-639-080-22

Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 91.7%; Pred. No. 9e+02;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGANNNNNN 18  
DB 1 CTGAGANNNNNN 12

RESULT 24  
US/09/647/c  
Sequence 39, Application US/09647344A  
Patent No. 6586180  
GENERAL INFORMATION:  
APPLICANT: Ruffner, Duane E.  
APPLICANT: Pierce, Michael L.  
APPLICANT: Chen, Zhidong  
TITLE OF INVENTION: Directed Antisense Libraries  
FILE REFERENCE: 16678.PCT.US  
CURRENT APPLICATION NUMBER: US/09/647,344A  
CURRENT FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: PCT/US99/06742  
PRIOR FILING DATE: 1999-03-28  
NUMBER OF SEQ ID NOS: 50  
SEQ ID NO 39  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 6..19  
OTHER INFORMATION: 14 bp variable sequence fragment of a deletion library including  
US/09/647,344A-39

Query Match 66.7%; Score 12; DB 4; Length 25;  
Best Local Similarity 91.7%; Pred. No. 8.9e+02;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGANNNNNN 18  
DB 25 CTGAGANNNNNN 14

RESULT 25  
US-09-647-344A-47/c  
Sequence 47, Application US/09647344A  
Patent No. 6586180  
GENERAL INFORMATION:  
APPLICANT: Ruffner, Duane E.  
APPLICANT: Pierce, Michael L.  
APPLICANT: Chen, Zhidong  
TITLE OF INVENTION: Directed Antisense Libraries  
FILE REFERENCE: 16678.PCT.US  
CURRENT APPLICATION NUMBER: US/09/647,344A  
CURRENT FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: PCT/US99/06742  
PRIOR FILING DATE: 1999-03-28  
NUMBER OF SEQ ID NOS: 50  
SEQ ID NO 47  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 14..19  
OTHER INFORMATION: Sequence flanking the chloramphenicol (CAT) gene after insertion  
US-09-647-344A-47

Query Match 66.7%; Score 12; DB 4; Length 25;  
Best Local Similarity 91.7%; Pred. No. 8.9e+02;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGANNNNNN 18  
DB 25 CTGAGANNNNNN 14

RESULT 26  
US-08-397-220B-98/c  
Sequence 98, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289



FILING DATE: 10-SEP-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Maasey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 98:  
US-08-397-220B-98  
Query Match 66.7%; Score 12; DB 3; Length 26;  
Best Local Similarity 83.3%; Pred. No. 8.9e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCUGAG 12  
|||:|:|  
Db 20 GGGGTCTCGAG 9  
RESULT 27  
US-08-650-093C-98/c  
Sequence 98, Application US/08650093C  
Patent No. 6391542  
GENERAL INFORMATION:  
APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Maasey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 98:  
US-08-650-093C-98  
Query Match 66.7%; Score 12; DB 3; Length 26;  
Best Local Similarity 83.3%; Pred. No. 8.9e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCUGAG 12  
|||:|:|  
Db 20 GGGGTCTCGAG 9  
RESULT 28  
US-08-240-547-7/c  
Sequence 7, Application US/08240547  
Patent No. 5527669  
GENERAL INFORMATION:  
APPLICANT: Resnick, Robert M.  
APPLICANT: Young, Karen K.Y.  
TITLE OF INVENTION: Primers and Probes for Detection of  
Hepatitis C and No. 5527669el Variants  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingdland Street  
CITY: Nutley  
STATE: NJ  
COUNTRY: U.S.A.  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/240,547  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/918,844  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sias Ph.D., Stacey R.  
REGISTRATION NUMBER: 32,630  
REFERENCE/DOCKET NUMBER: 8586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2977  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-240-547-7  
Query Match 66.7%; Score 12; DB 1; Length 30;  
Best Local Similarity 83.3%; Pred. No. 8.8e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCUGAG 12  
|||:|:|  
Db 13 GGGGTCTCGAG 2  
RESULT 29  
US-08-530-492-66/c  
Sequence 66, Application US/08530492  
Patent No. 5689052  
GENERAL INFORMATION:  
APPLICANT: Brown, Sherri M.  
APPLICANT: Dean, Duff A.

```

APPLICANT: Fromm, Michael E.
APPLICANT: Sanders, Patricia R.
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
TITLE OF INVENTION: Expression in Monocytledonous Plants and Method For
TITLE OF INVENTION: Preparation Thereof
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B94F
STREET: 700 Chesterfield Parkway No. 5689052th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,492
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/172,333
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10605)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6047
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-530-492-66

Query Match
Best Local Similarity 66.7%; Score 12; DB 1; Length 39;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12
DB 20 GGGGCTCTGGAG 9

RESULT 30
US-08-906-517-66/c
Sequence 66, Application US/08906517
Patent No. 6180774
GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Dean, Duff A.
APPLICANT: Fromm, Michael E.
APPLICANT: Sanders, Patricia R.
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
TITLE OF INVENTION: Expression in Monocytledonous Plants and Method For
TITLE OF INVENTION: Preparation Thereof
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,517
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-906-517-66

Query Match
Best Local Similarity 66.7%; Score 12; DB 3; Length 39;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12
DB 20 GGGGCTCTGGAG 9

RESULT 31
US-09-647-344A-48/c
Sequence 48, Application US/09647344A
Patent No. 6586180
GENERAL INFORMATION:
APPLICANT: Ruffner, Duane E.
APPLICANT: Pierce, Michael L.
APPLICANT: Chen, Zhidong
TITLE OF INVENTION: Directed Antisense Libraries
FILE REFERENCE: T6678.PCT.US
CURRENT APPLICATION NUMBER: US/09/647,344A
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/US99/06742
PRIOR FILING DATE: 1999-03-28
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 48
LENGTH: 46
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: 6..12 and 35..40
OTHER INFORMATION: Hammerhead ribozyme library with flanking sequences.
US-09-647-344A-48

Query Match
Best Local Similarity 66.7%; Score 12; DB 4; Length 46;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18
DB 46 CTGAGNNNNNN 35

RESULT 32
US-09-422-978-2597
Sequence 2597, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumentfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

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FILE REFERENCE: GENSET.020CP1  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 2597  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 99-1211-59 : polymorphic base C or T  
US-09-422-978-2597

Query Match 66.7%; Score 12; DB 4; Length 47;  
Best Local Similarity 83.3%; Pred. No. 8.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCUGAG 12  
|||:|||||  
Db 25 GGGGTCTGAG 36

RESULT 33  
US-09-621-976-10142  
Sequence 10142, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 10142  
LENGTH: 61  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 6  
OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-10142

Query Match 66.7%; Score 12; DB 4; Length 61;  
Best Local Similarity 83.3%; Pred. No. 8.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCUGAG 12  
|||:|||||  
Db 29 GGGGTCTGAG 40

RESULT 34  
US-08-474-700B-41  
Sequence 41, Application US/08474700B  
Patent No. 6001990  
GENERAL INFORMATION:  
APPLICANT: Maeda, Jack  
APPLICANT: Makita, Takaji  
APPLICANT: Moradpour, Darius  
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C  
TITLE OF INVENTION: VIRUS  
NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,700B  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,382  
FILING DATE: 10 May 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/279001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-474-700B-41

Query Match 66.7%; Score 12; DB 3; Length 155;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCUGAG 12  
|||:|||||  
Db 33 GGGGTCTGAG 44

RESULT 35  
US-08-256-568B-61/c  
Sequence 61, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: bea2 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-61

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 26 GGGGTCTCGAG 15

RESULT 36  
US-08-256-568B-67/c  
Sequence 67, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gp48  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-67

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 26 GGGGTCTCGAG 15

RESULT 37  
US-08-256-568B-68/c  
Sequence 68, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb116  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
US-08-256-568B-68

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTGGAG 15

## RESULT 38

US-08-256-568B-69/c  
Sequence 69, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8002  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb569  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
US-08-256-568B-69

Query Match 66.7%; Score 12; DB 2; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTGGAG 15

## RESULT 39

US-08-256-568B-70/c  
Sequence 70, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb358  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
US-08-256-568B-70

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTGGAG 15

## RESULT 40

US-08-256-568B-72/c  
; Sequence 72, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,568B  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: Cam600  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
US-08-256-568B-72  
  
Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGUCGUGAG 12  
DB 26 GGGGCTCTGGAG 15  
  
RESULT 41  
US-08-256-568B-73/c  
; Sequence 73, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,568B  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: Cam736  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
US-08-256-568B-73  
  
Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGUCGUGAG 12  
DB 26 GGGGCTCTGGAG 15  
  
RESULT 42  
US-08-256-568B-74/c  
; Sequence 74, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: gb809
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-08-256-568B-74

Query Match      66.7%; Score 12; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGCUCCUGAG 12
        |||:|:|:|:|
Db      26 GGGGTCTCTGAG 15

RESULT 43
US-08-256-568B-75/c
Sequence 75, Application US/08256568B
Patent No. 5846704
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03325
```

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FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: gb487
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-08-256-568B-75

Query Match      66.7%; Score 12; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGCUCCUGAG 12
        |||:|:|:|:|
Db      26 GGGGTCTCTGAG 15

RESULT 44
US-08-256-568B-76/c
Sequence 76, Application US/08256568B
Patent No. 5846704
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
```

REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-76

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
|||:|:|:|:|  
Db 26 GGGGTCTCTGAG 15

RESULT 45  
US-08-256-568B-77/c  
Sequence 77, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-77

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
|||:|:|:|:|  
Db 26 GGGGTCTCTGAG 15

RESULT 46  
US-08-256-568B-78/c  
Sequence 78, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-78



Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTGAG 15

RESULT 47  
US-08-256-568B-79/c  
; Sequence 79, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,568B  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: be96  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-08-256-568B-79

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTGAG 15

RESULT 48  
US-08-256-568B-80/c  
; Sequence 80, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,568B  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: be98  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-08-256-568B-80

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTGAG 15

RESULT 49  
US-09-038-369B-61/c  
; Sequence 61, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES

```

NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESSES:
ADDRESS: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,369B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: be82 (also referred to as be99)
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-038-369B-61

Query Match          66.7%; Score 12; DB 3; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12
    |||:|||||
DB 26 GGGGTCTGTGAG 15

RESULT 50
US-09-038-369B-67/c
; Sequence 67, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESSES:
; ADDRESS: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
```

```

ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,369B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 9b48
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-038-369B-67

Query Match          66.7%; Score 12; DB 3; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12
    |||:|||||
DB 26 GGGGTCTGTGAG 15

RESULT 51
US-09-038-369B-68/c
; Sequence 68, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESSES:
; ADDRESS: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb116  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-68

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 52  
US-09-038-369B-69/c  
Sequence 69, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb569  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-69

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 53  
US-09-038-369B-70/c  
Sequence 70, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: g9358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-70

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|:|:|  
Db 26 GGGGCTCTGGAG 15

RESULT 54  
US-09-038-369B-72/c  
Sequence 72, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam600  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-72

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|:|:|  
Db 26 GGGGCTCTGGAG 15

RESULT 55  
US-09-038-369B-73/c  
Sequence 73, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:  
CLONE: cam736  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-73

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCCTGAG 15

RESULT 56  
US-09-038-369B-74/c  
Sequence 74, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gp809  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-74

Query Match 66.7%; Score 12; DB 3; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCCTGAG 15

RESULT 57  
US-09-038-369B-75/c  
Sequence 75, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gp487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-75

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCCTGAG 15

RESULT 58  
US-09-038-369B-76/C  
; Sequence 76, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,369B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 76:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gp724  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-038-369B-76  
Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 26 GGGGTCTGAG 15  
RESULT 59  
US-09-038-369B-77/C  
; Sequence 77, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,369B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: be97  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-038-369B-77

APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-77  
Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 26 GGGGTCTGAG 15  
RESULT 60  
US-09-038-369B-78/C  
; Sequence 78, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,369B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: be97  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-038-369B-78

```

; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,369B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be95
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
;
US-09-038-369B-78
;
Query Match 66.7%; Score 12; DB 3; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12
Db 26 GGGGTCTCGAG 15

RESULT 61
US-09-038-369B-79/c
; Sequence 79, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,369B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be96
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
;
US-09-038-369B-79
;
Query Match 66.7%; Score 12; DB 3; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12
Db 26 GGGGTCTCGAG 15

RESULT 62
US-09-038-369B-80/c
; Sequence 80, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,369B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369b-80

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 63  
US-09-378-900A-61/c  
Sequence 61, Application US/09378900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-61

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 64  
US-09-378-900A-67/c  
Sequence 67, Application US/09378900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004



```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: gb48
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
US-09-378-900A-67

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      26 GGGGTCCTGGAG 15

RESULT 65
US-09-378-900A-68/c
; Sequence 68, Application US/093789900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; NUMBER OF SEQUENCES: 97
; ADDRESS: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
```

```
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: gb116
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
US-09-378-900A-68

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      26 GGGGTCCTGGAG 15

RESULT 66
US-09-378-900A-69/c
; Sequence 69, Application US/093789900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; NUMBER OF SEQUENCES: 97
; ADDRESS: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: gb569
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
```

US-09-378-900A-69

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 26 GGGGCTCTGGAG 15

RESULT 67

US-09-378-900A-70/c  
; Sequence 70, Application US/09378900A  
; Patent No. 6495670

; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/378,900A

; FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/256,568

FILING DATE: 18-JUL-1994

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/93/402,123.6

FILING DATE: 31-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410,004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: 9B358

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

US-09-378-900A-70

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12

Db 26 GGGGCTCTGGAG 15  
||||:|||||

RESULT 68

US-09-378-900A-72/c  
; Sequence 72, Application US/09378900A  
; Patent No. 6495670

; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/378,900A

; FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/256,568

FILING DATE: 18-JUL-1994

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/93/402,123.6

FILING DATE: 31-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410,004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: cam600

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

US-09-378-900A-72

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 26 GGGGCTCTGGAG 15

RESULT 69  
US-09-378-900A-73/c  
; Sequence 73, Application US/09378900A

```
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: cam736
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
;
; US-09-378-900A-73
;
; Query Match          66.7%; Score 12; DB 4; Length 177;
; Best Local Similarity 83.3%; Pred. No. 7.4e+02;
; Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; Qy      1 GGGGUCUCCUGAG 12
;         ||||:|||||
; Db      26 GGGGTCTCTGGAG 15
;
; RESULT 70
; US-09-378-900A-74/c
; Sequence 74, Application US/09378900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: gb809
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
;
; US-09-378-900A-74
;
; Query Match          66.7%; Score 12; DB 4; Length 177;
; Best Local Similarity 83.3%; Pred. No. 7.4e+02;
; Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; Qy      1 GGGGUCUCCUGAG 12
;         ||||:|||||
; Db      26 GGGGTCTCTGGAG 15
;
; RESULT 71
; US-09-378-900A-75/c
; Sequence 75, Application US/09378900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 9b487
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-378-900A-75

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
DB      26 GGGGTCTCTGGAG 15

RESULT 72
US-09-378-900A-76/C
Sequence 76, Application US/09378900A
Patent No. 6495670
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
```

```
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 9b724
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-378-900A-76

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
DB      26 GGGGTCTCTGGAG 15

RESULT 73
US-09-378-900A-77/C
Sequence 77, Application US/09378900A
Patent No. 6495670
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: be97
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; US-09-378-900A-77

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCCTGGAG 12
        |||:|||||
Db      26 GGGCTCTGGAG 15

RESULT 74
US-09-378-900A-78/c
; Sequence 78, Application US/093789900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be95
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; US-09-378-900A-78

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCCTGGAG 12
        |||:|||||
Db      26 GGGCTCTGGAG 15

RESULT 75
US-09-378-900A-79/c
; Sequence 79, Application US/093789900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 79:

```

SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-79

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCUCCUGAG 12  
Db 26 GGGGTCTCTGGAG 15

RESULT 76  
US-09-378-900A-80/c  
Sequence 80, Application US/09378900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:

CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-80

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCUCCUGAG 12  
Db 26 GGGGTCTCTGGAG 15

RESULT 77  
US-09-899-044-61/c  
Sequence 61, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 61:  
US-09-899-044-61

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGAG 12  
| | | | : | : | : | | |  
Db 26 GGGGTCTGAG 15

## RESULT 78

US-09-899-044-67/c

; Sequence 67, Application US/09899044

; Patent No. 6548244

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO

; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV

; ISOLATES

; NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN &amp; MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/899,044

; FILING DATE: 06-Jul-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/378,900

; FILING DATE: &lt;Unknown&gt;

; APPLICATION NUMBER: PCT/EP93/03325

; FILING DATE: 26-NOV-1993

; APPLICATION NUMBER: EP/93/402,129.6

; FILING DATE: 31-AUG-1993

; APPLICATION NUMBER: EP/92/403,222.0

; FILING DATE: 27-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410.004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 67:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

; IMMEDIATE SOURCE:

; CLONE: gb48

; POSITION IN GENOME:

; MAP POSITION: 5' untranslated region

; SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-899-044-67

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGAG 12  
| | | | : | : | : | | |  
Db 26 GGGGTCTGAG 15

RESULT 79  
US-09-899-044-68/c

; Sequence 68, Application US/09899044

; Patent No. 6548244

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO

; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV

; ISOLATES

; NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN &amp; MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/899,044

; FILING DATE: 06-Jul-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/378,900

; FILING DATE: &lt;Unknown&gt;

; APPLICATION NUMBER: PCT/EP93/03325

; FILING DATE: 26-NOV-1993

; APPLICATION NUMBER: EP/93/402,129.6

; FILING DATE: 31-AUG-1993

; APPLICATION NUMBER: EP/92/403,222.0

; FILING DATE: 27-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410.004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

; IMMEDIATE SOURCE:

; CLONE: gb116

; POSITION IN GENOME:

; MAP POSITION: 5' untranslated region

; SEQUENCE DESCRIPTION: SEQ ID NO: 68:

US-09-899-044-68

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGAG 12  
| | | | : | : | : | | |  
Db 26 GGGGTCTGAG 15

## RESULT 80

US-09-899-044-69/c

; Sequence 69, Application US/09899044

; Patent No. 6548244

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO

; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV

; ISOLATES

; NUMBER OF SEQUENCES: 97

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BIERMAN & MUSERLIAN  
;; STREET: 600 THIRD AVENUE  
;; CITY: NEW YORK  
;; STATE: NEW YORK  
;; COUNTRY: USA  
;; ZIP: 10016  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: ASCII  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/899,044  
;; FILING DATE: 06-Jul-2001  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/378,900  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: PCT/EP93/03325  
;; FILING DATE: 26-NOV-1993  
;; APPLICATION NUMBER: EP/93/402,129.6  
;; FILING DATE: 31-AUG-1993  
;; APPLICATION NUMBER: EP/92/403,222.0  
;; FILING DATE: 27-NOV-1992  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CHARLES A. MUSERLIAN  
;; REGISTRATION NUMBER: 19,683  
;; REFERENCE/DOCKET NUMBER: 410.004  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 661-8000  
;; TELEFAX: (212) 661-8002  
;;  
;; INFORMATION FOR SEQ ID NO: 69:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 177 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; IMMEDIATE SOURCE:  
;; CLONE: 9B569  
;; POSITION IN GENOME:  
;; MAP POSITION: 5', untranslated region  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-899-044-69  
;  
Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 GGGGUCCUGAG 12  
Db 26 GGGGTCTCGAG 15  
;  
RESULT 81  
US-09-899-044-70/c  
; Sequence 70, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: ASCII  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/899,044  
;; FILING DATE: 06-Jul-2001  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/378,900  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: PCT/EP93/03325  
;; FILING DATE: 26-NOV-1993  
;; APPLICATION NUMBER: EP/93/402,129.6  
;; FILING DATE: 31-AUG-1993  
;; APPLICATION NUMBER: EP/92/403,222.0  
;; FILING DATE: 27-NOV-1992  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CHARLES A. MUSERLIAN  
;; REGISTRATION NUMBER: 19,683  
;; REFERENCE/DOCKET NUMBER: 410.004  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 661-8000  
;; TELEFAX: (212) 661-8002  
;;  
;; INFORMATION FOR SEQ ID NO: 70:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 177 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; IMMEDIATE SOURCE:  
;; CLONE: 9B358  
;; POSITION IN GENOME:  
;; MAP POSITION: 5', untranslated region  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-09-899-044-70  
;  
Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 GGGGUCCUGAG 12  
Db 26 GGGGTCTCGAG 15  
;  
RESULT 82  
US-09-899-044-72/c  
; Sequence 72, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: cam600
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-899-044-72

Query Match          66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCGCGAG 12
        |||:|||||
Db      26 GGGGTCTCGAG 15

RESULT 83
US-09-899-044-73/c
; Sequence 73, Application US/09899044
; Patent No. 6548244
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,044
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002

```

```

; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: cam736
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-899-044-73

Query Match          66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCGCGAG 12
        |||:|||||
Db      26 GGGGTCTCGAG 15

RESULT 84
US-09-899-044-74/c
; Sequence 74, Application US/09899044
; Patent No. 6548244
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,044
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002

```

INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb809  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-899-044-74

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 26 GGGGTCCTGAG 15

RESULT 85  
US-09-899-044-75/c  
Sequence 75, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:

CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 75:  
US-09-899-044-75

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 26 GGGGTCCTGAG 15

RESULT 86  
US-09-899-044-76/c  
Sequence 76, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/399,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-09-899-044-76

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
DB 26 GGGGTCTCGAG 15

## RESULT 87

US-09-899-044-77/c

; Sequence 77, Application US/09899044  
; Patent No. 6548244

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

; ROSSAU, RUDI; VAN HEUVERSWMY, HUGO

; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV

; ISOLATES

; NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN &amp; MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/899,044

; FILING DATE: 06-Jul-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/378,900

; FILING DATE: &lt;Unknown&gt;

; APPLICATION NUMBER: PCT/EP93/03325

; FILING DATE: 26-Nov-1993

; APPLICATION NUMBER: EP/93/402,129,6

; FILING DATE: 31-Aug-1993

; APPLICATION NUMBER: EP/92/403,222,0

; FILING DATE: 27-Nov-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410,004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 77:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; LIBRARY: be97

; POSITION IN GENOME:

; MAP POSITION: 5' untranslated region

; SEQUENCE DESCRIPTION: SEQ ID NO: 77:

US-09-899-044-77

Query Match 66.7%; Score 12; DB 4; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.4e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
DB 26 GGGGTCTCGAG 15

## RESULT 88

US-09-899-044-78/c

; Sequence 78, Application US/09899044  
; Patent No. 6548244

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

; ROSSAU, RUDI; VAN HEUVERSWMY, HUGO

; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV

; ISOLATES

; NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN &amp; MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/899,044

; FILING DATE: 06-Jul-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/378,900

; FILING DATE: &lt;Unknown&gt;

; APPLICATION NUMBER: PCT/EP93/03325

; FILING DATE: 26-Nov-1993

; APPLICATION NUMBER: EP/93/402,129,6

; FILING DATE: 31-Aug-1993

; APPLICATION NUMBER: EP/92/403,222,0

; FILING DATE: 27-Nov-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410,004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 78:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; CLONE: be95

; POSITION IN GENOME:

; MAP POSITION: 5' untranslated region

; SEQUENCE DESCRIPTION: SEQ ID NO: 78:

US-09-899-044-78

Query Match 66.7%; Score 12; DB 4; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.4e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
DB 26 GGGGTCTCGAG 15

## RESULT 89

US-09-899-044-79/c

; Sequence 79, Application US/09899044  
; Patent No. 6548244

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

; ROSSAU, RUDI; VAN HEUVERSWMY, HUGO

; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV

; ISOLATES

NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
US-09-899-044-79  
Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15  
RESULT 90  
US-09-899-044-80/c  
; Sequence 80, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN,  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,568B  
; FILING DATE: 18-JUL-1994

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 80:  
US-09-899-044-80  
Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15  
RESULT 91  
US-08-256-568B-59/c  
; Sequence 59, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN,  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,568B  
; FILING DATE: 18-JUL-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: bu74  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-59

Query Match 66.7%; Score 12; DB 2; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 92  
US-08-256-568B-71/C  
Sequence 71, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gb549  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-71

Query Match 66.7%; Score 12; DB 2; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 93  
US-08-038-369B-59/C  
Sequence 59, Application US/09038369B.  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; IMMEDIATE SOURCE:  
; CLONE: bu74  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-038-369B-59

Query Match 66.7%; Score 12; DB 3; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCCTGGAG 15

RESULT 94  
US-09-038-369B-71/c  
; Sequence 71, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,369B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

MOLECULE TYPE: CDNA  
; IMMEDIATE SOURCE:  
; CLONE: pb549  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-038-369B-71

Query Match 66.7%; Score 12; DB 3; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCCTGGAG 15

RESULT 95  
US-09-378-900A-59/c  
; Sequence 59, Application US/09378900A  
; Patent No. 6495670  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/378,900A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; IMMEDIATE SOURCE:  
; CLONE: bu74  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-378-900A-59

Query Match 66.7%: Score 12; DB 4; Length 178;  
Best Local Similarity 83.3%: Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:||||  
Db 26 GGGGTCCTGGAG 15

RESULT 96  
US-09-378-900A-71/c  
; Sequence 71, Application US/09378900A  
; Patent No. 6495670  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWIN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/378, 900A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gbs49  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-378-900A-71

Query Match 66.7%: Score 12; DB 4; Length 178;  
Best Local Similarity 83.3%: Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
|||:||||  
Db 26 GGGGTCCTGGAG 15

RESULT 97  
US-09-899-044-59/c  
; Sequence 59, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWIN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-JUL-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378, 900  
; FILING DATE: <unknown>  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: bu74  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
; US-09-899-044-59

Query Match 66.7%: Score 12; DB 4; Length 178;  
Best Local Similarity 83.3%: Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
|||:||||  
Db 26 GGGGTCCTGGAG 15

RESULT 98  
US-09-899-044-71/c  
; Sequence 71, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

ROSSAU, RUDI; VAN HEUVERSMYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gds49  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 71:  
US-09-899-044-71  
Query Match 66.7%; Score 12; DB 4; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 26 GGGGTCCTGGAG 15  
RESULT 99  
US-08-441-971-50/c  
Sequence 50, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts

COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE: US/07/881,528  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TEXT: EZEKIEL  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sa3  
US-08-441-971-50  
Query Match 66.7%; Score 12; DB 3; Length 180;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 34 GGGGTCCTGGAG 23  
RESULT 100  
US-08-441-971-51/c  
Sequence 51, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653



```

; FILING DATE:
; APPLICATION NUMBER: US/07/881,528
; FILING DATE: 07/697,326
; APPLICATION NUMBER: 07/697,326
; FILING DATE: 8 May 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janluk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 720-3500
; TELEFAX: (617) 720-2441
; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: sa4
;
US-08-441-971-51
Query Match 66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12
Db 34 GGGGTCCTGAG 23

RESULT 101
US-08-221-653-50/c
; Sequence 50, Application US/08221653
; Patent No. 6190864
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,653
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/881,528
; FILING DATE:
; APPLICATION NUMBER: 07/697,326
; FILING DATE: 8 May 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janluk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 720-3500
; TELEFAX: (617) 720-2441
; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 180 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: sa3
;
US-08-221-653-50
Query Match 66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12
Db 34 GGGGTCCTGAG 23

RESULT 102
US-08-221-653-51/c
; Sequence 51, Application US/08221653
; Patent No. 6190864
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; OPERATING SYSTEM: IBM compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,653
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/881,528
; FILING DATE:
; APPLICATION NUMBER: 07/697,326
; FILING DATE: 8 May 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janluk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 720-3500
; TELEFAX: (617) 720-2441
; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: sa4
;
US-08-221-653-51
Query Match 66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12
Db 34 GGGGTCCTGAG 12
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Db 34 GGGGCTCTGGAG 23

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RESULT 103
US-08-442-144A-50/c
; Sequence 50, Application US/08442144A
; Patent No. 6214583
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; APPLICANT: Eileen Beall
; APPLICANT: Bruce Irvine
; APPLICANT: Michael Kolberg
; APPLICANT: Michael S. Urdea
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 Inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,144A
; FILING DATE: MAY 16, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,653
; FILING DATE: APRIL 1, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yacko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CHIR-0121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 Nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: sa3
US-08-442-144A-50

Query Match 66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTCTGGAG 12
Db 34 GGGGCTCTGGAG 23

RESULT 104
US-08-442-144A-51/c
; Sequence 51, Application US/08442144A
; Patent No. 6214583
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; APPLICANT: Eileen Beall
; APPLICANT: Bruce Irvine
; APPLICANT: Michael Kolberg
; APPLICANT: Michael S. Urdea
```

```
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 Inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,144A
; FILING DATE: MAY 16, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,653
; FILING DATE: APRIL 1, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yacko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CHIR-0121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 Nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: sa4
US-08-442-144A-51

Query Match 66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGGGCTCTGGAG 12
Db 34 GGGGCTCTGGAG 23

RESULT 105
US-08-441-970-50/c
; Sequence 50, Application US/08441970
; Patent No. 6297370
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,970
```

FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 MAY 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sa3  
US-08-441-970-50

Query Match 66.7%; Score 12; DB 3; Length 180;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGCCCGAG 12  
Db 34 GGGGTCCTGGAG 23

RESULT 106  
US-08-441-970-51/c  
Sequence 51, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sa4  
US-08-441-970-51

Query Match 66.7%; Score 12; DB 3; Length 180;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGCCCGAG 12  
Db 34 GGGGTCCTGGAG 23

RESULT 107  
US-08-634-797-46/c  
Sequence 46, Application US/08634797  
Patent No. 5851759  
GENERAL INFORMATION:  
APPLICANT: WEINER, AMY J.  
TITLE OF INVENTION: HETEROIDUPLEX TRACKING ASSAY (HTA) FOR  
TITLE OF INVENTION: GENOTYPING HCV  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street - R440  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,797  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hardin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 1226,001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-3274  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-634-797-46

Query Match 66.7%; Score 12; DB 2; Length 194;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGCCCGAG 12  
Db 56 GGGGTCCTGGAG 45

RESULT 108  
US-08-634-797-47/c

Sequence 47, Application US/08634797  
Patent No. 5851759  
GENERAL INFORMATION:  
APPLICANT: WEINER, AMY J.  
TITLE OF INVENTION: HETERODUPLEX TRACKING ASSAY (HTA) FOR  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street - R440  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,797  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hardin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 1226.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-3274  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-634-797-47

Query Match 66.7%; Score 12; DB 2; Length 194;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 56 GGGGTCTGAG 45

RESULT 109  
US-08-634-797-48/C  
Sequence 48, Application US/08634797  
Patent No. 5851759  
GENERAL INFORMATION:  
APPLICANT: WEINER, AMY J.  
TITLE OF INVENTION: HETERODUPLEX TRACKING ASSAY (HTA) FOR  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street - R440  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,797  
FILING DATE: 19-APR-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hardin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 1226.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-3274  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-634-797-48

Query Match 66.7%; Score 12; DB 2; Length 194;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 56 GGGGTCTGAG 45

RESULT 110  
US-09-270-767-28457/C  
Sequence 28457, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 28457  
LENGTH: 201  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-28457

Query Match 66.7%; Score 12; DB 4; Length 201;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 102 GGGGTCTGAG 91

RESULT 111  
US-09-513-999C-29549  
Sequence 29549, Application US/0951399C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513, 999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pn  
SEQ ID NO 29549  
LENGTH: 221

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-29549

Query Match      66.7%; Score 12; DB 4; Length 221;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
      |||:|||||
Db      15 GGGGTCTCTGGAG 26

RESULT 112
US-09-034-205-37/c
; Sequence 37, Application US/09034205
; Patent No. 6194149
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034.205
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-034-205-37

Query Match      66.7%; Score 12; DB 3; Length 232;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
      |||:|||||
Db      47 GGGGTCTCTGGAG 36

RESULT 113
US-08-934-097A-37/c
; Sequence 37, Application US/08934097A
; Patent No. 6210880
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
```

```
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; TITLE OF INVENTION: Structure Probing With Structure-Bridging
; TITLE OF INVENTION: Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934.097A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-934-097A-37

Query Match      66.7%; Score 12; DB 3; Length 232;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
      |||:|||||
Db      47 GGGGTCTCTGGAG 36

RESULT 114
US-08-851-588-37/c
; Sequence 37, Application US/08851588
; Patent No. 6214545
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Prudent, James R.
; APPLICANT: Dahlberg, James E.
; APPLICANT: Fors, Lance
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; TITLE OF INVENTION: Structure Probing
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-37

Query Match 66.7%; Score 12; DB 3; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
Db 47 GGGGTCCTGGAG 36

RESULT 115  
US-09-677-218B-37/C  
Sequence 37, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamachev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-677-218B-37

Query Match 66.7%; Score 12; DB 3; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
Db 47 GGGGTCCTGGAG 36

RESULT 116  
US-09-677-192-37/C  
Sequence 37, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamachev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-37

Query Match 66.7%; Score 12; DB 3; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
Db 47 GGGGTCCTGGAG 36

RESULT 117  
US-09-402-618B-37/C  
Sequence 37, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamachev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot:  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA

ORGANISM: Hepatitis C virus  
US-09-402-618B-37

Query Match 66.7%; Score 12; DB 4; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
Db 47 GGGGCTCTGGAG 36

RESULT 118  
US-09-825-574-37/C  
Sequence 37, Application US/09825574  
Patent No. 6709819

GENERAL INFORMATION:  
APPLICANT: Lyamachev, Victor I.  
Fors, Lance  
Neil, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-825-574-37

Query Match 66.7%; Score 12; DB 4; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
Db 47 GGGGCTCTGGAG 36

RESULT 119  
US-09-676-768-37/C

Sequence 37, Application US/09676768  
Patent No. 6780585

GENERAL INFORMATION:

APPLICANT: Dong, Fang  
Lyamachev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-676-768-37

Query Match 66.7%; Score 12; DB 4; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
Db 47 GGGGCTCTGGAG 36

RESULT 120  
US-09-034-205-32/C

Sequence 32, Application US/09034205  
Patent No. 6194149

GENERAL INFORMATION:

APPLICANT: Lyamachev, Victor I.  
Fors, Lance  
Neil, Bruce P.

APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco

```
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,205
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-034-205-32

Query Match      66.7% Score 12; DB 3; Length 239;
Best Local Similarity 83.3% Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12
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Db 54 GGGGTCTGGAG 43

RESULT 121
US-09-034-205-36/c
Sequence 36, Application US/09034205
Patent No. 6194149
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Fors, Lance P.
APPLICANT: Neri, Bruce P.
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
STRUCTURE-BRIDGING OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,205
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
```

```
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-034-205-36
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```
Query Match      66.7% Score 12; DB 3; Length 239;
Best Local Similarity 83.3% Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GGGGUCGAG 12
    |||:|:|:|
Db 54 GGGGTCTGGAG 43
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RESULT 122
US-08-934-097A-32/c
Sequence 32, Application US/08934097A
Patent No. 6210880
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Fors, Lance P.
APPLICANT: Neri, Bruce P.
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
STRUCTURE PROBING WITH STRUCTURE-BRIDGING
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,097A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-02980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-934-097A-32
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Query Match      66.7% Score 12; DB 3; Length 239;
Best Local Similarity 83.3% Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGGGUCGAG 12
    |||:|:~|:|
Db 54 GGGGTCTGGAG 43
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RESULT 123  
US-08-934-097A-36/c  
; Sequence 36, Application US/08934097A  
; Patent No. 6210680  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neil, Bruce P.  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; TITLE OF INVENTION: Structure Probing With Structure-Bridging  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk.  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,097A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-02980  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; US-08-934-097A-36  
Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGCGANG 12  
Db 54 GGGGTCTCGANG 43  
RESULT 124  
US-08-851-588-32/c  
; Sequence 32, Application US/08851588  
; Patent No. 6214545  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Prudent, James R.  
; APPLICANT: Dahlberg, James E.  
; APPLICANT: Fors, Lance  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; TITLE OF INVENTION: Structure Probing  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-32  
Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGCGANG 12  
Db 54 GGGGTCTCGANG 43  
RESULT 125  
US-08-851-588-36/c  
; Sequence 36, Application US/08851588  
; Patent No. 6214545  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Prudent, James R.  
; APPLICANT: Dahlberg, James E.  
; APPLICANT: Fors, Lance  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; TITLE OF INVENTION: Structure Probing  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851,588  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ingolia, Diane E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET NUMBER: FORS-02777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-36

Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

## RESULT 126

US-09-677-218B-32/c

Sequence 32, Application US/09677218B  
Patent No. 6355437

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B

FILING DATE: 02-Oct-2000

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/034,205

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: F0RS-03268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-677-218B-32

Query Match 66.7%; Score 12; DB 3; Length 239;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

## RESULT 127

US-09-677-218B-36/c

Sequence 36, Application US/09677218B  
Patent No. 6355437

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B

FILING DATE: 02-Oct-2000

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/034,205

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: F0RS-03268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-677-218B-36

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

## RESULT 128

US-09-677-192-32/c

Sequence 32, Application US/09677192  
Patent No. 6358691

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING

;; TITLE OF INVENTION: OLIGONUCLEOTIDES  
;; FILE REFERENCE: FORS-04708  
;; CURRENT APPLICATION NUMBER: US/09/677,192  
;; CURRENT FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 09/034,205  
;; PRIOR FILING DATE: 1998-03-03  
;; NUMBER OF SEQ ID NOS: 68  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 32  
;; LENGTH: 239  
;; TYPE: DNA  
;; ORGANISM: Hepatitis C virus  
US-09-677-192-32

Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

RESULT 129  
US-09-677-192-36/c  
; Sequence 36, Application US/09677192  
; Patent No. 6358691  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
; FILE REFERENCE: FORS-04708  
; CURRENT APPLICATION NUMBER: US/09/677,192  
; CURRENT FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/034,205  
; PRIOR FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-677-192-36

Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

RESULT 130  
US-09-402-618B-32/c  
; Sequence 32, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/09/402,618B  
; CURRENT FILING DATE: 2000-07-18

;; PRIOR APPLICATION NUMBER: PCT/US98/03194  
;; PRIOR FILING DATE: 1998-05-05  
;; NUMBER OF SEQ ID NOS: 128  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 32  
;; LENGTH: 239  
;; TYPE: DNA  
;; ORGANISM: Hepatitis C virus  
US-09-402-618B-32

Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

RESULT 131  
US-09-402-618B-36/c  
; Sequence 36, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/09/402,618B  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-402-618B-36

Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

RESULT 132  
US-09-825-574-32/c  
; Sequence 32, Application US/09825574  
; Patent No. 6709819  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; Structure Probing With Structure-Bridging  
; Oligonucleotides.  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA

COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-825-574-32  
Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 54 GGGGTCCTGGAG 43  
RESULT 133  
US-09-825-574-36/C  
Sequence 36, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-825-574-36  
Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 54 GGGGTCCTGGAG 43  
RESULT 134  
US-09-676-768-32/C  
Sequence 32, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-676-768-32

Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
DB 54 GGGGTCCTGGAG 43

## RESULT 135

US-09-676-768-36/C  
Sequence 36, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lymachev, Victor I.  
Prudent, James R.  
Danberg, James E.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-676-768-36

Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
DB 54 GGGGTCCTGGAG 43

## RESULT 136

US-09-034-205-33/C  
Sequence 33, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lymachev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-09-034-205-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
DB 55 GGGGTCCTGGAG 44

## RESULT 137

US-09-034-205-38/C  
Sequence 38, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lymachev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
||||:|||||  
Db 56 GGGGTCCTGGAG 45

RESULT 138  
US-08-934-097A-33/c  
Sequence 33, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
||||:|||||  
Db 55 GGGGTCCTGGAG 44

RESULT 139  
US-08-934-097A-38/c  
Sequence 38, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
||||:|||||  
Db 56 GGGGTCCTGGAG 45

RESULT 140  
US-08-851-588-33/c

Sequence 33, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGUGAG 12  
Db 55 GGGGCTCTGGAG 44

RESULT 141  
US-08-851-588-38/C  
Sequence 38, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGUGAG 12  
Db 56 GGGGCTCTGGAG 45

RESULT 142  
US-09-677-218B-33/C  
Sequence 33, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Neri, Bruce P.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-677-218B-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 55 GGGGTCTCTGGAG 44

## RESULT 143

US-09-677-218B-38/c  
Sequence 38, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Karmin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-677-218B-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 56 GGGGTCTCTGGAG 45

## RESULT 144

US-09-677-192-33/c  
Sequence 33, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 33  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 55 GGGGTCTCTGGAG 44

## RESULT 145

US-09-677-192-38/c  
Sequence 38, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 38  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 56 GGGGTCTCTGGAG 45

## RESULT 146

US-09-402-618B-33/c



Sequence 33, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 33  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-33

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
||||:|||||  
Db 55 GGGGTCTCGAG 44

RESULT 147  
US-09-402-618B-38/c  
Sequence 38, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 2000-07-18  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 38  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-38

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
||||:|||||  
Db 56 GGGGTCTCGAG 45

RESULT 148  
US-09-825-574-33/c  
Sequence 33, Application US/09825574

Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-825-574-33

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
||||:|||||  
Db 55 GGGGTCTCGAG 44

RESULT 149  
US-09-825-574-38/c  
Sequence 38, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-825-574-38

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 56 GGGGCTCTGGAG 45

RESULT 150  
US-09-676-768-33/C  
Sequence 33, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588

FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-676-768-33

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 55 GGGGCTCTGGAG 44

RESULT 151  
US-09-676-768-38/C  
Sequence 38, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/576,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-676-768-38

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 56 GGGGTCTCGAG 45

RESULT 152  
US-08-335-595-1/c  
; Sequence 1, Application US/08335595  
; Patent No. 5914228  
; GENERAL INFORMATION:  
; APPLICANT: VIERLING, JOHN M  
; APPLICANT: HU, KE-QIN  
; TITLE OF INVENTION: DIRECT DETECTION OF HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LYON & LYON  
; STREET: 611 WEST 6TH STREET  
; CITY: LOS ANGELES  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335.595  
; FILING DATE: 08-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/175.473  
; FILING DATE:  
; APPLICATION NUMBER: US/07/758.862  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SCHNEIDER, CAROL A  
; REGISTRATION NUMBER: 34,923  
; REFERENCE/DOCKET NUMBER: 194/285  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 213-489-1600  
; TELEFAX: 213-955-0440  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-335-595-1

Query Match 66.7%; Score 12; DB 2; Length 242;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 100 GGGGTCTCGAG 89

RESULT 153  
US-09-034-205-26/c  
; Sequence 26, Application US/09034205  
; Patent No. 6194149

GENERAL INFORMATION:  
; APPLICANT: Lyamchev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neil, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034.205  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamtin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; US-09-034-205-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 56 GGGGTCTCGAG 45

RESULT 154  
US-09-034-205-29/c  
; Sequence 29, Application US/09034205  
; Patent No. 6194149  
; GENERAL INFORMATION:  
; APPLICANT: Lyamchev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neil, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
|||:|||||  
DB 56 GGGGTCTCGAG 45

RESULT 155  
US-09-034-205-31/C  
Sequence 31, Application US/09034205  
Patent No. 6194149

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"  
US-09-034-205-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
|||:|||||  
DB 55 GGGGTCTCGAG 44

RESULT 156

US-08-934-097A-26/C  
Sequence 26, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing with Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12  
|||:|||||  
DB 56 GGGGTCTCGAG 45

RESULT 157

US-08-934-097A-29/C  
Sequence 29, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.

APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||||:  
Db 56 GGGGTCTCTGGAG 45

RESULT 158  
US-08-934-097A-31/c  
Sequence 31, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||||:  
Db 55 GGGGTCTCTGGAG 44

RESULT 159  
US-08-851-588-26/c  
Sequence 26, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 56 GGGGTCCTGGAG 45

RESULT 160  
US-08-851-588-29/C  
Sequence 29, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 397-8338  
TELEFAX: (415) 705-8410  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 56 GGGGTCCTGGAG 45

RESULT 161  
US-08-851-588-31/C  
Sequence 31, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 55 GGGGTCCTGGAG 44

RESULT 162  
US-09-677-218B-26/C  
Sequence 26, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Fors, Lance  
APPLICANT: Brown, Mary Ann D.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-677-218B-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCUCCGAG 12  
||||:|||||  
Db 56 GGGGTCTCTGGAG 45

RESULT 163  
US-09-677-218B-29/c  
Sequence 29, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-677-218B-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCUCCGAG 12  
||||:|||||  
Db 56 GGGGTCTCTGGAG 45

RESULT 164  
US-09-677-218B-31/c  
Sequence 31, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-677-218B-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 55 GGGGTCTCGAG 44

RESULT 165  
US-09-677-192-26/C  
; Sequence 26, Application US/09677192  
; Patent No. 6358691  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
; FILE REFERENCE: FORS-04708  
; CURRENT APPLICATION NUMBER: US/09/677,192  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/034,205  
; PRIOR FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-677-192-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 56 GGGGTCTCGAG 45

RESULT 166  
US-09-677-192-29/C  
; Sequence 29, Application US/09677192  
; Patent No. 6358691  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
; FILE REFERENCE: FORS-04708  
; CURRENT APPLICATION NUMBER: US/09/677,192  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/034,205  
; PRIOR FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-677-192-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 56 GGGGTCTCGAG 45

RESULT 167  
US-09-677-192-31/C

; Sequence 31, Application US/09677192  
; Patent No. 6358691  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
; FILE REFERENCE: FORS-04708  
; CURRENT APPLICATION NUMBER: US/09/677,192  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/034,205  
; PRIOR FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-677-192-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 55 GGGGTCTCGAG 44

RESULT 168  
US-09-402-618B-26/C  
; Sequence 26, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-402-618B-26

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 56 GGGGTCTCGAG 45

RESULT 169  
US-09-402-618B-29/C  
; Sequence 29, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang



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; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-29
```

```
Query Match      66.7%; Score 12; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GGGGUCCTGGAG 12
      |||:|||||
DB      56 GGGGTCTGGAG 45
```

```
RESULT 170
US-09-402-618B-31/C
; Sequence 31, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-31
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```
Query Match      66.7%; Score 12; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GGGGUCCTGGAG 12
      |||:|||||
DB      55 GGGGTCTGGAG 44
```

```
RESULT 171
US-09-402-618B-124
; Sequence 124, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
```

```
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-124
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```
Query Match      66.7%; Score 12; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GGGGUCCTGGAG 12
      |||:|||||
DB      189 GGGGTCTGGAG 200
```

```
RESULT 172
US-09-402-618B-127
; Sequence 127, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 127
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-127
```

```
Query Match      66.7%; Score 12; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGUCCTGGAG 12
      |||:|||||
DB      189 GGGGTCTGGAG 200
```

```
RESULT 173
US-09-402-618B-128
; Sequence 128, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
```

APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 128  
LENGTH: 244  
TYPE: DNA  
US-09-402-618B-128

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 189 GGGGUCCTGGAG 200

## RESULT 174

US-09-825-574-26/c  
Sequence 26, Application US/09825574  
Patent No. 6709819

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26;  
US-09-825-574-26

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 56 GGGGUCCTGGAG 45

## RESULT 175

US-09-825-574-29/c  
Sequence 29, Application US/09825574  
Patent No. 6709819

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 29;

US-09-825-574-29

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 56 GGGGUCCTGGAG 45

RESULT 176  
US-09-825-574-31/C  
Sequence 31, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neil, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-825-574-31

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
DB 55 GGGGTCTTGAG 44

RESULT 177  
US-09-676-768-26/C  
Sequence 26, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-676-768-26

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
DB 56 GGGGTCTTGAG 45

RESULT 178  
US-09-676-768-29/C  
Sequence 29, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-676-768-29

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
Db 56 GGGGCTCGAG 45

RESULT 179  
US-09-676-768-31/C  
Sequence 31, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fore, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-676-768-31

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
Db 55 GGGGCTCGAG 44

RESULT 180  
US-08-441-971-33/C  
Sequence 33, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,523  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiak, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: (ATCC # 40394)  
INDIVIDUAL ISOLATE: hcv1  
US-08-441-971-33

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

Db 34 GGGGTCTGTGAG 23

RESULT 181

US-08-441-971-34/c  
Sequence 34, Application US/08441971

Patent No. 6071693

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971

FILING DATE: 16-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

APPLICATION NUMBER: 07/697,326

FILING DATE: 8 May 1991

ATTORNEY/AGENT INFORMATION:

NAME: Janiuk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: u85

US-08-441-971-34

Query Match 66.7%; Score 12; DB 3; Length 252;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 34 GGGGTCTGTGAG 23

RESULT 182

US-08-441-971-35/c

Sequence 35, Application US/08441971

Patent No. 6071693

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971

FILING DATE: 16-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

APPLICATION NUMBER: 07/697,326

FILING DATE: 8 May 1991

ATTORNEY/AGENT INFORMATION:

NAME: Janiuk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: aue1

US-08-441-971-35

Query Match 66.7%; Score 12; DB 3; Length 252;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 34 GGGGTCTGTGAG 23

RESULT 183

US-08-441-971-36/c

Sequence 36, Application US/08441971

Patent No. 6071693

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp2  
US-08-441-971-36

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
||||:|||||  
Db 34 GGGGTCTGAG 23

RESULT 184  
US-08-441-971-37/c  
Sequence 37, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-441-971-37

REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-441-971-37

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
||||:|||||  
Db 34 GGGGTCTGAG 23

RESULT 185  
US-08-441-971-38/c  
Sequence 38, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 121  
US-08-441-971-38

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 34 GGGGTCCTGGAG 23

## RESULT 186

US-08-441-971-39/C  
Sequence 39, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441.971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221.653  
FILING DATE:  
APPLICATION NUMBER: US/07/881.528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us4  
US-08-441-971-39

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 34 GGGGTCCTGGAG 23

RESULT 187

US-08-441-971-40/C  
Sequence 40, Application US/08441971  
Patent No. 6071693

GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441.971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221.653  
FILING DATE:  
APPLICATION NUMBER: US/07/881.528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: jh1  
US-08-441-971-40

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 34 GGGGTCCTGGAG 23

## RESULT 188

US-08-441-971-41/C  
Sequence 41, Application US/08441971  
Patent No. 6071693

GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE: US/07/881,528  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: nacs  
US-08-441-971-41

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 34 GGGGCTCTGGAG 23

RESULT 189  
US-08-441-971-42/c  
Sequence 42, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
NUMBER OF SEQUENCES: 147  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653

FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: arg2  
US-08-441-971-42

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 34 GGGGCTCTGGAG 23

RESULT 190  
US-08-441-971-43/c  
Sequence 43, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
NUMBER OF SEQUENCES: 147  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL



INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: spl  
US-08-441-971-43

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGAG 12  
|||:|||||  
Db 34 GGGGTCTGAG 23

RESULT 191  
US-08-441-971-44/c  
Sequence 44, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ghl  
US-08-441-971-44

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGAG 12  
|||:|||||  
Db 34 GGGGTCTGAG 23

RESULT 192  
US-08-441-971-45/c  
Sequence 45, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: i15  
US-08-441-971-45

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGAG 12  
|||:|||||  
Db 34 GGGGTCTGAG 23

RESULT 193  
US-08-441-971-49/c  
Sequence 49, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE: US/07/881,528  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 9161329  
US-08-441-971-49  
Query Match 66.7%; Score 12; DB 3; Length 252;  
Best local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 34 GGGGTCCTGGAG 23  
RESULT 194  
US-08-221-653-33/c  
Sequence 33, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: (ATCC # 40394)  
INDIVIDUAL ISOLATE: hcvi  
US-08-221-653-33

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 34 GGGGTCCTGGAG 23

RESULT 195  
US-08-221-653-34/c  
Sequence 34, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-221-653-34

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|:|  
Db 34 GGGGTCTCGAG 23

RESULT 196  
US-08-221-653-35/C  
Sequence 35, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221.653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881.528  
FILING DATE:  
APPLICATION NUMBER: 07/697.326  
FILING DATE: 8 MAY 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-221-653-35

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|:|  
Db 34 GGGGTCTCGAG 23

RESULT 197  
US-08-221-653-36/C  
Sequence 36, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221.653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881.528  
FILING DATE:  
APPLICATION NUMBER: 07/697.326  
FILING DATE: 8 MAY 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp2  
US-08-221-653-36

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:~|:|  
Db 34 GGGGTCTCGAG 23

RESULT 198  
US-08-221-653-37/C  
Sequence 37, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKTEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-221-653-37

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
Db 34 GGGGTCCTGGAG 23

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Sequence 38, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKTEL  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 121  
US-08-221-653-38

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
Db 34 GGGGTCCTGGAG 23

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Sequence 39, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441  
 TELETYPE: EZEKIEL  
 INFORMATION FOR SEQ ID NO: 39:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 252 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: us4  
 US-08-221-653-39

Query Match 66.7%; Score 12; DB 3; Length 252;  
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 Db 34 GGGGTCCTCGAG 23

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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:45:46 ; Search time 252.474 Seconds  
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Perfect score: 18

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Gapop 60.0 , Gapext 60.0

Searched: 5633728 seqs, 3035525691 residues

Word size : 0

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	13	72.2	20	US-10-008-1408-30	Sequence 30, Appl
6	13	72.2	3286	US-10-723-860-5700	Sequence 5700, Ap
7	13	72.2	5132	US-10-723-860-5700	Sequence 5700, Ap
8	13	72.2	92726	US-09-997-722-193	Sequence 193, App
9	13	72.2	165221	US-10-087-192-1015	Sequence 1015, App
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146	12	66.7	177	9	US-09-899-082A-70	Sequence 70, Appl	C 219	12	66.7	201	18	US-10-719-993-9591	Sequence 9591, App
147	12	66.7	177	9	US-09-899-082A-72	Sequence 72, Appl	C 220	12	66.7	201	18	US-10-719-993-26387	Sequence 26387, A
148	12	66.7	177	9	US-09-899-082A-73	Sequence 73, Appl	C 221	12	66.7	201	18	US-10-719-993-26388	Sequence 26388, A
149	12	66.7	177	9	US-09-899-082A-74	Sequence 74, Appl	C 222	12	66.7	201	18	US-10-719-993-26511	Sequence 26511, A
150	12	66.7	177	9	US-09-899-082A-75	Sequence 75, Appl	C 223	12	66.7	201	18	US-10-719-993-26602	Sequence 26602, A
151	12	66.7	177	9	US-09-899-082A-76	Sequence 76, Appl	C 224	12	66.7	201	18	US-10-719-993-50021	Sequence 50021, A
152	12	66.7	177	9	US-09-899-082A-77	Sequence 77, Appl	C 225	12	66.7	201	18	US-10-719-993-50033	Sequence 50033, A
153	12	66.7	177	9	US-09-899-082A-78	Sequence 78, Appl	C 226	12	66.7	201	18	US-10-719-993-50034	Sequence 50034, A
154	12	66.7	177	9	US-09-899-082A-79	Sequence 79, Appl	C 227	12	66.7	201	18	US-10-719-993-52863	Sequence 52863, A
155	12	66.7	177	9	US-09-899-082A-80	Sequence 80, Appl	C 228	12	66.7	201	19	US-10-741-600-16871	Sequence 16871, A
156	12	66.7	177	9	US-09-899-302-61	Sequence 61, Appl	C 229	12	66.7	201	19	US-10-741-600-16872	Sequence 16872, A
157	12	66.7	177	9	US-09-899-302-67	Sequence 67, Appl	C 230	12	66.7	201	19	US-10-741-600-16902	Sequence 16902, A















TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-67

Query Match 100.0%; Score 18; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAGANNNNN 18  
Db 1 GGGGUCUGAGANNNNN 18

RESULT 3  
US-10-053-883-10  
Sequence 10, Application US/10053883  
Publication No. US20030113737A1  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Morten Lorentz  
TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
FILE REFERENCE: PEDERSEN-1A  
CURRENT APPLICATION NUMBER: US/10/053.883  
CURRENT FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: PA 2001 00126  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: US 60/267,704  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
NAME/KEY: misc feature  
LOCATION: (12)-(29)  
OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-10

Query Match 83.3%; Score 15; DB 15; Length 29;  
Best Local Similarity 86.7%; Pred. No. 19;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 GUCCUGAGANNNNN 18  
Db 3 GTCTCGAGANNNNN 17

RESULT 4  
US-10-053-883-11/c  
Sequence 11, Application US/10053883  
Publication No. US20030113737A1  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Morten Lorentz  
TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
FILE REFERENCE: PEDERSEN-1A  
CURRENT APPLICATION NUMBER: US/10/053.883  
CURRENT FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: PA 2001 00126  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: US 60/267,704

PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
NAME/KEY: misc feature  
LOCATION: (1)-(18)  
OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-11

Query Match 83.3%; Score 15; DB 15; Length 29;  
Best Local Similarity 86.7%; Pred. No. 19;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 GUCCUGAGANNNNN 18  
Db 27 GTCTCGAGANNNNN 13

RESULT 5  
US-10-008-140B-30/c  
Sequence 30, Application US/10008140B  
Publication No. US20030124512A1  
GENERAL INFORMATION:  
APPLICANT: Stuyver, Lieven  
TITLE OF INVENTION: Simultaneous Quantification of Nucleic Acids in Diseased Cells  
FILE REFERENCE: 08841.105021  
CURRENT APPLICATION NUMBER: US/10/008.140B  
CURRENT FILING DATE: 2001-10-18  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 30  
LENGTH: 20  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: labelled oligonucleotide (probe) used to detect HCV viral load  
NAME/KEY: misc\_feature  
LOCATION: (1)-(1)  
OTHER INFORMATION: n=FAM modified cytosine  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (20)-(20)  
OTHER INFORMATION: n=TAMRA modified cytosine  
US-10-008-140B-30

Query Match 72.2%; Score 13; DB 15; Length 20;  
Best Local Similarity 84.6%; Pred. No. 3.2e+02;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAGN 13  
Db 13 GGGGTCCTCGAGN 1

RESULT 6  
US-10-723-860-5790/c  
Sequence 5790, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsburg, Wendy M.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
FILE REFERENCE: 05882.0193.NPUS01

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; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5790
; LENGTH: 3286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (248)..(271)
; OTHER INFORMATION: "n" is a, c, g, or t
US-10-723-860-5790

Query Match      72.2%; Score 13; DB 18; Length 3286;
Best Local Similarity 92.3%; Pred. No. 88;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      6 CCUGAGNNNNNN 18
Db      278 CCTGAGNNNNNN 266

RESULT 7
US-10-723-860-5700/c
; Sequence 5700, Application US/10723860
; Publication No. US2004025606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natacha
; APPLICANT: Gineburg, Wendy M.
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882, 0193, NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5700
; LENGTH: 5132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (974)..(1005)
; OTHER INFORMATION: "n" is a, c, g, or t
US-10-723-860-5700

Query Match      72.2%; Score 13; DB 18; Length 5132;
Best Local Similarity 92.3%; Pred. No. 78;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      6 CCUGAGNNNNNN 18
Db      1012 CCTGAGNNNNNN 1000

RESULT 8
US-09-997-722-193/c
; Sequence 193, Application US/09997722
; Publication No. US2004007215A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377

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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 92726
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (122)..(148)
; OTHER INFORMATION: "n" at positions 122 through 148 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3122)..(3263)
; OTHER INFORMATION: "n" at positions 3122 through 3263 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7485)..(8927)
; OTHER INFORMATION: "n" at positions 7485 through 8927 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24884)..(25439)
; OTHER INFORMATION: "n" at positions 24884 through 25439 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36036)..(36055)
; OTHER INFORMATION: "n" at positions 36036 through 36055 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (46607)..(46729)
; OTHER INFORMATION: "n" at positions 46607 through 46729 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (77651)..(77670)
; OTHER INFORMATION: "n" at positions 77651 through 77670 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (81264)..(81462)
; OTHER INFORMATION: "n" at positions 81264 through 81462 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (89156)..(89175)
; OTHER INFORMATION: "n" at positions 89156 through 89175 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (90342)..(90361)
; OTHER INFORMATION: "n" at positions 90342 through 90361 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (91379)..(91398)
; OTHER INFORMATION: "n" at positions 91379 through 91398 can be any base.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (92723)..(92726)
; OTHER INFORMATION: "n" at positions 92723 through 92726 can be any base.
US-09-997-722-193

Query Match      72.2%; Score 13; DB 11; Length 92726;
Best Local Similarity 92.3%; Pred. No. 38;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      6 CCUGAGNNNNNN 18
Db      155 CCTGAGNNNNNN 143

RESULT 9
US-10-087-192-1015
; Sequence 1015, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:

```



```

; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 165221
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(165221)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1015

Query Match      72.2%; Score 13; DB 13; Length 165221;
Best Local Similarity 92.3%; Pred. No. 33;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCUGAGNNNNNN 18
      ||:|||||
Db      59475 CCTGAGNNNNNN 59487

RESULT 10
US-10-394-948-31
; Sequence 31, Application US/10394948
; Publication No. US20040023267A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NO. US20040023267A1 Compositions and Methods in Cancer
; FILE REFERENCE: 529452000900
; CURRENT APPLICATION NUMBER: US/10/394,948
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US 60/367,025
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 167163
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(167163)
; OTHER INFORMATION: n = A,T,C or G
US-10-394-948-31

Query Match      72.2%; Score 13; DB 17; Length 167163;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCUGAGNNNNNN 18
      ||:|||||
Db      62041 CCTGAGNNNNNN 62053

RESULT 11
US-08-887-505-47
; Sequence 47, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kiluskie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
```

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; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walcher, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-887-505-47

Query Match      66.7%; Score 12; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTUGAG 12
      |||||||
Db      1 GGGGUCCTUGAG 12

RESULT 12
US-10-291-230-43/c
; Sequence 43, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: 76678.US.A
; CURRENT APPLICATION NUMBER: US/10/291,230
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
```

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; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A portion of an antisense library including a Bpm1 site.
; NAME/KEY: misc.feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
US-10-291-230-43

Query Match
Best Local Similarity 66.7%; Score 12; DB 15; Length 12;
Pred. No. 1.4e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy
12 CTGAGAGNNNNNN 18
|:|||||
Db
12 CTGAGAGNNNNNN 1

RESULT 13
US-10-291-249-43/c
; Sequence 43, Application US/10291249
; Publication No. US20030119041A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678 US B
; CURRENT APPLICATION NUMBER: US/10/291,249
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A portion of an antisense library including a Bpm1 site.
; NAME/KEY: misc.feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
US-10-291-249-43

Query Match
Best Local Similarity 66.7%; Score 12; DB 15; Length 12;
Pred. No. 1.4e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy
7 CUGAGAGNNNNNN 18
|:|||||
Db
12 CTGAGAGNNNNNN 1

RESULT 14
US-10-322-138-5/c
; Sequence 5, Application US/10322138
; Publication No. US20030175765A1
; GENERAL INFORMATION:
; APPLICANT: Kessler, Christoph
```

```

; APPLICANT: Haberkusen, Gerd
; APPLICANT: Bartl, Knut
; APPLICANT: Orum, Henrik
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS
; FILE REFERENCE: 4817/OO
; CURRENT APPLICATION NUMBER: US/10/322,138
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/530,746B
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: probe
US-10-322-138-5

Query Match
Best Local Similarity 66.7%; Score 12; DB 16; Length 12;
Pred. No. 1.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy
1 GGGGUCCTGAG 12
|:|||||
Db
12 GGGGUCCTGAG 1

RESULT 15
US-09-504-231A-1587/c
; Sequence 1587, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwigen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Maciejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT-
; FILE REFERENCE: TP1 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1587
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1587

Query Match
Best Local Similarity 66.7%; Score 12; DB 9; Length 15;
Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy
1 GGGGUCCTGAG 12
|:|||||
Db
15 GGGGUCCTGAG 4

RESULT 16
US-09-274-553D-1587/c
; Sequence 1587, Application US/09274553D
```

Patent No. US20020082225A1  
GENERAL INFORMATION:  
APPLICANT: Blatt, Lawrence  
APPLICANT: McSwiggen, James  
APPLICANT: Roberts, Beth  
APPLICANT: Pavco, Pamela  
APPLICANT: Maccejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
FILE REFERENCE: rpl 247/282  
CURRENT APPLICATION NUMBER: US/09/274,553D  
CURRENT FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3148  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 1587  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553D-1587

Query Match 66.7%; Score 12; DB 9; Length 15;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
|||||  
Db 15 GGGGTCTCTGGAG 4

RESULT 17  
US-09-740-332-26/c  
Sequence 26, Application US/09740332  
Publication No. US20030125270A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
TITLE OF INVENTION: Hepatitis C Virus Infection  
FILE REFERENCE: RPI 400/003  
CURRENT APPLICATION NUMBER: US/09/740,332  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9704  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 26  
LENGTH: 17  
TYPE: RNA  
ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-26

Query Match 66.7%; Score 12; DB 10; Length 17;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
|||||  
Db 13 GGGGTCTCTGGAG 2

RESULT 18  
US-09-740-332-4529  
Sequence 4529, Application US/09740332  
Publication No. US20030125270A1

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
TITLE OF INVENTION: Hepatitis C Virus Infection  
FILE REFERENCE: RPI 400/003  
CURRENT APPLICATION NUMBER: US/09/740,332  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9704  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 4529  
LENGTH: 17  
TYPE: RNA  
ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-4529

Query Match 66.7%; Score 12; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
|||||  
Db 6 GGGGUCCTGGAG 17

RESULT 19  
US-09-817-879-26/c  
Sequence 26, Application US/09817879  
Publication No. US20030171311A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
TITLE OF INVENTION: Hepatitis C Virus Infection  
FILE REFERENCE: MBH00-801-F  
CURRENT APPLICATION NUMBER: US/09/817,879  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9703  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 26  
LENGTH: 17  
TYPE: RNA  
ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-26

Query Match 66.7%; Score 12; DB 10; Length 17;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
|||||  
Db 13 GGGGTCTCTGGAG 2

RESULT 20  
US-09-817-879-4529  
Sequence 4529, Application US/09817879  
Publication No. US20030171311A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
TITLE OF INVENTION: Hepatitis C Virus Infection  
FILE REFERENCE: MBH00-801-F  
CURRENT APPLICATION NUMBER: US/09/817,879  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9703  
SOFTWARE: Patentin version 3.0

```
/ SEQ ID NO 4529
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4529

Query Match      66.7%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCGCGAG 12
Db      6 GGGGUCGCGAG 17

RESULT 21
US-10-298-255-4/c
/ Sequence 4, Application US/10298255
/ Publication No. US20030134312A1
/ GENERAL INFORMATION:
/ APPLICANT: BURGOME, LEIGH A.
/ TITLE OF INVENTION: METHODS AND MATERIALS FOR DETECTING GENETIC MATERIAL
/ FILE REFERENCE: 45858-56064
/ CURRENT APPLICATION NUMBER: US/10/298,255
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: 60/336,005
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-298-255-4

Query Match      66.7%; Score 12; DB 15; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCGCGAG 12
Db      16 GGGGUCGCGAG 5

RESULT 22
US-10-669-841-2619/c
/ Sequence 2619, Application US/10669841
/ Publication No. US20040127446A1
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Lawrence, Blact
/ APPLICANT: Dennis, Macejak
/ APPLICANT: James, McSwiggen
/ APPLICANT: David, Morrissey
/ APPLICANT: Pamela, Pavco
/ APPLICANT: Patricia, Lee
/ APPLICANT: Kenneth, Draper
/ APPLICANT: Elisabeth, Roberts
/ TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPV
/ TITLE OF INVENTION: VIRUS REPLICATION
/ FILE REFERENCE: 400/042US (MBH02-249-E)
/ CURRENT APPLICATION NUMBER: US/10/669,841
/ PRIOR FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: PCT/US02/09187
/ PRIOR FILING DATE: 2002-03-26
/ PRIOR APPLICATION NUMBER: US 60/236,876
/ PRIOR FILING DATE: 2001-06-08
```

```
/ PRIOR APPLICATION NUMBER: US 60/335,059
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: US 60/337,055
/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US 09/817,879
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: US 09/740,332
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: US 09/611,931
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: US 09/504,321
/ PRIOR FILING DATE: 2000-02-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 16207
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2619
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-2619

Query Match      66.7%; Score 12; DB 18; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCGCGAG 12
Db      13 GGGGUCGCGAG 2

RESULT 23
US-10-669-841-7122
/ Sequence 7122, Application US/10669841
/ Publication No. US20040127446A1
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Lawrence, Blact
/ APPLICANT: Dennis, Macejak
/ APPLICANT: James, McSwiggen
/ APPLICANT: David, Morrissey
/ APPLICANT: Pamela, Pavco
/ APPLICANT: Patricia, Lee
/ APPLICANT: Kenneth, Draper
/ APPLICANT: Elisabeth, Roberts
/ TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPV
/ TITLE OF INVENTION: VIRUS REPLICATION
/ FILE REFERENCE: 400/042US (MBH02-249-E)
/ CURRENT APPLICATION NUMBER: US/10/669,841
/ PRIOR FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: PCT/US02/09187
/ PRIOR FILING DATE: 2002-03-26
/ PRIOR APPLICATION NUMBER: US 60/296,876
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: US 60/335,059
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: US 60/337,055
/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US 09/817,879
/ PRIOR FILING DATE: 2001-03-26
```

```

; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7122
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-7122

Query Match      66.7%; Score 12; DB 18; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTCGAG 12
DB      6 GGGGUCCTCGAG 17

RESULT 24
US-08-887-505-39
; Sequence 39, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilbuckie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 39:
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHEICAL: NO
; ANTI-SENSE: YES
US-08-887-505-39

Query Match      66.7%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTCGAG 12
DB      1 GGGGUCCTCGAG 12

RESULT 25
US-08-887-505-40
; Sequence 40, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilbuckie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHEICAL: NO
; ANTI-SENSE: YES
US-08-887-505-40

Query Match      66.7%; Score 12; DB 8; Length 18;
```

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0;

QY 1 GGGGUCUGAG 12  
Db 7 GGGGUCUGAG 18

## RESULT 26

US-08-887-505-41  
; Sequence 41, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-5000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-41

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
Db 1 GGGGUCUGAG 12

RESULT 27  
US-08-887-505-42  
; Sequence 42, Application US/08887505

; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-42

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
Db 7 GGGGUCUGAG 18

## RESULT 28

US-08-887-505-43  
; Sequence 43, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
ATTORNEY/AGENT INFORMATION:  
NAME: Keener, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-43

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
DB 1 GGGGUCGCGAG 12

RESULT 29  
US-08-887-505-44  
Sequence 44, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuksie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
ATTORNEY/AGENT INFORMATION:  
NAME: Keener, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-44

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
DB 7 GGGGUCGCGAG 18

RESULT 30  
US-08-887-505-45  
Sequence 45, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuksie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-45

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12

## RESULT 31

US-08-887-505-46  
Sequence 46, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walcher, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-46

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCUGAG 12  
Db 7 GGGGUCCUGAG 18

## RESULT 32

US-08-887-505-49  
Sequence 49, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walcher, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-49

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCUGAG 12



Db 1 GGGGUCGAG 12

## RESULT 33

US-08-887-505-50  
; Sequence 50, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US2002081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-50

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 7 GGGGUCGAG 18

## RESULT 34

US-08-887-505-51  
; Sequence 51, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-51

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 1 GGGGUCGAG 12

## RESULT 35

US-08-887-505-52  
; Sequence 52, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US2002081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP

STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-52

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 7 GGGGTCCTGGAG 18

RESULT 36  
US-08-887-505-53  
Sequence 53, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-53

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12

RESULT 37  
US-08-887-505-54  
Sequence 54, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-54

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 7 GGGGUCCUGAG 18

RESULT 38  
US-08-887-505-141  
Sequence 141, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kiluskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 141:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES

US-08-887-505-141

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 7 GGGGUCCUGAG 18

RESULT 39  
US-08-887-505-142  
Sequence 142, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kiluskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 142:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-142

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 7 GGGGUCCUGAG 18

RESULT 40  
US-08-887-505-143  
; Sequence 143, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 143:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-143

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12  
Db 7 GGGGUCCUGGAG 18

RESULT 41  
US-08-887-505-144  
; Sequence 144, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walthers, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 144:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-144

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12  
Db 7 GGGGUCCUGGAG 18

RESULT 42  
US-08-887-505-145  
; Sequence 145, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-145

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
Db 1 GGGGUCGAG 12

RESULT 43  
US-08-887-505-146  
Sequence 146, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilruskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 146:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-146

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
Db 1 GGGGUCGAG 12

RESULT 44  
US-08-887-505-147  
Sequence 147, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilruskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-887-505-147

Query Match          66.7%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12
Db 1 GGGGUCCUGGAG 12

RESULT 45
US-09-782-361-14
; Sequence 14, Application US/09782361
; Patent No. US20020064778A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Ya-Wen
; TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GEN
; FILE REFERENCE: 2883-4757US
; CURRENT APPLICATION NUMBER: US/09/782,361
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer for PSMEA
; US-09-782-361-14

Query Match          66.7%; Score 12; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12
Db 2 GGGGTCTCTGGAG 13

RESULT 46
US-10-461-790-121/c
; Sequence 121, Application US/10461790
; Publication No. US2004002911A1
; GENERAL INFORMATION:
; APPLICANT: Lannen, Jeffery M.
; APPLICANT: Kolik, Daniel P.
; APPLICANT: Dockter, Daniel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: US/10/461,790
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 121
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Hepatitis C Virus
```

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US-10-461-790-121

Query Match          66.7%; Score 12; DB 17; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12
Db 15 GGGGTCTCTGGAG 4

RESULT 47
US-10-667-271-466/c
; Sequence 466, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 466
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
; US-10-667-271-466

Query Match          66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12
Db 13 GGGGTCTCTGGAG 2

RESULT 48
US-10-667-271-467/c
; Sequence 467, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwigen, James
```

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; APPLICANT: Macejak, Dennis
; APPLICANT: Belgelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 467
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-467

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      12 GGGGTCTCTGGAG 1

RESULT 49
US-10-667-271-498/c
; Sequence 498, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Belgelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: US/10/667,271
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
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; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 498
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-667-271-498

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      16 GGGGTCTCTGGAG 5

RESULT 50
US-10-667-271-500/c
; Sequence 500, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Belgelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: US/10/667,271
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 500
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
```





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; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 544
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-544

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      19 GGGGTCTCTGGAG 8

RESULT 54
US-10-667-271-545/c
; Sequence 545, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 545
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
```

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-667-271-545

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      17 GGGGTCTCTGGAG 6

RESULT 55
US-10-667-271-1162
; Sequence 1162, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1162
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1162

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      7 GGGGUCCTGGAG 18

RESULT 56
US-10-667-271-1163
; Sequence 1163, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
```

```
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1163
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sirna antisense region
US-10-667-271-1163

Query Match      66.7% Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUGGAG 12
Db      8 GGGGUCUGGAG 19

RESULT 57
US-10-667-271-1194
Sequence 1194, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
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PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1194
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sirna antisense region
US-10-667-271-1194

Query Match      66.7% Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUGGAG 12
Db      4 GGGGUCUGGAG 15

RESULT 58
US-10-667-271-1196
Sequence 1196, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1196
LENGTH: 19
TYPE: RNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1198

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGAG 12
        |||||
Db       6 GGGGUCGAG 17

RESULT 59
US-10-667-271-1198
; Sequence 1198, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: US/10/667,271
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1198
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1198

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGAG 12
        |||||
Db       5 GGGGUCGAG 16

RESULT 60
US-10-667-271-1234
; Sequence 1234, Application US/10667271
; Publication No. US20040209831A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: US/10/667,271
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1234

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGAG 12
        |||||
Db       2 GGGGUCGAG 13

RESULT 61
US-10-667-271-1240
; Sequence 1240, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: US/10/667,271
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
```

```

; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1240
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1240
```

```

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 GGGGUCGAG 12
        |||||
Db      1 GGGGUCGAG 12
```

```

RESULT 62
US-10-667-271-1241
; Sequence 1241, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1241
; LENGTH: 19
```

```

; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1241
```

```

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 GGGGUCGAG 12
        |||||
Db      3 GGGGUCGAG 14
```

```

RESULT 63
US-08-887-505-19
; Sequence 19, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilkuskie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Keirner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-887-505-19
```

```

Query Match      66.7%; Score 12; DB 8; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 GGGGUCGAG 12
```

Db 2 GGGGCTCTGGAG 13

RESULT 64  
US-08-887-505-20  
Sequence 20, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-20

Query Match 66.7%; Score 12; DB 8; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTCTGGAG 12  
Db 6 GGGGCTCTGGAG 17

RESULT 65  
US-10-291-230-49/c  
Sequence 49, Application US/10291230  
Publication No. US20030108939A1  
GENERAL INFORMATION:  
APPLICANT: Ruffner, Duane E.  
APPLICANT: Pierce, Michael L.

APPLICANT: Chen, Zhidong  
TITLE OF INVENTION: Directed Antisense Libraries  
FILE REFERENCE: T6678.US.A  
CURRENT APPLICATION NUMBER: US/10/291,230  
CURRENT FILING DATE: 2002-11-07  
PRIOR APPLICATION NUMBER: US 09/647,344  
PRIOR FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: PCT/US99/06742  
PRIOR FILING DATE: 1999-03-28  
PRIOR APPLICATION NUMBER: US 60/079,792  
PRIOR FILING DATE: 1998-03-28  
PRIOR APPLICATION NUMBER: US 60/107,504  
PRIOR FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 49  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Deletion fragment in a deletion fragment library, including a po  
FEATURE:  
OTHER INFORMATION: tion of a multiple cloning site.  
NAME/KEY: misc\_feature  
LOCATION: (1)-(14)  
OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
US-10-291-249-49

Query Match 66.7%; Score 12; DB 15; Length 20;

QY 7 CUGAGNNNNNN 18  
Db 20 CTGAGNNNNNN 9

RESULT 66  
US-10-291-249-49/c  
Sequence 49, Application US/10291249  
Publication No. US20030119041A1  
GENERAL INFORMATION:  
APPLICANT: Ruffner, Duane E.  
APPLICANT: Pierce, Michael L.  
APPLICANT: Chen, Zhidong  
TITLE OF INVENTION: Directed Antisense Libraries  
FILE REFERENCE: T6678.US.B  
CURRENT APPLICATION NUMBER: US/10/291,249  
CURRENT FILING DATE: 2002-11-07  
PRIOR APPLICATION NUMBER: US 09/647,344  
PRIOR FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: PCT/US99/06742  
PRIOR FILING DATE: 1999-03-28  
PRIOR APPLICATION NUMBER: US 60/079,792  
PRIOR FILING DATE: 1998-03-28  
PRIOR APPLICATION NUMBER: US 60/107,504  
PRIOR FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 49  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Deletion fragment in a deletion fragment library, including a po  
FEATURE:  
OTHER INFORMATION: tion of a multiple cloning site.  
NAME/KEY: misc\_feature  
LOCATION: (1)-(14)  
OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
US-10-291-249-49

Query Match 66.7%; Score 12; DB 15; Length 20;

Best Local Similarity 91.7%; Pred. No. 1.3e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGNNNNNN 18  
Db 20 CTGAGNNNNNN 9

## RESULT 67

US-10-008-140B-12/c  
; Sequence 12, Application US/10008140B  
; Publication No. US20030124512A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmasset, Ltd.  
; APPLICANT: Stuyver, Lieven  
; TITLE OF INVENTION: Simultaneous Quantification of Nucleic Acids in Diseased Cells  
; FILE REFERENCE: 08841. 105021  
; CURRENT APPLICATION NUMBER: US/10/008.140B  
; CURRENT FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide (probe) used to detect HCV viral load  
US-10-008-140B-12

Query Match 66.7%; Score 12; DB 15; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCUGAG 12  
Db 13 GGGGTCTCGAG 2

## RESULT 68

US-10-169-371-48/c  
; Sequence 48, Application US/10169371  
; Publication No. US20030175729A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN ELK, Michael Josephus Theresia  
; APPLICANT: HOGERS, Rene Cornelis Josephus  
; APPLICANT: HEIJNEN, Leo  
; TITLE OF INVENTION: Method for generating oligonucleotides, in particular for the  
; FILE REFERENCE: VAN ELK-2  
; CURRENT APPLICATION NUMBER: US/10/169.371  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: EPC 99204614.4  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: PCT/NL00/00963  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 48  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: misc\_feature  
; LOCATION: (1)-(14)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-169-371-48

Query Match 66.7%; Score 12; DB 16; Length 20;  
Best Local Similarity 91.7%; Pred. No. 1.3e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGNNNNNN 18  
Db 20 CTGAGNNNNNN 9

## RESULT 69

US-09-747-419-7/c  
; Sequence 7, Application US/09747419  
; Patent No. US20020155582A1  
; GENERAL INFORMATION:  
; APPLICANT: Lemon, Stanley  
; APPLICANT: Yi, Minkyung  
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
; FILE REFERENCE: 265.0007 0101  
; CURRENT APPLICATION NUMBER: US/09/747.419  
; CURRENT FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/171.909  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Red probe  
; NAME/KEY: misc\_difference  
; LOCATION: (1)-(1)  
; OTHER INFORMATION: LC640 labeled  
US-09-747-419-7

Query Match 66.7%; Score 12; DB 9; Length 21;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCUGAG 12  
Db 21 GGGGTCTCGAG 10

## RESULT 70

US-10-259-275-7/c  
; Sequence 7, Application US/10259275  
; Publication No. US20030125541A1  
; GENERAL INFORMATION:  
; APPLICANT: Lemon, Stanley M.  
; APPLICANT: Yi, Minkyung  
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
; FILE REFERENCE: 265.0007 0120  
; CURRENT APPLICATION NUMBER: US/10/259.275  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/171.909  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 09/747.419  
; PRIOR FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/325.236  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/338.123  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Red probe  
; NAME/KEY: misc\_difference  
; LOCATION: (1)-(1)  
; OTHER INFORMATION: LC640 labeled  
US-10-259-275-7

Query Match 66.7%; Score 12; DB 9; Length 21;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match 66.7%; Score 12; DB 15; Length 21;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 21 GGGGCTCTGAG 10

## RESULT 71

US-10-291-230-38/c  
; Sequence 38, Application US/10291230  
; Publication No. US20030108939A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruffner, Duane E.  
; APPLICANT: Pierce, Michael L.  
; TITLE OF INVENTION: Directed Antisense Libraries  
; FILE REFERENCE: T6678, US A  
; CURRENT APPLICATION NUMBER: US/10/291,230  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 09/647,344  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/US99/06742  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/079,792  
; PRIOR FILING DATE: 1998-03-28  
; PRIOR APPLICATION NUMBER: US 60/107,504  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Portion of an intermediate in the making of a deletion library,  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(16)  
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t/u.  
US-10-291-230-38

Query Match 66.7%; Score 12; DB 15; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18  
|||:|||||  
Db 22 CTGAGNNNNNN 11

## RESULT 72

US-10-291-249-38/c  
; Sequence 38, Application US/10291249  
; Publication No. US20030119041A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruffner, Duane E.  
; APPLICANT: Pierce, Michael L.  
; TITLE OF INVENTION: Directed Antisense Libraries  
; FILE REFERENCE: T6678, US B  
; CURRENT APPLICATION NUMBER: US/10/291,249  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 09/647,344  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/US99/06742  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/079,792  
; PRIOR FILING DATE: 1998-03-28  
; PRIOR APPLICATION NUMBER: US 60/107,504  
; PRIOR FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Portion of an intermediate in the making of a deletion library,  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(16)  
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t/u.  
US-10-291-249-38

Query Match 66.7%; Score 12; DB 15; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18  
|||:|||||  
Db 22 CTGAGNNNNNN 11

## RESULT 73

US-10-169-371-47  
; Sequence 47, Application US/10169371  
; Publication No. US20030175729A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN EIJK, Michael Josephus Theresia  
; APPLICANT: HOGERS, Rene Cornelis Josephus  
; APPLICANT: HEIJNEN, Leo  
; TITLE OF INVENTION: Method for generating oligonucleotides, in particular for the  
; FILE REFERENCE: VAN EIJK-2  
; CURRENT APPLICATION NUMBER: US/10/169,371  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: ERC 99204614.4  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: PCT/NL00/00963  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: misc\_feature  
; LOCATION: (7)..(22)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-169-371-47

Query Match 66.7%; Score 12; DB 16; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18  
|||:|||||  
Db 1 CTGAGNNNNNN 12

## RESULT 74

US-10-092-885-59  
; Sequence 59, Application US/10092885  
; Publication No. US20030190618A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMAL, BABRU  
; APPLICANT: LI, YUAN  
; APPLICANT: HERMIDA, LEANDRO C.  
; APPLICANT: HOPPA, NANCY L.

APPLICANT: JOHE, KARL K.  
TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG  
FILE REFERENCE: 0109015/026  
CURRENT APPLICATION NUMBER: US/10/092,885  
CURRENT FILING DATE: 2002-03-06  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 59  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: modified base  
LOCATION: (7)..(22)  
OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-092-885-59

Query Match 66.7%; Score 12; DB 16; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGANNNNNN 18  
|:|||||  
DB 1 CTGAGANNNNNN 12

## RESULT 75

US-10-045-674-375  
Sequence 3/5, Application US/10045674  
Publication No. US200302333A1  
GENERAL INFORMATION:  
APPLICANT: LADNER, ROBERT C.  
APPLICANT: COHEN, EDWARD H.  
APPLICANT: NASTRI, HORACIO G.  
APPLICANT: ROOKEY, KRISTIN L.  
APPLICANT: HOET, RENE  
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.  
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING  
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY  
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL  
TITLE OF INVENTION: LIBRARIES  
FILE REFERENCE: DYAX/002 CIP2  
CURRENT APPLICATION NUMBER: US/10/045,674  
CURRENT FILING DATE: 2001-10-25  
PRIOR APPLICATION NUMBER: 60/198,069  
PRIOR FILING DATE: 2000-04-17  
PRIOR APPLICATION NUMBER: 09/837,306  
PRIOR FILING DATE: 2001-04-17  
NUMBER OF SEQ ID NOS: 635  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 375  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide  
FEATURE:  
NAME/KEY: modified base  
LOCATION: (7)..(22)  
OTHER INFORMATION: A, T, C, G, other or unknown  
US-10-045-674-375

Query Match 66.7%; Score 12; DB 17; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGANNNNNN 18  
|:|||||  
DB 1 CTGAGANNNNNN 12

## RESULT 76

US-10-399-843-4  
Sequence 4, Application US/10399843  
Publication No. US20040053284A1  
GENERAL INFORMATION:  
APPLICANT: Andrus, Linda  
APPLICANT: Nichols, Carmen Nicola  
TITLE OF INVENTION: Universal Multi-Variant Detection System  
FILE REFERENCE: 454-30 PCT/US  
CURRENT APPLICATION NUMBER: US/10/399,843  
CURRENT FILING DATE: 2003-04-22  
PRIOR APPLICATION NUMBER: PCT/US02/12035  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: 60/284,334  
PRIOR FILING DATE: 2001-04-17  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(22)  
OTHER INFORMATION: Nucleotide sequence encoding a primer  
US-10-399-843-4

Query Match 66.7%; Score 12; DB 17; Length 22;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTCUGGAG 12  
|||||  
DB 11 GGGGCTCCTGAG 22

## RESULT 77

US-10-678-961B-22  
Sequence 22, Application US/10678961B  
Publication No. US2005007483A1  
GENERAL INFORMATION:  
APPLICANT: Slater, Michael R.  
APPLICANT: Straus, Ethan Edward  
APPLICANT: Wood, Keith V.  
APPLICANT: Hartnett, James Robert  
APPLICANT: Promega Corporation  
TITLE OF INVENTION: Vectors for Directional Cloning  
FILE REFERENCE: 341.023US1  
CURRENT APPLICATION NUMBER: US/10/678,961B  
CURRENT FILING DATE: 2003-10-03  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: A synthetic DNA fragment  
OTHER INFORMATION:  
NAME/KEY: misc feature  
LOCATION: 7-22  
OTHER INFORMATION: n = A, T, G, or C  
US-10-678-961B-22

Query Match 66.7%; Score 12; DB 19; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGANNNNNN 18  
|:|||||  
DB 1 CTGAGANNNNNN 12



RESULT 78  
US-10-702-228A-22  
; Sequence 22, Application US/10702228A  
; Publication No. US20050074785A1  
; GENERAL INFORMATION:  
; APPLICANT: Slater, Michael R.  
; APPLICANT: Wood, Keith V.  
; APPLICANT: Hartnett, James Robert  
; TITLE OF INVENTION: Vectors for Directional Cloning  
; FILE REFERENCE: 341.030US1  
; CURRENT APPLICATION NUMBER: US/10/702,228A  
; PRIOR FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: 10/678,961  
; PRIOR FILING DATE: 2003-10-03  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A synthetic DNA fragment  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 7-22  
; OTHER INFORMATION: n = A, T, G, or C  
US-10-702-228A-22

Query Match 66.7%; Score 12; DB 19; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGANNNNNN 18  
|:|||||  
Db 1 CTGAGANNNNNN 12

RESULT 79  
US-10-053-883-111  
; Sequence 111, Application US/10053883  
; Publication No. US20030113737A1  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Morten Lorentz  
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
; FILE REFERENCE: PEDERSEN-A  
; CURRENT APPLICATION NUMBER: US/10/053,883  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: PA 2001 00126  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 60/267,704  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 111  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (7)..(23)  
; OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-111

Query Match 66.7%; Score 12; DB 15; Length 23;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGANNNNNN 18

Db 1 CTGAGANNNNNN 12

RESULT 80  
US-10-053-883-112/c  
; Sequence 112, Application US/10053883  
; Publication No. US20030113737A1  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Morten Lorentz  
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
; FILE REFERENCE: PEDERSEN-A  
; CURRENT APPLICATION NUMBER: US/10/053,883  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: PA 2001 00126  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 60/267,704  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 112  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(17)  
; OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-112

Query Match 66.7%; Score 12; DB 15; Length 23;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGANNNNNN 18  
|:|||||  
Db 23 CTGAGANNNNNN 12

RESULT 81  
US-08-887-505-48  
; Sequence 48, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kiluskie, Robert E.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-48

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 1 GGGGTCTCGAG 12

RESULT 82  
US-08-887-505-55  
Sequence 55, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilukkie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-55

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 1 GGGGTCTCGAG 12

RESULT 83  
US-08-887-505-56  
Sequence 56, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilukkie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-56

Query Match 66.7%; Score 12; DB 8; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 1 GGGGUCCTGGAG 12

## RESULT 84

US-08-887-505-57  
; Sequence 57, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilbuckie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-57

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 13 GGGGUCCTGGAG 24

RESULT 85  
US-08-887-505-58  
; Sequence 58, Application US/08887505

; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilbuckie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-58

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 13 GGGGUCCTGGAG 24

## RESULT 86

US-08-887-505-59  
; Sequence 59, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilbuckie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-59

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 13 GGGGTCTGTGAG 24

RESULT 87  
US-08-887-505-60  
Sequence 60, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-60

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 1 GGGGTCTGTGAG 12

RESULT 88  
US-08-887-505-61  
Sequence 61, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-61

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|  
Db 13 GGGGCTCGAG 24

RESULT 89  
US-08-887-505-62  
Sequence 62, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilnuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-62

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|  
Db 1 GGGGCTCGAG 12

RESULT 90  
US-08-887-505-63  
Sequence 63, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilnuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-63

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12

Db 13 GGGGCTCTGGAG 24

```

RESULT 91
US-08-887-505-64
; Sequence 64, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilkuskie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHEICAL: NO
; ANTI-SENSE: YES
; US-08-887-505-64

Query Match 66.7%; Score 12; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGGGCTCTGGAG 12  
 Db 1 GGGGCTCTGGAG 12

```

RESULT 92
US-08-887-505-65
; Sequence 65, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilkuskie, Robert E.
; APPLICANT: Frank, Bruce L.

```

```

; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHEICAL: NO
; ANTI-SENSE: YES
; US-08-887-505-65

Query Match 66.7%; Score 12; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGGGCTCTGGAG 12  
 Db 13 GGGGCTCTGGAG 24

```

RESULT 93
US-08-887-505-66
; Sequence 66, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilkuskie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP

```

STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-66

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0;

Qy 1 GGGGUCUUGAG 12  
Db 1 GGGGTCCTGGAG 12

RESULT 94  
US-08-887-505-148  
Sequence 148, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-148

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GGGGUCUUGAG 12  
Db 7 GGGGUCUUGAG 18

RESULT 95  
US-08-887-505-149  
Sequence 149, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 149:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-149

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
|||||  
Db 7 GGGGUCUCGAG 18

RESULT 96  
US-08-887-505-150  
Sequence 150, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-5000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES

US-08-887-505-150

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
|||||  
Db 7 GGGGUCUCGAG 18

RESULT 97

US-08-887-505-151  
Sequence 151, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 151:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-151

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
|||||  
Db 13 GGGGUCUCGAG 24



RESULT 98  
US-08-887-505-152  
Sequence 152, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 152:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-152

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
Db 7 GGGGUCUCGAG 18

RESULT 99  
US-08-887-505-153  
Sequence 153, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 153:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-153

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
Db 13 GGGGUCUCGAG 24

RESULT 100  
US-08-887-505-154  
Sequence 154, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 154:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-154

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 GGGGUCGAG 12  
Db 7 GGGGUCGAG 18

RESULT 101  
US-08-887-505-155  
Sequence 155, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 155:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-155

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 GGGGUCGAG 12  
Db 13 GGGGUCGAG 24

RESULT 102  
US-08-887-505-156  
Sequence 156, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 156:  
SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-156

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUCGAG 12  
DB 7 GGGGUCUCGAG 18

## RESULT 103

US-08-887-505-157  
Sequence 157, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckle, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 157:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-157

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUCGAG 12  
DB 7 GGGGUCUCGAG 18

## RESULT 104

US-08-887-505-158  
Sequence 158, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckle, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-158

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUCGAG 12  
DB 7 GGGGUCUCGAG 18

RESULT 105  
US-10-098-263B-87040/C  
Sequence 87040, Application US/10098263B  
Publication No. US20030104410A1

```
;; GENERAL INFORMATION:
;; APPLICANT: Miltman, Michael
;; TITLE OF INVENTION: Human Microarray
;; FILE REFERENCE: 3118.1
;; CURRENT APPLICATION NUMBER: US/10/098,263B
;; PRIOR FILING DATE: 2003-01-08
;; PRIOR APPLICATION NUMBER: 60/276,759
;; PRIOR FILING DATE: 2001-03-16
;; NUMBER OF SEQ ID NOS: 131066
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 87040
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-10-098-263B-87040

Query Match      66.7%; Score 12; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGGAG 12
Db 24 GGGGTCCTGGAG 13

RESULT 106
US-10-291-230-39/c
;; Sequence 39, Application US/10291230
;; Publication No. US20030108939A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruffner, Duane E.
;; APPLICANT: Pierce, Michael L.
;; APPLICANT: Chen, Zhidong
;; TITLE OF INVENTION: Directed Antisense Libraries
;; FILE REFERENCE: T6678.US.A
;; CURRENT APPLICATION NUMBER: US/10/291,230
;; CURRENT FILING DATE: 2002-11-07
;; PRIOR APPLICATION NUMBER: US 09/647,344
;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: PCT/US99/06742
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/079,792
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/107,504
;; PRIOR FILING DATE: 1998-11-06
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 39
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: 14 bp variable sequence fragment of a deletion library including
;; OTHER INFORMATION: flanking portions of multiple cloning site.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (6)..(19)
;; OTHER INFORMATION: The "n" in the sequence means a or g or c or t/u.
US-10-291-230-39

Query Match      66.7%; Score 12; DB 15; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18
Db 25 CTGGAGNNNNNN 14

RESULT 107
US-10-291-230-47/c
;; Sequence 47, Application US/10291230
;; Publication No. US20030108939A1
```

```
;; GENERAL INFORMATION:
;; APPLICANT: Ruffner, Duane E.
;; APPLICANT: Pierce, Michael L.
;; APPLICANT: Chen, Zhidong
;; TITLE OF INVENTION: Directed Antisense Libraries
;; FILE REFERENCE: T6678.US.A
;; CURRENT APPLICATION NUMBER: US/10/291,230
;; CURRENT FILING DATE: 2002-11-07
;; PRIOR APPLICATION NUMBER: US 09/647,344
;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: PCT/US99/06742
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/079,792
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/107,504
;; PRIOR FILING DATE: 1998-11-06
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 47
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Sequence flanking the chloramphenicol (CAT) gene after insertion
;; OTHER INFORMATION: into the antisense library.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (14)..(19)
;; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
US-10-291-230-47
```

```
Query Match      66.7%; Score 12; DB 15; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 7 CUGAGNNNNNN 18
Db 25 CTGGAGNNNNNN 14

RESULT 108
US-10-291-249-39/c
;; Sequence 39, Application US/10291249
;; Publication No. US20030119041A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruffner, Duane E.
;; APPLICANT: Pierce, Michael L.
;; APPLICANT: Chen, Zhidong
;; TITLE OF INVENTION: Directed Antisense Libraries
;; FILE REFERENCE: T6678.US.B
;; CURRENT APPLICATION NUMBER: US/10/291,249
;; CURRENT FILING DATE: 2002-11-07
;; PRIOR APPLICATION NUMBER: US 09/647,344
;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: PCT/US99/06742
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/079,792
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/107,504
;; PRIOR FILING DATE: 1998-11-06
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 39
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: 14 bp variable sequence fragment of a deletion library including
;; OTHER INFORMATION: flanking portions of multiple cloning site.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (6)..(19)
;; OTHER INFORMATION: The "n" in the sequence means a or g or c or t/u.
```

US-10-291-249-39

Query Match 66.7%; Score 12; DB 15; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
DB 25 CTGAGNNNNNN 14

RESULT 109

US-10-291-249-47/c  
; Sequence 47, Application US/10291249  
; Publication No. US20030115041A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruffner, Duane E.  
; APPLICANT: Pierce, Michael L.  
; APPLICANT: Chen, Zhidong  
; TITLE OF INVENTION: Directed Antisense Libraries  
; FILE REFERENCE: 16678, US.B  
; CURRENT APPLICATION NUMBER: US/10/291,249  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 09/647,344  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/US99/06742  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/079,792  
; PRIOR FILING DATE: 1998-03-28  
; PRIOR APPLICATION NUMBER: US 60/107,504  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 47  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence flanking the chloramphenicol (CAT) gene after insertion  
; NAME/KEY: misc feature  
; LOCATION: (14)-(19)  
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
US-10-291-249-47

Query Match 66.7%; Score 12; DB 15; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
DB 25 CTGAGNNNNNN 14

RESULT 110

US-10-719-900-205441/c  
; Sequence 205441, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 205441  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus

US-10-719-900-205441

Query Match 66.7%; Score 12; DB 19; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAG 12  
|:|:|:|:|:|  
DB 22 GGGGTCTCGAG 11

RESULT 111

US-10-053-883-12  
; Sequence 12, Application US/10053883  
; Publication No. US20030113737A1  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Morten Lorentz  
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
; FILE REFERENCE: PEDERSEN-1A  
; CURRENT APPLICATION NUMBER: US/10/053,883  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: PA 2001 00126  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 60/267,704  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: misc feature  
; LOCATION: (11)-(27)  
; OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-12

Query Match 66.7%; Score 12; DB 15; Length 27;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
DB 5 CTGAGNNNNNN 16

RESULT 112

US-10-053-883-13/c  
; Sequence 13, Application US/10053883  
; Publication No. US20030113737A1  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Morten Lorentz  
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
; FILE REFERENCE: PEDERSEN-1A  
; CURRENT APPLICATION NUMBER: US/10/053,883  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: PA 2001 00126  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 60/267,704  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: misc feature  
; LOCATION: (1)-(17)

```
; OTHER INFORMATION: n is a, c, g or t
US-10-053-883-13

Query Match      66.7%; Score 12; DB 15; Length 27;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7  CUGAGANNNNNN 18
      |||:|||||
Db      23  CTGAGANNNNNN 12

RESULT 113
US-09-935-338-192/c
; Sequence 192, Application US/09935338
; Publication No. US20030073081A1
; GENERAL INFORMATION:
; APPLICANT: MUKAI, Hiroyuki
; APPLICANT: SAGAWA, Hiroaki
; APPLICANT: UEMORI, Takashi
; APPLICANT: YAMAMOTO, Junko
; APPLICANT: TOMONO, Jun
; APPLICANT: KOBAYASHI, Ei-ji
; APPLICANT: ENOKI, Tatsuji
; APPLICANT: TAKEDA, Osamu
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: SATO, Yoshimi
; APPLICANT: MORIYAMA, Mariko
; APPLICANT: SAMURAGI, Haruhisa
; APPLICANT: HIGITA, Michio
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikumoshin
; TITLE OF INVENTION: A method for amplification of nucleic acids
; FILE REFERENCE: MUKAI-1
; CURRENT APPLICATION NUMBER: US/09/935,338
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: JP11-076966
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: JP11-370035
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP2000-251981
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: JP2000-284419
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: JP2000-288750
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP2001-104191
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PCT/JP00/01534
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed oligonucleotide probe to detect a DNA fragment amplifying
; OTHER INFORMATION: portion of HCV.
US-09-935-338-192

Query Match      66.7%; Score 12; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGGGUCUGGAG 12
      |||:|||||
Db      30  GGGGTCCTGAG 19

RESULT 114
US-10-169-371-71
; Sequence 71, Application US/10169371
```

```
; Publication No. US20030175729A1
; GENERAL INFORMATION:
; APPLICANT: VAN EIJK, Michael Josephus Theresia
; APPLICANT: HOGERS, Rene Cornelis Josephus
; APPLICANT: HEIJNEN, Leo
; TITLE OF INVENTION: Method for generating oligonucleotides, in particular for the
; TITLE OF INVENTION: detection of amplified restriction fragments obtained using AFLP
; FILE REFERENCE: VAN EIJK-2
; CURRENT APPLICATION NUMBER: US/10/169,371
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: EPC 99204614.4
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/NL00/00963
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(36)

US-10-169-371-71

Query Match      66.7%; Score 12; DB 16; Length 36;
Best Local Similarity 91.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7  CUGAGANNNNNN 18
      |||:|||||
Db      17  CTGAGANNNNNN 28

RESULT 115
US-10-169-371-79
; Sequence 79, Application US/10169371
; Publication No. US20030175729A1
; GENERAL INFORMATION:
; APPLICANT: VAN EIJK, Michael Josephus Theresia
; APPLICANT: HOGERS, Rene Cornelis Josephus
; APPLICANT: HEIJNEN, Leo
; TITLE OF INVENTION: Method for generating oligonucleotides, in particular for the
; TITLE OF INVENTION: detection of amplified restriction fragments obtained using AFLP
; FILE REFERENCE: VAN EIJK-2
; CURRENT APPLICATION NUMBER: US/10/169,371
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: EPC 99204614.4
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/NL00/00963
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(36)
```

```
; OTHER INFORMATION: n is a, c, g, or t
US-10-169-371-79
Query Match      66.7%; Score 12; DB 16; Length 36;
Best Local Similarity 91.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      7 CUGAGNNNNNN 18
       ||:|||||
Db      17 CTGAGNNNNNN 28

RESULT 116
US-10-291-230-48/c
; Sequence 48, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.A
; CURRENT APPLICATION NUMBER: US/10/791,230
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hammerhead ribozyme library with flanking sequences.
; NAME/KEY: misc feature
; LOCATION: (6)..(12)
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (35)..(40)
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
US-10-291-230-48

Query Match      66.7%; Score 12; DB 15; Length 46;
Best Local Similarity 91.7%; Pred. No. 1e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      7 CUGAGNNNNNN 18
       ||:|||||
Db      46 CTGAGNNNNNN 35

RESULT 117
US-10-291-249-48/c
; Sequence 48, Application US/10291249
; Publication No. US20030119041A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.B
; CURRENT APPLICATION NUMBER: US/10/291,249
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
```

```
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hammerhead ribozyme library with flanking sequences.
; NAME/KEY: misc feature
; LOCATION: (6)..(12)
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (35)..(40)
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
US-10-291-249-48

Query Match      66.7%; Score 12; DB 15; Length 46;
Best Local Similarity 91.7%; Pred. No. 1e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      7 CUGAGNNNNNN 18
       ||:|||||
Db      46 CTGAGNNNNNN 35

RESULT 118
US-10-349-143-2597
; Sequence 2597, Application US/10349143
; Publication No. US2004000584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSRT.020C01
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2597
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-1211-59 : polymorphic base C or T
US-10-349-143-2597

Query Match      66.7%; Score 12; DB 17; Length 47;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 GGGGUCUGAG 12
       ||||:||||
Db      25 GGGGTCTGAG 36
```

RESULT 119  
US-10-156-306-7157  
; Sequence 7157, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn Version 3.0  
; SEQ ID NO 7157  
; LENGTH: 48  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-156-306-7157

Query Match 66.7%; Score 12; DB 15; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
Db 1 GGGGUCUCGAG 12

RESULT 120  
US-10-322-138-6/C  
; Sequence 6, Application US/10322138  
; Publication No. US20030175765A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Christoph  
; APPLICANT: Haberkusen, Gerd  
; APPLICANT: Bartl, Knut  
; APPLICANT: Otum, Henrik  
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS  
; FILE REFERENCE: 4817/OO  
; CURRENT APPLICATION NUMBER: US/10/322,138  
; CURRENT FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: US/09/530,746B  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Version 3.1  
; SEQ ID NO 6  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: HCV  
US-10-322-138-6

Query Match 66.7%; Score 12; DB 16; Length 48;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
Db 31 GGGGUCUCGAG 20

RESULT 121  
US-10-322-138-7/C  
; Sequence 7, Application US/10322138  
; Publication No. US20030175765A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Christoph  
; APPLICANT: Haberkusen, Gerd  
; APPLICANT: Bartl, Knut  
; APPLICANT: Otum, Henrik  
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS

; FILE REFERENCE: 4817/OO  
; CURRENT APPLICATION NUMBER: US/10/322,138  
; CURRENT FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: US/09/530,746B  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Version 3.1  
; SEQ ID NO 7  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-322-138-7

Query Match 66.7%; Score 12; DB 16; Length 48;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
Db 31 GGGGUCUCGAG 20

RESULT 122  
US-10-461-790-141/C  
; Sequence 141, Application US/10461790  
; Publication No. US2004002911A1  
; GENERAL INFORMATION:  
; APPLICANT: Linmen, Jeffery M.  
; APPLICANT: Kolk, Daniel P.  
; APPLICANT: Dockter, Janel M.  
; APPLICANT: German, Damon K.  
; APPLICANT: Yoshimura, Tadashi  
; APPLICANT: Ho-Sing-Loy, Marcy  
; APPLICANT: Stringfellow, Leslie A.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP134-02 UT  
; CURRENT APPLICATION NUMBER: US/10/461,790  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: 60/389,393  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 141  
; LENGTH: 86  
; TYPE: DNA  
; ORGANISM: Hepatitis C Virus  
US-10-461-790-141

Query Match 66.7%; Score 12; DB 17; Length 86;  
Best Local Similarity 83.3%; Pred. No. 8.7e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
Db 32 GGGGUCUCGAG 21

RESULT 123  
US-10-029-386-15052  
; Sequence 15052, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: ABEMTCA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1



SEQ ID NO 15052  
LENGTH: 97  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC024195.2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EST\_HUMAN HIT: AL538246.1, EVALUATE 1.80e+00  
US-10-029-386-15052

Query Match 66.7%; Score 12; DB 16; Length 97;  
Best Local Similarity 83.3%; Pred. No. 8.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 78 GGGGTCTGGAG 89

RESULT 124  
US-10-029-386-14059/c  
Sequence 14059, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AECOMICA-X-2  
CURRENT FILING DATE: 2001-12-20  
CURRENT APPLICATION NUMBER: US/10/029,386  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 14059

LENGTH: 124  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL136366.3  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6  
OTHER INFORMATION: NT HIT: g115303560, EVALUATE 1.60e+00  
OTHER INFORMATION: EST\_HUMAN HIT: W90458.1, EVALUATE 1.50e-01  
OTHER INFORMATION: SWISSPROT HIT: O15529, EVALUATE 2.30e-01  
US-10-029-386-14059

Query Match 66.7%; Score 12; DB 16; Length 124;  
Best Local Similarity 83.3%; Pred. No. 7.9e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 34 GGGGTCTGGAG 23

RESULT 125  
US-10-029-386-15594  
Sequence 15594, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AECOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 15594  
LENGTH: 138  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR19.1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.83  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.6  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6  
OTHER INFORMATION: SWISSPROT HIT: Q9ZSR8, EVALUATE 5.20e-01  
OTHER INFORMATION: NT HIT: g14786907, EVALUATE 3.00e-67  
OTHER INFORMATION: EST\_HUMAN HIT: BG479422.1, EVALUATE 4.00e-67  
US-10-029-386-15594

Query Match 66.7%; Score 12; DB 16; Length 138;  
Best Local Similarity 83.3%; Pred. No. 7.7e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 113 GGGGTCTGGAG 124

RESULT 126  
US-10-425-115-1205  
Sequence 1205, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovallik, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 1205  
LENGTH: 168  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_101098C.1  
US-10-425-115-1205

Query Match 66.7%; Score 12; DB 18; Length 168;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 133 GGGGTCTGGAG 144

RESULT 127  
US-10-424-599-11511  
Sequence 11511, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovallik, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 115511  
LENGTH: 175  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_75317C.1  
US-10-424-599-115511

Query Match 66.7%; Score 12; DB 17; Length 175;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 140 GGGGTCCTGGAG 151

RESULT 128  
US-09-294-121A-61/c  
Sequence 61, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCY  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:  
CLONE: De82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-61

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 26 GGGGTCCTGGAG 15

RESULT 129  
US-09-294-121A-67/c  
Sequence 67, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCY  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb48  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-67

Query Match 66.7%; Score 12; DB 9; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15

## RESULT 130

US-09-294-121A-68/c  
; Sequence 68, Application US/09294121A  
; Patent No. US20020069422A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,121A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gp16  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-294-121A-68

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15

RESULT 131  
US-09-294-121A-69/c

; Sequence 69, Application US/09294121A  
; Patent No. US20020069422A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,121A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gp569  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-294-121A-69

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15

RESULT 132  
US-09-294-121A-70/c  
; Sequence 70, Application US/09294121A  
; Patent No. US20020069422A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

```

APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESS: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: gp358
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-294-121A-70

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
DB      26 GGGGTCCTGGAG 15

RESULT 133
US-09-294-121A-72/c
Sequence 72, Application US/09294121A
Patent No. US20020069422A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESS: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible

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CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: cam600
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-294-121A-72

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
DB      26 GGGGTCCTGGAG 15

RESULT 134
US-09-294-121A-73/c
Sequence 73, Application US/09294121A
Patent No. US20020069422A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESS: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: cam736
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-294-121A-73

Query Match          66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGCCCGAG 12
        ||||:|||||
Db      26 GGGGTCCTGGAG 15

RESULT 135
US-09-294-121A-74/C
Sequence 74, Application US/09294121A
Patent No. US20020069422A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
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APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: gb809
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-294-121A-74

Query Match          66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGCCCGAG 12
        ||||:|||||
Db      26 GGGGTCCTGGAG 15

RESULT 136
US-09-294-121A-75/C
Sequence 75, Application US/09294121A
Patent No. US20020069422A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: GP487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-75

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
DB 26 GGGGTCTCGAG 15

RESULT 137  
US-09-294-121A-76/c  
Sequence 76, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: GP724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-76

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
DB 26 GGGGTCTCGAG 15

RESULT 138  
US-09-294-121A-77/c  
Sequence 77, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-77

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
DB 26 GGGGCTCTGGAG 15

RESULT 139  
US-09-294-121A-78/c  
Sequence 78, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region

US-09-294-121A-78

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
DB 26 GGGGCTCTGGAG 15

RESULT 140  
US-09-294-121A-79/c  
Sequence 79, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-79

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

Db 26 GGGGTCTCTGGAG 15

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||||:||||:
RESULT 141
US-09-294-121A-80/c
; Sequence 80, Application US/09294121A
; Patent No. US20020069422A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,121A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8000
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be98
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
US-09-294-121A-80

Query Match 66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12
||||:||||:
Db 26 GGGGTCTCTGGAG 15

RESULT 142
US-09-899-082A-61/c
; Sequence 61, Application US/09899082A
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; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8000
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be82 (also referred to as be99)
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-899-082A-61

Query Match 66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12
||||:||||:
Db 26 GGGGTCTCTGGAG 15

RESULT 143
US-09-899-082A-67/c
; Sequence 67, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
```



NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb48  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-899-082A-67

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTGGAG 15

RESULT 144  
US-09-899-082A-68/C  
Sequence 68, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK

COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb116  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-899-082A-68

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTGGAG 15

RESULT 145  
US-09-899-082A-69/C  
Sequence 69, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/899,082A
  FILING DATE: 06-JUL-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/378,900
  FILING DATE: <Unknown>
  APPLICATION NUMBER: 08/256,568
  FILING DATE: 18-JUL-1994
  APPLICATION NUMBER: PCT/EP93/03325
  FILING DATE: 26-NOV-1993
  APPLICATION NUMBER: EP/93/402,129.6
  FILING DATE: 31-AUG-1993
  APPLICATION NUMBER: EP/92/403,222.0
  FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410.004
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 69:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 177 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  IMMEDIATE SOURCE:
  CLONE: gB569
  POSITION IN GENOME:
  MAP POSITION: 5' untranslated region
  SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-899-082A-69

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTCGAG 12
Db      26 GGGGCTCTCGAG 15

RESULT 146
US-09-899-082A-70/c
; Sequence 70, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEYVERSWMYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-JUL-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/378,900
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410.004
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 70:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 177 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  IMMEDIATE SOURCE:
  CLONE: gB358
  POSITION IN GENOME:
  MAP POSITION: 5' untranslated region
  SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-09-899-082A-70

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTCGAG 12
Db      26 GGGGCTCTCGAG 15

RESULT 147
US-09-899-082A-72/c
; Sequence 72, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEYVERSWMYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-JUL-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
```

APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam600  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-899-082A-72

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|:|  
Db 26 GGGGTCTGGAG 15

RESULT 148  
US-09-899-082A-73/c  
Sequence 73, Application US/09899082A  
Patent No. US2002010638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam736  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-899-082A-73

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|:|  
Db 26 GGGGTCTGGAG 15

RESULT 149  
US-09-899-082A-74/c  
Sequence 74, Application US/09899082A  
Patent No. US2002010638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb809  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-899-082A-74

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 150  
US-09-899-082A-75/c  
Sequence 75, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:  
CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 75:  
US-09-899-082A-75

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 151  
US-09-899-082A-76/c  
Sequence 76, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-09-899-082A-76

Query Match 66.7% Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAG 12  
||||:|||||  
26 GGGGTCTGAG 15

## RESULT 152

US-09-899-082A-77/c  
; Sequence 77, Application US/09899082A  
; Patent No. US2002010638A1

## GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA

ZIP: 10016

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>

APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994

APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993

APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993

APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

LIBRARY: b697

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 77:

US-09-899-082A-77

Query Match 66.7% Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAG 12

Db 26 GGGGTCTGAG 15  
||||:|||||

## RESULT 153

US-09-899-082A-78/c  
; Sequence 78, Application US/09899082A  
; Patent No. US2002010638A1

## GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA

ZIP: 10016

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>

APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994

APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993

APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993

APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: b695

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 78:

US-09-899-082A-78

Query Match 66.7% Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAG 12  
||||:|||||  
26 GGGGTCTGAG 15

RESULT 154  
US-09-899-082A-79/c

```
; Sequence 79, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-Jul-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-Nov-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-Aug-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-Nov-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be96
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-899-082A-79

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGUCUUGAG 12
        |||:|||||
DB      26 GGGGTCTGAG 15
```

```
RESULT 155
US-09-899-082A-80/c
; Sequence 80, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
```

```
ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-Jul-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-Nov-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-Aug-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-Nov-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be98
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-899-082A-80

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGUCUUGAG 12
        |||:|||||
DB      26 GGGGTCTGAG 15
```

```
RESULT 156
US-09-899-302-61/c
; Sequence 61, Application US/09899302
; Patent No. US2002016826A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
```

```
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,302
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/378,900
FILING DATE:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
FAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: be82 (also referred to as be99)
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-899-302-61

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
      ||||:|||||
      26 GGGGCTCTGGAG 15

RESULT 157
US-09-899-302-67/c
Sequence 67, Application US/09899302
Patent No. US20020168626A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,302
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/378,900
FILING DATE:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
FAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: gp48
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-899-302-67

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
      ||||:|||||
      26 GGGGCTCTGGAG 15

RESULT 158
US-09-899-302-68/c
Sequence 68, Application US/09899302
Patent No. US20020168626A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,302
```

```

      FILING DATE:
      CLASSIFICATION:
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 09/378,900
      FILING DATE:
      APPLICATION NUMBER: 08/256,568
      FILING DATE: 18-JUL-1994
      APPLICATION NUMBER: PCT/EP93/03325
      FILING DATE: 26-NOV-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: EP/93/402,129.6
      FILING DATE: 31-AUG-1992
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: EP/92/403,222.0
      FILING DATE: 27-NOV-1992
      ATTORNEY/AGENT INFORMATION:
      NAME: CHARLES A. MUSERLIAN
      REGISTRATION NUMBER: 19,683
      REFERENCE/DOCKET NUMBER: 410.004
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 661-8000
      TELEFAX: (212) 661-8002
      INFORMATION FOR SEQ ID NO: 68:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 177 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      IMMEDIATE SOURCE:
      CLONE: gbl16
      POSITION IN GENOME:
      MAP POSITION: 5' untranslated region
US-09-899-302-68

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCUCUGAG 12
Db      26 GGGGTCTCTGAG 15

RESULT 159
US-09-899-302-69/c
; Sequence 69, Application US/09899302
; Patent No. US20020168626A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:

```

```

      APPLICATION NUMBER: 08/256,568
      FILING DATE: 18-JUL-1994
      APPLICATION NUMBER: PCT/EP93/03325
      FILING DATE: 26-NOV-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: EP/93/402,129.6
      FILING DATE: 31-AUG-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: EP/92/403,222.0
      FILING DATE: 27-NOV-1992
      ATTORNEY/AGENT INFORMATION:
      NAME: CHARLES A. MUSERLIAN
      REGISTRATION NUMBER: 19,683
      REFERENCE/DOCKET NUMBER: 410.004
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 661-8000
      TELEFAX: (212) 661-8002
      INFORMATION FOR SEQ ID NO: 69:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 177 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      IMMEDIATE SOURCE:
      CLONE: gp569
      POSITION IN GENOME:
      MAP POSITION: 5' untranslated region
US-09-899-302-69

```

```

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCUCUGAG 12
Db      26 GGGGTCTCTGAG 15

```

```

RESULT 160
US-09-899-302-70/c
; Sequence 70, Application US/09899302
; Patent No. US20020168626A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:

```



APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-70

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 161  
US-09-899-302-72/c  
Sequence 72, Application US/09899302  
Patent No. US20020168626A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam600  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-72

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 162  
US-09-899-302-73/c  
Sequence 73, Application US/09899302  
Patent No. US20020168626A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:

```

;
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: cam36
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
US-09-899-302-73

Query Match          66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCUGAG 12
Db      26 GGGGTCCTGGAG 15

RESULT 163
US-09-899-302-74/c
; Sequence 74, Application US/09899302
; Patent No. US20020168626A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs

```

```

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: gb809
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
US-09-899-302-74

Query Match          66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCUGAG 12
Db      26 GGGGTCCTGGAG 15

RESULT 164
US-09-899-302-75/c
; Sequence 75, Application US/09899302
; Patent No. US20020168626A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:

```

CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-75

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
||||:||||  
Db 26 GGGGTCTGGAG 15

RESULT 165  
US-09-899-302-76/c  
Sequence 76, Application US/09899302  
Patent No. US2002016826A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN,  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899.302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378.900  
FILING DATE:  
APPLICATION NUMBER: 08/256.568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402.129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403.222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-76

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
||||:||||  
Db 26 GGGGTCTGGAG 15

RESULT 166  
US-09-899-302-77/c  
Sequence 77, Application US/09899302  
Patent No. US2002016826A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN,  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899.302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378.900  
FILING DATE:  
APPLICATION NUMBER: 08/256.568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402.129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403.222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-77

OY 1 GGGGUCGAG 12

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 26 GGGGTCTCGAG 15

RESULT 167  
US-09-899-302-78/c  
; Sequence 78, Application US/09899302  
; Patent No. US20020168626A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,302  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: be95  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
US-09-899-302-78

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 168

US-09-899-302-79/c  
; Sequence 79, Application US/09899302  
; Patent No. US20020168626A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,302  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: be96  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
US-09-899-302-79

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 169  
US-09-899-302-80/c  
; Sequence 80, Application US/09899302  
; Patent No. US20020168626A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129,6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222,0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-80  
Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGGAG 15  
RESULT 170  
US-09-899-044-61/c  
Sequence 61, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129,6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222,0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 61:  
US-09-899-044-61  
Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGGAG 15  
RESULT 171  
US-09-899-044-67/c  
Sequence 67, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/899,044
  FILING DATE: 06-Jul-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/378,900
  FILING DATE: <Unknown>
  APPLICATION NUMBER: PCT/EP93/03325
  FILING DATE: 26-NOV-1993
  APPLICATION NUMBER: EP/93/402,129.6
  FILING DATE: 31-AUG-1993
  APPLICATION NUMBER: EP/92/403,222.0
  FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 67:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 177 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
  CLONE: 9b48
POSITION IN GENOME:
  MAP POSITION: 5' untranslated region
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-899-044-67

Query Match      66.7%; Score 12; DB 10; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
        |||:|||||
Db      26 GGGGTCTCTGAG 15

RESULT 172
US-09-899-044-68/c
; Sequence 68, Application US/09899044
; Publication No. US20030036053A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWM, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
COMPUTER READABLE FORM:
  MEDIUM TYPE: floppy disk
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/899,044
  FILING DATE: 06-Jul-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 09/378,900
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 68:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 177 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
  CLONE: 9b16
POSITION IN GENOME:
  MAP POSITION: 5' untranslated region
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-899-044-68

Query Match      66.7%; Score 12; DB 10; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
        |||:|||||
Db      26 GGGGTCTCTGAG 15

RESULT 173
US-09-899-044-69/c
; Sequence 69, Application US/09899044
; Publication No. US20030036053A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWM, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
COMPUTER READABLE FORM:
  MEDIUM TYPE: floppy disk
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/899,044
  FILING DATE: 06-Jul-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/378,900
  FILING DATE: <Unknown>
  APPLICATION NUMBER: PCT/EP93/03325
  FILING DATE: 26-NOV-1993
  APPLICATION NUMBER: EP/93/402,129.6
  FILING DATE: 31-AUG-1993
  APPLICATION NUMBER: EP/92/403,222.0
  FILING DATE: 27-NOV-1992
```

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: gb569  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-899-044-69

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGCGAG 12  
|||:|:|:|  
Db 26 GGGGTCTCGAG 15

RESULT 174  
US-09-899-044-70/c  
Sequence 70, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: gb358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-09-899-044-70

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGCGAG 12  
|||:|:|:|  
Db 26 GGGGTCTCGAG 15

RESULT 175  
US-09-899-044-72/c  
Sequence 72, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: cam600

POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-899-044-72

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 176  
US-09-899-044-73/c  
; Sequence 73, Application US/09899044  
; Publication No. US20030036053A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: cam736  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-899-044-73

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 177  
US-09-899-044-74/c  
; Sequence 74, Application US/09899044  
; Publication No. US20030036053A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 74:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gb809  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-899-044-74

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 178  
US-09-899-044-75/c



Sequence 75, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 75:  
US-09-899-044-75  
Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGTCTGAG 15  
RESULT 179  
US-09-899-044-76/c  
Sequence 76, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-09-899-044-76  
Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGTCTGAG 15  
RESULT 180  
US-09-899-044-77/c  
Sequence 77, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-09-899-044-77  
Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGAG 15  
RESULT 181  
US-09-899-044-78/c  
Sequence 78, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVESWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 78:  
US-09-899-044-78  
Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGAG 15  
RESULT 182  
US-09-899-044-79/c  
Sequence 79, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVESWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
US-09-899-044-79

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTGTGAG 15

RESULT 183  
US-09-899-044-80/C  
Sequence 80, Application US/09899044  
Publication No. US20030036053a1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 80:  
US-09-899-044-80

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTGTGAG 15

RESULT 184  
US-10-822-711-61/C  
Sequence 61, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-APR-2004  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-JUL-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 61  
US-10-822-711-61

Query Match  
Best Local Similarity 66.7%; Score 12; DB 18; Length 177;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 26 GGGGTCCTGGAG 15

RESULT 185  
US-10-822-711-67/c  
Sequence 67, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:

CLONE: gb48  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 67  
US-10-822-711-67

Query Match  
Best Local Similarity 66.7%; Score 12; DB 18; Length 177;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 26 GGGGTCCTGGAG 15

RESULT 186  
US-10-822-711-68/c  
Sequence 68, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/922,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb116  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 68;

US-10-822-711-68

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|:|:|:  
Db 26 GGGGCTCGAG 15

RESULT 187

US-10-822-711-69/c

; Sequence 69, Application US/10822711

; Publication No. US20040191768A1

; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGOTITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN &amp; MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/822,711

FILING DATE: 13-Apr-2004

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/899,082A

FILING DATE: 06-Jul-2001

APPLICATION NUMBER: US/09/378,900

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: 08/256,568

FILING DATE: 18-Jul-1994

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-Nov-1993

APPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 31-Aug-1993

APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-Nov-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: gb569

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 69:

US-10-822-711-69

Query Match 66.7%; Score 12; DB 18; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

|||:|:|:|:

Db 26 GGGGCTCGAG 15

RESULT 188

US-10-822-711-70/c

; Sequence 70, Application US/10822711

; Publication No. US20040191768A1

; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGOTITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN &amp; MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/822,711

FILING DATE: 13-Apr-2004

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/899,082A

FILING DATE: 06-Jul-2001

APPLICATION NUMBER: US/09/378,900

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: 08/256,568

FILING DATE: 18-Jul-1994

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-Nov-1993

APPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 31-Aug-1993

APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-Nov-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: gb358

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 70:

US-10-822-711-70

Query Match 66.7%; Score 12; DB 18; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

|||:|:~|:|:|:

Db 26 GGGGCTCGAG 15

Db 26 GGGGTCCTCGAG 15

## RESULT 189

US-10-822-711-72/c  
; Sequence 72, Application US/10822711  
; Publication No. US20040191768A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/822,711  
; FILING DATE: 13-Apr-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,082A  
; FILING DATE: 06-Jul-2001  
; APPLICATION NUMBER: US/09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-Jul-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-Nov-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-Aug-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-Nov-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: cam600  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-10-822-711-72

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTCGAG 12

Db 26 GGGGTCCTCGAG 15

RESULT 190

US-10-822-711-73/c  
; Sequence 73, Application US/10822711  
; Publication No. US20040191768A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/822,711  
; FILING DATE: 13-Apr-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,082A  
; FILING DATE: 06-Jul-2001  
; APPLICATION NUMBER: US/09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-Jul-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-Nov-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-Aug-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-Nov-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: cam736  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-10-822-711-73

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTCGAG 12

Db 26 GGGGTCCTCGAG 15

RESULT 191

US-10-822-711-74/c  
; Sequence 74, Application US/10822711  
; Publication No. US20040191768A1  
; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb809  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-10-822-711-74  
Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCCTGGAG 15  
RESULT 192  
US-10-822-711-75/c  
Sequence 75, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 75:  
US-10-822-711-75  
Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCCTGGAG 15  
RESULT 193  
US-10-822-711-76/c  
Sequence 76, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE

CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gbt24  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-10-822-711-76  
Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGCTCTGGAG 15  
RESULT 194  
US-10-822-711-77/c  
; Sequence 77, Application US/10822711  
; Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-10-822-711-77  
Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGCTCTGGAG 15  
RESULT 195  
US-10-822-711-78/c  
; Sequence 78, Application US/10822711  
; Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 78:  
US-10-822-711-78

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGANG 12  
|||:|:|:|  
Db 26 GGGGTCTCTGAG 15

RESULT 196  
US-10-822-711-79/c  
Sequence 79, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
US-10-822-711-79

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGANG 12  
|||:|:|:|  
Db 26 GGGGTCTCTGAG 15

RESULT 197  
US-10-822-711-80/c  
Sequence 80, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001

APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-10-822-711-80

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 198  
US-09-294-121A-59/c  
Sequence 59, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: bu74  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-59

Query Match 66.7%; Score 12; DB 9; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 199  
US-09-294-121A-71/c  
Sequence 71, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb549  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-71

Query Match 66.7%; Score 12; DB 9; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGCGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 200  
US-09-899-082A-59/c  
Sequence 59, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: bu74  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-899-082A-59

Query Match 66.7%; Score 12; DB 9; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGCGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

Search completed: April 25, 2005, 16:27:33  
Job time : 264.474 secs

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